SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
15584	45952	A	15674	1	1640	MSCDTNGEVEGGRVDSKTRGR
						QEVERNTETHLGSGLNCDIPLIF
	1	ļ				LTYEWRGILEYKIFSVKTGEVL
						GKPGQLGHPTGQTTFFETGTQV
	1					TSMQEMGSYSFGQPHPVALQG
	ļ.					TAPLPAAFTGWRLASVAFPGTQ
	ŀ				i	CKLSVDLPIWGLEDSGPLLTAP
	i	l				LGSAPVGPLCGGSDPTFPFCTA
		1				LTGPSAASLLEFARGPLQTLFA
						WVSAEVSAEQGFFVNHECCCLI
	1					VPLEVLSQRSTRPCEVSVCPYW
						GVPPRDRSNQCPSGFTLDSVGP
	I	1				FCADEDECAAGNPCSHSCHNA
		ŀ				MGTYYCSCPKGLTIAADGRTC
	1			l		QDIDECALGRHTCHAGQDCDN
						TIGSYRCVVRCGSGFRRTSDGL
		l				SCQDINECQESSPCHQRCFNAIG
		1				SFHCGCEPGYQLKGRKCMDVN
	i i					ECRONVCRPDQHCKNTRGGYK
	1	1	l			CIDLCPNGMTKAENGTCIGECL
		l				AVSVTEIS/CAVNKSNIDECKDG
		1		ŀ		THQCRYNQICENTRGSYRCVCP
	1	l				RGYRSQGVGRPCMDIDECENT
		1				DACQHECKNTFGSYQCICPPGY
		1				QLTHNGKTCQGKLPFKQIESGG
15585	45953	Α	15675	1	669	MGFCHDGRSIAFRGERGNDESA
		1				IEMIKVSHLKQYLAVVFRDKPL
			1			ELWDVRTCTLLREMSKNFPTIT
		1	ļ			ALILTGRCASLKWRSKPKKEEF
		l				MGYRQWNPTQESSKGDFEIQL
	i	1				EGGPSMATVYRTEMQPVQIGIE
		1				LLPSPLSFHPSPNSGIPNDPSWL
				l		LSTATLHPPTGVERSSSPATEQR
		1				WTENDFDELREEGFRRSNYSEL
				ļ		REDTQTKGKEVENFEK\NLEECI
15586	45954	A	15676	1	323	MAHESAEDLFHFNVGGWHFSV
1		1	l	I		PRSKLSQFPDSLLWKEASALTS\
		1	1	1		SESQRLFIDRDGSTFRHVHYYL
						YTSKLSFSSCAELNLLYEQALG
						LQLMPLLQVRCSCFLGVVDQ
15587	45955	В	15677	1	1443	

SEO ID	SEO ID NO:	Met	SEO ID NO.	Nucleotide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codun, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
15588	45956	Α	15678	1	708	EVTASPOGVSAVSKGDOKWI
				1		ALGKGLTFIKAVGSIORNRWRG
						WOLKALYOCTTIAGATGVFLR
						VYRALDVLOMEEEDVLKFLAA
						GIHLGGTNLDFQMKQYIYKKK
		l				CDGVYIINLKRTWEKLLLAACA
						IVAIENPADVRVISSRNTGORAI
		1				LKFAAATGATPIAGRFTPGIFTN
		1		1		OIOATFOEPOHLFFTDSRADH/S
		l				PLTEASYVNLHTIAPRNTDSPLC
		l				YVDIAIPCKKGAHSVGL
15589	45957	Ā	15679	78	757	REIFINVRSLLMACFVKEEDVL
1						KFLAAGTHLGGTNLDFQMEQY
			-			IYKRKSDGIYIINLKRTWEKLLL
						AARAIVAIENPADVSVISSRNTG
				1		QRAVLKFAAATGATPIAGRFTP
				Į.		GTFTNQIQAAFRE\PRLLVVTDP
	-	1				RADHQPLTEASYVNLPTIALCN
						TDSPLRYVDIAIPCNNKGAHSV
						GLMWWMLAREVLRMRGTISR
						EHPWEVMPDLYFYRDPEEIEKE
		ĺ				EQAAAEE
15590	45958	В	15680	1	1767	
15591	45959	Α	15681	98	412	
15592	45960	A	15682	521	600	PSPGES/PPLQPDPPVPPWPPPEE EPRA
15593	45961	Α	15683	117	285	
15594	45962	С	15684	12	468	
15595	45963	В	15685	1	840	
15596	45964	Λ	15686	1	1173	
15597	45965	Α	15687	1	2931	MDLFMNVAMLRAARYLWSEA
	ļ	1				VSGFGAQDPKSLALRTHCQTSG
						WSLTEQDPYNNVIRTTIEALAA
		1		1		TLGGTQSLHTNVFDEALGLPTD
						FSARIARNTQIIIQEESELCRTVD
						PLAGSYYIESLTDQIVKQARAII
						QQIDEAGGMAKAIEAGLPKRMI
						EEASAREQSLIDQGKRVIVGVN
				1		KYKLDHEDETDVLEIDNVMVR
				1		NEQIASLERIRATRODAASDTR
		ŀ		•		EIVDLTNGNIKTFNGSIIIYARFD TGRHLFSGGNT
15500	45066	С	15688	11	1779	TGRHLFSGGNT
15598	45966 45967	В	15688	22	1531	<del> </del>
15600	45968	A	15690	98	412	
15601	45969	Ā	15691	521	600	PSPGES/PPLQPDPPVPPWPPPEE
						EPRA EPRA
15602	45970	С	15692	175	454	
15603	45971	Α	15693	332	494	RKEMASGFSKGPTLGCC\RRAL
l	l	1				PDGDTQLQLLLRGNHDSVLGA
		Ь.	L		L	KRRDKGEAGPD

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first		
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
15604	45972	A	15694	2	1276	HTLHSLVTILGTWALHSGPALL
						LPRPGSGLDFLLSPVLPSPOPPG
		1				LPTPTPFTNAVOLLLTLKLVSLA
						SEVQDLHLAQRKEMASGFSKG
						PTLGLL/RRRALPDGDTQLQLLL
		1			1	RGNHDRPVLPLPHLPGLAGAAL
	l .	1				PRGSA\SLRPLLRRAWPAPLFGL
						LFLLSSHLFPLEAVREDAFYARP
		1				LPARLFYMIPVFFAFRMRFYVA
						WIAAECGCIAAGFGAYPVAAK
ľ	1					ARA\GGGPTLOCPPPSSPEKAAS
						LEYDYETIRNIDCYSTDFCVRV
ŀ			i			RDGMRYWNMTVQWWLAQYI
	i .					YKSAPARSYVLRTAWTMLLSA
	į.					YWHGLHPGYYLSFLTIPLCLAA
						EGRLESALRGRLSPGGQKAWD
	i		i			WVHWFLKMRAYDYMCMGFV
	i		İ			LLSLADTLRYWASIYFCIHFLAL
						AALGLGLALGGGSPSRRKAAS
		1				QPTSLAPEKLREE
15605	45973	Α	15695	134	601	RDGEQPLWAWGSPCSPVAPTL
	1					CILWAPSSGPGPSFRPSPAPATP
l			l			WLWPGLSPISCDSEPSASWACP
l						LPCPSPKPDRWLLTLKLVSLAS
1		ŀ				EVQDLHLAQRKEMASGFSKGP
1						TLGLL/RRRALPDGDTQLQLLL
	1					RGNHDSVLGAKRRDKGGQTTII
						FVQV
15606	45974	В	15696	76	504	
15607	45975	Α	15697	13	706	HITRGRSCTRWTSSAMAKGAPR
1						VILLCLFGAALCLTGSRALQCY
	1					SFEHTYFGPFDLRAMKLPSISCP
						HERFEAILSLDTGYRAPVTLAR
						KGCWTGPPAGQDAIEPGRAAA
						RLLG\VRGCTTDKCNAHLMTH
l	1	1		i		DALPNLSQAPDPPTLSGAECYA
		1		l		CIGVHQDDCAIGRSRRVQCHQD
	1	l				QTACFQGNGRMTVGKGLEGW
		1		l		KGLGKGYGGRAAMRVVIPDRP
l	1	ı	i	l		NRETWPCSEVGGMTLV

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
15608	45976	IA	15698	2	1642	DEGRAKGHHTWOOTRENESOA
13008	43970	^	13096	1	1042	KGETPYKTIRFRETYYHKNSMO
						ETTPMIQLSPTGSLPQHVGIMG
						ATIODKIWVRTGLPGFPGTPGL
						PVSSGFPGSPGFPGLQGPPVSYG
		1				PTGIPGPIGPPGPPGLMVSSGPP
						GLPGPKVILGLNFQGPKGEKVS
						KGLQGPPGPPGQISEQKRPIDVE
		1			•	FOKGDOVSNGDRGPPGPPGIRG
			}			PPVSTGGEKGEKGEOGEPGKR
		ļ.				
		ļ	1			VSEGKDGENGQPGIPVSSGDPG YPGEPGRDG/EKGKNVMGPPGP
1		1	1			PGFPGERGOKGDEGPPGISIPGP
į.		ŀ				
			1			PGLDGQPGAPGLPGPPGPAGPH
			1		-	IPPSKLGDTCFNCIGTGISGPPGQ PGLPGLPGPPGKL\GAPGAPGFP
			İ			GSKGEPGDILTFPGMKGDKGEL
					ŀ	GSPGAPGLPGLPGTPGQDGLPG
						LPGPKGEPVSCTFKGERGPPGN PGLPGLPGNIGPMGPPGFGPPGP
	ĺ					
	l					VGEKGIQGVAGNPGQPGIPGKF
			1			GDPGQTITQPGKPGLPGNPGRD
				İ		GDVGLPGM*GLPGQPGLPGIPG SKGEPGIPGIGLPGPPGPKGMLL
15609	45977	A	15699	246	433	GLFPLEPGANGI*GC/SGRIRAO
1300)	43311	1	13077	1-70	1-33	RWLPGRPKFTGESFIR*PPRVAK
	Ì	1		l		ESGQLIWFGCVPTQISS
15610	45978	A	15700	179	5262	RSCGSRRRMKLRGVSLAAGLFL
13010	43576	,,	13700	l'''	3202	LALSLWGQPAEAAACYGCSPG
				į .		SKCDCSGIKGEKGERGFPGLEG
i						HPGLPGFPGPEGPPGPRGQKGD
		1			i	DGIPGPPGPKGIRGPPGLPGFPG
		1				TPGLPGMPGHDGAPGPOGIPGC
						NGTKGERGFPGSPGFPGLQGPP
					· ·	GPPGIPGMKGEPGSIIMSSLPGP
			l			KGNPGYPGPPGIQGLPGPTGIPG
			ŀ			PIGPPGPPGLMGPPGPPGLPGPK
						GNMGLNFQGPKGEKGEQGLQG
						PPGPPGQISEQ
15611	45979	A	15701	155	623	FNYLPPGPSHN/DVGIMGATIOD
15011			10,100			KIWGPPGLPGFPGTPGLPGERG
1				ļ		FPGSPGFPGLQGPPGLPGPTGIP
1		1	1			GPIGPPGPPGLMGPPGPPGLPGP
	1	1	1			KGNMGLNFQGPKGEKGEQGLQ
	1	1	1	1		GPPGPPGQISEQKRPIDVEFQKG
1		I	1			DQVSNGDRGPPGPPGIRGPPVS
15612	45980	A	15702	581	687	KKGAGQVV/DDVQLAQRLAQA
13012	1.5560	ľ.	13,02	I		NEIVLSWNCWMLCKQY
15613	45981	A	15703	7	123	
.5015	.5501	۲.	1.5,05	<u> </u>		

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nuclcotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
15614	45982	A	15704		374	RFRKAQCTIVERLTNSMMMHG RNNGKKLMTVRIVKHAFEIIHL LTGENPLQVLVNAIIN/DVSPLR RVNHAIWLLCTGAREAAFRNIK TIAECLADELINAAKGSSNSYAI KNKDELERVAKSNR
15615	45983	A	15705	2	892	QAFLEITPDOLSNYKVFAKKTA LWONDDVHSQHKGEVRNAAG EFKYRNSVTTHSEGKWQSEKG KDLGVGYWSMACYKLGHIAG NEQQKHICGGIAKKWKQPKCP PTGKWPAVVKFATESEGGGAK KEEKAHLPRVVEKELHESSRII RHSIESVLLQAFTQKDYTAVKE KYAKYLPIISAERYAAKFEKA QCPIVECLTYSMMTHGRNNRK KLMIMRIVKHAFEIIQLLTGDNP LQVLVNAINSGPREDSTLTGRA RIVRRQAVAVSPLSKVNQAIWP QCTGALEMAFRINKTIA
15616	45984	Α	15706	1	536	
15617	45985	Α	15707	8	437	
15618	45986	В	15708	255	1058	
15619	45987	A	15709	609	1489	LPLSLPRAARPAVAPHLPPREPGPALPLPPPGPPPSLPGSAGO NS*RTGTAAAGAGPFAPASMSL RVQTPCWPQRGAREPPGSCAS WLFCAVWQMYRAHSGCPLAPP PAAAAWVAAQLQP*DGHEGPG G*ET/S*VLRLRPTPTPPLPTWCC TVRPRRPVLPFCLIMRRRTAGPP CAPIAAAPTTPSSLRRGKVPTGR PPUL*G*PAVMLTMAVTITRTV TTSCNAAAVMPKTGTAHRAP LTPGTV*RDLCLVKPTAQMPPS APPWTAPPRAVAPVIVLPAIS NGAFA
15620	45988	Α	15710	173	530	GRERGDKGGAVQTLQDLVNV HLGLTYPPRPCGHSPPSWASPQ APLQPPLRGEPGHGWGS/PSGL GQGKSEGLGPAHLPRAARPAV APHLPPREPGPALPLPPPQPPRPP SLPGSAQGCNS
15621	45989	Α	15711	1	227	
15622	45990	A	15712	238	498	
15623	45991	В	15713	1	1017	
15624	45992	В	15714	590	649	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540.217	codon for peptide sequence	of peptide sequence	deletion, \*possible nucleotide insertion)
15625	45993	Λ	15715	3	843	AVFLSTSNEAVYKIFDDSPCPFT
				l		AKTCNPETFPSSNESRQCPNAR
		l				COFAFYGGESGYHRALLGLOIF
1		l		1		NAFMFFWLANFVLALGOVTLA
				1		GAFASYYWALRKPDDLPAFPLF
						SAFGRALRYHTGSLAFGALILAI
						VQIIRVILEYLDQRLKAAENKFS
				1		Y\CLMTCLKCCFWCLEKFIKFL
						NRNAYIMIAIYGTNFCTSAR\NA
				1		CFLLMRNIIRVDVLDKITDFLFL
		1		1		*GKLLIVGIVGILAFFFFTHRIRI
				1		VQDTSPPLNYYWVPILTVIVGS
		1		1		YLIAHGFFQRY
15626	45994	Α	15716	I	449	FRGMGDERPHYYGKHGTPQKY
						DPTFKGPIYNRGCTDIICCVFLL
	1					LAIVGYVAVGIIAWTHGDPRKV
						IYPTDSRGEFCGQKGTKNENKP
	1					YLFYFNIVKCASPLVLAGI\QCP
}						TPQICVEKCPDRYLTYLNARSS
	1					RDFEYYKQFCVPGV/PRTIKKA
		ļ				NGVLEAGNSPCAYLKITPSLGT
		ľ				DY/PWFLLEFQCPTPQICVEKCP
1	1					DRYLTYLNARSSRDFEYYKQFC
						VPGVQEQ
15627	45995	A	15717	627	1665	EQAGQALSTAPVGDGHELLCE
l						VGSSSFRDVLGT\$MGLCGGY/G
	1					GAS/GMGGITAVTVNQNVLSPL
				į		NLEVDPNMQGMHTQEKEQVK
						TLNKSASFVDKVLFLEQQNKM
ļ		1		1		LETNWSLLQQQKPAQSNMDN
	ŀ	}				MFESYINNLLGQLEILGQEKLK
		1		İ		LEAELGNMQGLCMFFVKEDFK
		į.				KKYEDEINKPTEMENEFVLIKK
		ĺ				DVDDAYMNKVELEFRLEGLTD
		1				EINFLRQLYEEEIPELQSQILDTS
		1				VVLSMDNSRSLDMDSIIAEIKY
						EELQTLAGKHWDDRRLTKTKIS
		1				EMNRNISRLQAEIEGLPQRPEQ
l	1		1			RASLESVIADAEQRGELAIKDA
l	i .	1	1	1	1	KTKLSELEAAQQRAKQDMAHG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *-Stop codon, /-possible nucleotide delction, \-possible nucleotide insertion)
15628	45996	A	15718	3	3908	STQQKTARSNMDNMFESYINN
13028	43770	^	13710	ľ	3700	LRRHVETLGQEKLKLEAEL\GN
		1				MOGLVEDFKNKYEDEINKRTE
						MENEFVLIKKD\VDEAYINKVE
						LESRLEGLTDEINFLROLYEEEI
						RELOSWISDTSVVLSMDNSRSL
		1				DMNSVIAEVKAQYEEIANRSQA
1		l				EAESMYQIKDEELQSLAGKHG
		l				DNLRCTKT*DLLR*TRNISRLQA
		l				EIEGLKGORAFLEAAIADAEOC
1		l				GELAIKDANAKI/SELEAALOR
		l				AKODMA WOLR\LMN
15629	45997	A	15719	1	804	MKPRTLVVSVTVLKDGVSRVC
1		l				SFRCSDVSRISSFQWVRGLADF
1		l		ŀ		RNEATDPHGLLDDILTLRQDKG
		1				SFMICWLKGKAPPGDPAPPRITP
		1				TVRFSTMDLSAASHRIP\LSDGN
ı	İ	1			1	SIPIIGLGTYSEPKSLWATNHVP
		1			ŀ	EMVRPTLERTLRVLQLDYVDL
		1		1		YIIEVPMAFKPGDEIYPRDENGK
		ļ				WLYHKSNLCATW\EAM\EACK\
		1	ŀ			DAGLVKSLGVSNFNRRQLELIL
		1		ŀ		NKPGLKHKPVSNQVECHPYFT
		1				QPKLLKFCQQHDIVITAYSPLW
						TSTNP
15630	45998	Α	15720	476	906	WKQHSHHQTWYLLTSEACKD
		l			1	AGLVKSLGVSSFNSR\QLELIQN
		l	l	İ		NPGLKPKPVSNEVECHPYYTQP
			İ	İ		KLLKFRQQHDIVMIAYSPLGTT
	ł	1		ľ	1	RNPTWTNMSSLPSLKDALLKR
	1	l	ļ	İ		CNKITAQVILRFNIQQGVVVIPK
		Ļ.				SFNPEKIKENLQA
15631	45999	A	15721	138	217	RHAPQVLGGLSEGT*GGHRCPA
		_	1.5000			RGHW
15632	46000	В	15722	8	578 3087	
15633	46001	A	15723	1	2232	
15634	46002	A	15724	1	2085	
15635	46003	A	15725	1	1512	
15636	46004	A	15726	1	1260	
15637	46005	A B	15728	1	2145	
15639	46006	A	15729	1	1353	
15640	46007	A	15730	1	1741	
15641	46008	A	15731	1	1995	
15642	46010	В	15732	1	3464	
15643	46010	A	15732	2	109	FTFWHDFAAAGTGCSFPCLVLP
						SWW*QNLSAFACL
15644	46012	В	15734	90	1247	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
15645	46013	Α	15735	ı	1698	MELKAKAQELREECRSLRSRC
						NQLEESVSVMEDEMNEMKREG
1						KFREKRIKRNEQSLQEIWDYVK
1				1		RPNLRLTGVHESDGENGTKLEN
						TLQDIIQENFPNLARQANIQIQEI
1			1			QRTPQRYSSRRATPRHIIVRFTK
1						VEMKEKMLRAAREKGWVTHK
						GKPIRLTVDLSAETLQARREWG
						PIFNILKEKNFQPRISYPAKLSFI
						SEGEIKSFTDKQMLTDFVTTRP
				ļ		ALQELLKEALNMERKNRDTHR
						LKIKGWRKIYQANGKQKKAGV
				i		AILVSDKTDFKPTKILKDKEGH
				i		YIIVKGLIQQEELTILNTYAPSTG
						APRFIKQVRSDLQRDLDSHTLII
						GDFNTPLSTLDRSTRQKVNKDT
				ļ		QELNSALHQADLIDIYRTLHPK
1						STEYTFFSAPHHTYSKIDHIVGS
						KALLSKCKRTEIITNYLSDHSAI
		l				KLELRIKKLTQNHSTTWKLNNL
						LLNDYWVHNEMKAEIKMFFET
		l				NENKDTTYQNLWDTFKVVCTG
					İ	KFIALNAHKRKQERSKIDTLTS
				ľ		QLKELEKQEQTHSKASRRQEIT
		l				KIRAELKEIETQKTL/QKINESRS
		_				WFFERINKIDRPL
15646	46014	Α	15736	1043	1536	TSTELSTPNQQNIHFFQHHTTSI
				1		PKLTTYLEVKLSS*KKH*TWKG
Í				ļ		TTGTSCC/INHAKIVTHRLKIKG
						WRKIYQANGKQKKAGVANLV
		1				SDKTDFKPTKIKRDKEGHYIMV
		1				KGSIQQEELTTLNIYAPNTGAPR
		l				FIKQVLSDLQRDLDSHTLIMGD
						FNTPLLTLDRSTRQKVNKDTQE
						LNSALHQADLIDIYRTLHPKSTE
1						YTFFSAPHHIYSKTDHILGSKAL
1						LSKCKRTEIITNYLSDHSAIKLE
	į.					LRIKNLTKNRSTTWKLNNLLLN
				1		DYWVHNEMKAEMKMFFETNE
						NKDTTYQNLWDTFKAMCRGK
l						FIAVNAHKRKQERSKIDTLTSQ LKELEKQEQTHSKASRRQEITKI
15647	46015	A	15737	1208	1387	KPWOKNYVTHAQASVADLIK
13047	40013	^	13/3/	1208	1367	WKKGYQ*LKIK*MK*SKKRSLE
1			1			KKE*KETNKASKKYGTI
15648	46016	A	15738	308	487	KPWHKNYIMHAQASVANLINW
13048	40010	^	13/38	300	1407	KKGYQ*LKIK*VK*SEKRSLEK
1				l		
15649	46017	A	15739	220	1101	KE*KEMNKASKKYGTM
15650	46017	A	15740	1	1534	
	46019	A B		365	3904	
15651	40019	lα	15741	203	3904	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
15652	46020	A	15742	79	506	EPSQRIISQDLQGWSQEHQVCL HRVGWGHCATCILPAATASHE GPEAWTARLLVPQTAVGICSA FSGLPTSTHEPTGMHFLPSEAHE KPRTQPDQKRGRDDLPCTPSTC LHTSLFLDTGQEFGTCRMAGLK EHVAGDNKERRQ
15653	46021	Α	15743	2	71	ELKF**FPILSPSRKTSPLRQGS
15654	46022	A	15744	1	627	MKABIKMFFETNENKDTTYQN LWNTFKAVRRGKFIALNAHKR KQERSKIDTLTSQLKELERQEQ THSQASRRLNQEEVESLNRPIT GSEIEAIINSLPTKKRPGPDGFTA EFYQRYKEELPKYLLKQLQOS LRIPNQCAKITSIPKHQYQTNRE PPHIETTHINCFKONKIRNPITY KGREGPLQGELRTIAQRNKRGH KQMEEHSMLM
15655	46023	A	15746	1	3828	MQLPVOTIAADGYVIKLOKRTI EDGHOSPERICIPPHLSSYSEQE TTRYPFAKAVASGFPGDTTLVF CASPQPSPQVHLPTQAVADIFSE FHEHY ARISTABVTLSKANMM GSEPTARLSNSKYPETLEVGES AQPVPMYTWKTVAODRKDG SPPLLEKQSITKSISNKPVELSSK VVEVDASKADHMKKMASMGL VVEVDASKADHMKKMASMGL VSMAGSGLVLSKSELKEISSL RNGCAIVRSEPISTDSSWVVPR PRTNEENNGE

2008

SEO ID	ISEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1			sequence		
15656	46024	Α	15747	ī	1639	NCLSDHSAIKLELRIKKLTONCS
						TTWKLNNLLLNDYWVHNEMK
						AEIKIFFETNENKDTTYQNLWD
		1				TFKAVCRGKFTALNAHKRKQE
		1				RSKIDTLTSQLKELEKQEQTHS
						KASRRQEITKIRAELKEIETQKT
				l		LQNINESRSLFFEKINKIDRPLA
	İ	i			ļ	RLIKKKREKDQIEAIKNDKGDIT
	i	İ			İ	TDPTEIQTTIREY\YKH\LYANKL
						EY\LEEM\DKF\LDTYTLPRLT\Q
						EEVESLNRPTTGSEIEAIINSLPT
						KK\SPGPDGFTAEFYQRYKEEL
	1		l			VPFLLKLFQSIEKEGILPNSFYE
						ASIILIPKPGRDTTKKENFRPISL
	1					MNIDAKILNKILANRIQQHIKKL
			l			IHIIDQVGFIPGMQGWFNIRKSI
						NVIQHINRAKDKNHMIISIDAG
	J		1			KAFDKIQQSFMLKALNKLDIDG
	ł		1			TAIRQEKEIKGIQLGKEEVKLSL
		1				FADDMIVYLENPIVSAQNLLKLI
	l					SNFSKVSGYKINVQKSQAFLYT
				1		NNRQTESQIMSELPFTIASKRIK
				1		YLGIQLTRDVKDLFKENYKPLL
						KEIKEDINKWKNIPCSWVGRINI
15657	46025	В	15748	1	1563	
15658	46026	Α_	15749	1	4332	

2009

15659 46027 A 15750 1 2319 MRIDGAQELTLALPFASX DVKPGPRRPLRYRCFQ LGSASLGAGFWAGRRD, DDDPSGALFSVTMDRDL DRAENIELIAQORPPRRR* GKTLQEKLYDIYVECG PQELRSNVNLLEKLVRR LLVNLYPGNQGYSVMLC SFAETIKLPYEERALLDY LPPALGDVLDKASVNIFF IVEVRDYRQSSNMQPPG ILLRITMGTLAPFVKTM* KWSQEDKFPLESQLILAT CLDPSVAVACTANRLLY MNTDPMEQCLQRYSWP, QEQSDCPPPELRVSTSG RKVGQPEELNITKAGSC* KGRPCDLAVPSEVDVEK YQSVTAADPQLPVWPAG PFRHAWEAGCOQWDTK SFNDPLLCGKIRPRKARA KSPWOFFPDDISAWLRP	KPSNR
ASFWQFFPDIBAWLEF AGRAVSQAQESVQSKVB MSHSSSG PASVSQLSSWJ PDPVWVQSSVSGKGEKE QLPSSSGKISSGNSFPPQC LKRPFPAAPAVAAAAP PAAPALAAAAVAAAAA SHSQKPSVPLIKASRRPP TRFVKIAPAIQVRTGSTG QRGGPSGPGISGSGLQ LPDARFGSSAGCPAPLCI	EQAL YSPRA KEPED SSLPC QREDG SSLPC QREDG SSLPC QREDG QREDG QREDG QREDG YQSRH RRDGE VYQSRH RRDGE VDTW LAKG GSETDK GGSETDK GGSETDK GGSETDK GGSETDK GAGPAAGRP AAGRP AAGRP ASGPAAGRP SSGGP SSGGP

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
I5660	46028	Α	15751	409	1874	YDSYIVVIDDADITRGDDAVPR
						DHHSSTSMVVFRHIRLDVIVVD
						GDDQHRRMVGRRCRSAWFRR
						GSLDVDQVIGDTAAGRLNVMG
						DITRDARRDKVKNERYGVAPS
		l				VAFGLGTANRLYLNYLHVTQH
						NTPDGGIPTIGLPGYSAPSAGTA
						ALNHSGKVDTHNFYGTDSDYD
ŀ						DSTTDTATMRFEHDINDNTTIR
						NTTRWSR/S/WTWSRTANTKDV
1						SNKILTNQTNLTSTFYTGSIGHD
		l				VSTGVEFTRETQTNYGVNPVTL
ŀ		1				PAVNIYHPDSSIHPGGLTRNGA
		1				NANGQTDTFAIYAFDTLQITRD
		l	ĺ			FELNGGIRLDNYHTEYDSATAC
ĺ						GGSGRGAITCPTGVAKGSPVTT
1						VDTAKSGNLMNWKAGALYHL
ĺ				l		TENGNVYINYAVSQQPPGGNN
			ł			FALAQSGSGNSANRTDFNPQK
						ANTSEIGTKWQVRGSSRVNVM
				1		HEVNTPHQCVRFRPARSAPGCC
		l		1		QSPCHRSGKHMQYGLSKCQPG
						QYNSVKSGERVNGVTFQ
15661	46029	Α	15752	421	441	P*ARMPSPLGPPCLPVMDPETT
	1		l	ļ.		LEEPETARLRFRGFCYQEVAGP
	1	l				REALARLRELCCQWLQPEAHS
	ļ					KEQMLEMLVLEQFLGTLPTEIH
	ì					AWVRGQRPGSPEEAAALIEGLQ
						HDPGQLLG
15662	46030	Α	15753	1	346	PAFGGSAPSERLELHVDGPPPRP
						QAPGD/CGVGRSWRAEM/HDR
						ALRGTNPRRHLRSCCARARRRP
						*RRSAPPGPRAN\PS*SSWGPSTP
						GNYRCRYRSWVPHTFKSELND
						PVELLVA

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
15663	46031	A	15754	1	2091	MKPGLRRRRGRGLGCGLGPQL
						RATWSGAVLAGRDAVLRCEGP
						IPDVTFELLREGETKAVKTVRT
1						PGAGAKLELIFVGPQHAGNYRC
i						RYRSLVAHTFESELSDPVELLV
						AVAATLNIHLRLVHMLHIPAAG
				ļ		EGSFREGTHFLKPSPVKMPLVF
				ŀ		RVGRRRVLNQGPQGVPIPIPRSC
				l		EHLNWQKGLCGVTKCAAPLLR
			İ			GPPCPAVLRKEIPFVSLKPGLMS
				l		SKASEAEPLGPRLGSHQSTAAA
				l		LGPRYNGSADAIRPHTAWAVIQ
				1		TTISRFTWSLTQVNVPSRTVSLA
						VRRDRYMTSRTTTNPEEGCRG
1						TFWARRNGCSPSACAVAEAAL
ļ						EACLADVRYPVVALSCGRLQK
						RRDFRETNAAMSNKEKSLASA
						RFFVEVQVTLGALCTVQATGQ
						SMLVFSTTQMSSYSEKFLTSKH
						ASLSPRLQLADRWRDQGMKW
						QSPQWGELRPAASHTAEQEPGL
				ľ		AASKAFRDLQNLSNSAFLSLTS
						LSAGHQCISAIVVMMSKKEITP
1			1			QGQLAAASFGELQPVALKCPW LKSQHVESWL\RPEAHSKEQML
						EMLVLEQFLGTLPPEIQAWVRG
		١				QRPGSPEEAAALVEGLQHDPG
						QLLGWITAHVLKQEVLPAAQK
						TEEPLGSPHPSGTVESPGEGPQD
						TRIEGSVOLSCSVKEEPNVDGO
			ľ			EVAPSSPPLAAQSPEGNHGHQE
						PASTSFHPPRIQVSSPKWEV
15664	46032	A	15755	1	208	TANDEST THE TRACE OF THE TEXT
15665	46033	A	15756	3	373	EVAQMPRVSTPATLPSLPQPAL
1						MAPWTVPYDQLMEEEKARAR
1		l				YAGTIQKWTAAALQPLSRTSLK
						DSGEGTSKWGRSVDTTQPLSPA
						IPVIFQ*AHEQSGHSGMDGGYA
						WALQHGLALTNTDLA
15666	46034	Α	15757	3	266	
15667	46035	Α	15758	3	587	YPASAGLMLQNFGVIGLRYHF
						AIHSPAAGGLLDGLHAVAAIQG
						ITKIETTPNHQRAPAHWTLLTQ
						QAHLQPSPLHFNLPLTLCLMHC
				l		PTAIPHCFADARTWVNLPTSSLI
				l	1	GHKKENLKEFISGSLIVHEILEE
1				l	1	VLQAEGDFQPFTRVTVHWGKG
1				1		NDQTFRGLLDTGSELTLIPGDP
				l		KHHYGPPVKVG\AYGAQLL
15668	46036	Α	15759	1	1566	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
l				sequence		
		L				
15669	46037	A	15760	I	981	MVAIAKVLIAYKEDSDSHNQPN
i				l		TRMTVSKGPVSAVEGGRRGQD
						SDDCVEENDAVRTWPPSRILRT
1						ESHPSPHTCSWRRHLLSSCPYT
1						GMSFPIPSSGNISSTHAVISFPPL
				l		SEEMNPMLPKATVMTSLEAAA
						RQNLKSRQAPRCEVESVTHEEV
						YYTRKELFEFSNLYRKKSGEQI
		l				REWILRKTDGSWRITVDYRKL
1	l					NQMVTPIAAAVPDV/VVSLLEQ
	ŀ			1		INTSPGTW\LCHNLIWRDLDCFL
				l		LPONITLVHYTDDIMQIGSSEQE
İ		l				VANTLDLLPALMASW/ENSP*SI
	i		ŀ	Ì		DRGRED*SLVHKWFCTICRHHP
	l		i			KVDSCSTTAPF*DIPEGQQL
15670	46038	A	15761	349	718	AGPEGTTTAECP/I/COORPILS
13070	40036	l^	13701	1777	/10	LRYGTISWG/DOSATWWQVDY
			į	}		IRTLLSWKWOSASAKTTIHGLT
						KCLIHHDIPHSIASD*GTCFMAK
						EVWQWYCFSHSQDSRVQESRG
				ł		
14(7)	46000		147/0	140	400	GIGSCTTHHHPCSFPN
15671	46039	Α	15762	143	469	ARIQ/GSRNQGVEVEVAPLTVT
		l	l	1		PSDPLANVLLPVPATLPSAGLEI
						LVPEEGRLPPGDTTMMPLNWN
1		l			i	LRLPHGHFGLLLPLNQQAKKG
		_				VAVLGGVIALDCQDEISLLLYK
15672	46040	Α	15763	I	2712	
15673	46041	A	15764	3	578	LKSRQAPRCEVESVTHEEVYYT
	1					RKELFEFSNLYRKKSGEQIREWI
		1				LRKTDGSWRITVDYRKLNQMV
		l				TPIAAAVPDV/VVSLLEQINTSP
1						GTWLCHNLIWRDLDCFLLPQN
				1		ITLVHYTDDIMQIGSSEQEVAN
		l		l		TLDLLPALMASW/ENSP*SIDRG
		l		1		RED*SLVHKWFCTICRHHPKVD
				1		SCSTTAPF*DIPEGQQL
15674	46042	Α	15765	1	461	MTVDYRKFNOVVTPMAA/AVP
	1			I		DAVSLLEOINTFPGTWYAAIDL
		1		1		ANAFFSIPVHEAHOKQFAF\LPQ
	1	1		1	1	GYINFPALCHNLIRRELDFFLLL
1	1			1	1	QDITLVHYIDDILLIGSSEQEVV
1		1	1	I	1	NTLDLLIHKRSKEAEHTAASRIR
				1		VSCLPEOKSHEOTLPWEQVP
15675	46043	A	15766		1371	VSCLIEGRAMEQTERWEQVE
		_		54	864	
15676	46044	В	15767	124	004	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /-possible nucleotide deletion, \=possible nucleotide insertion)
15677	46045	Α	15768	2	1148	PRGRNRRRKTFQERRMTLNESP
				i		EKIGKWIECYGHPPASKLVEIYI
						HTVFVEDKLSICIRSFNKKADGS
						WRMTVDYCKLNQVVTAIAAAI
					l	P\EWFHCLSKLIHLLIPGMQPLT
ļ.						WQ/HALFSIPVHKGYINSLALC/
						Q*CYLERT*LLFTSTRYHTGPLH
						**HYADWIQCARSRKQTGLTG
						KGQRFVLTERDTY\YGFTYPAH
				ł		NASAKTTIHGCTECLTHPHVIPH
						SIASEQDTHFTAKEVWQWAHG
						NGIHWSYHVPHHPEIARLIEWW
						NGLLKSQVQCHLGDNTLQGW
						GKVLQKAVYALNQYPIYGTVS
				İ		PIARIHGSRNQGVEVEVAPLTIT
						PSDPLAKCLFPVPKTLCAACLE
1						VLLPGGGMLPPGDTTTIPLNRK
						LRFPLEHFGLL
15678	46046	Α	15769	917	2352	DTISHQLEWRSLKSQETTGIAEI
		l				SATIKDLKGAGVVIPTTSLFNSS
						VWPVQKTDKSWRMTVDYCKL
1						NQVLTPNAAAVPDVVPLLEQIN
						TSPGTWYAAIDLANAIFSIPVHK
						AQQKQFAFSWQGQQYTFTVLP
			İ			QGYISSLALCHNLIRRDLDGFLL
						LQNITLLVHYVDDIMLIGSSEQE
		1			1	VANALDLLVRHLCVRGWEISPT
1	1	1				KIQGPSTLVKFLGVQWCGACR
						DILSKVKDKLLHLAPPTTKKEA
1					1	QRLVGLFGFWRQHIPHLGGLLQ
1	ļ					PLYLVIQKAAIFEWNPEPEKVL
		l		ļ		QKVQAAVQAALPLGPYDPTDPI
		l				MLEVLVADRDAVWSLWQALI
		l				GESQQRPVGFWSMALPSSADN
				i		YSPFERQLFACSWALVETECLT
				l		MGHQVTMQPELPIMNWMLSDP
		1		i		SSHKVVQAQQH\QEVAQMPRV
		l				STPATLPSLPQPALMAPWTVPY
						DQLMEEEKARARYAGTIQKWT
10070	16045	ļ	15770		861	AAALQPLSRTSLKDSGEGTSKW
15679 15680	46047	A	15770	5	90	
15681	46049	A	15772	1	324	MVQEASEVIGQLQSSAAK*AM
13001	70047	ľ	13/12	ľ	727	HWAGFSYLTKKSLNAN
15682	46050	С	15773	1	726	
15683	46051	Ā	15774	364	543	ARGAARSMKHTSGDETKRQKL
1		1				D*VRLTGIRASREEVTKEAGPR
		l		l		KRIMCSGMDELNGGLQL
15684	46052	В	15775	1	1056	
15685	46053	A	15776	1	282	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	location of first	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *-Stop codon, /-possible nucleotide deletion, \*-possible nucleotide insertion)
15686	46054	A	15777	167	954	IKNTSKLESPRGSSPHCSRNPV LLRGIGRYSRSAMYSKAMYK, RKYSAAKSKYEKKKKEK VLAT VTKPVGGDKNGGTEVVKLRK PSQHVKKLRASITFGTILIILTG PLVLNRIVPLRRTHQKFVILLTG PLVLNRIVPLRRTHQKFVILATFI KIDISNVKIPKHLTDAYFKKK LEKPRHQGGEIPTEKEKYEITE QRKIDQKAVDSQLEPKIKAIPQL GOYLBSVEALTNGIVPIKIQL
15687	46055	A	15778	1054	1403	MVEGGILRVNTSVECKTGPFFF SPHILWREPFCSVQVGKKKKEK VLATVTKPVGGDKNGGTRVVK LRKMPRYYPTEDVPRKLLSHG KKPFSQHVRKLRPSITPG\TILIIL TGNRHG
15688	46056	Α	15779	1	388	
15689	46057	A	15780	1	456	MKLPEEGSLSDICCSAIFAVLQP LLVIPRETGSGVDLQQTPTDLQ LRQTESQIMSELPFTVASKRIKY LGIQLTKDVKDLFKEIYKPLLSE IKEDTNKWKSIPCSWLGRINIVK MAILPKVTYIFNAIHIKLPMTEL EKTKHIWNKKACI
15690	46058	Α	15781	1	504	
15691	46059	A	15782	1	1836	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	location of first	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				sequence		
15692	46060	Α	15783	285	1949	RGEMNSRGRNNLSIINKTDFPFI
						ALNAHKRKHERSKIDTLTSQLK
						ELEKQEQTNSKASRSHEITKIRA
	ì					ELKEIETHNKPFKKISESR\SWFF
	1					IFYF\ERINKIDRPLARLIKKKRE
						KNQIDTIKNDKGDITTDPTEIQT
	l	i		ŀ		TIREYYKHLYANKLENLEEMD
						KFLDTYTLPRLNQEEVESLNRPI
	1					TGSEIEAIINSLPTKRSPGPDGFT
				ŀ		AEFYQRLKQCRKAHLDPVSLT
l						HRSGPGAREDRLSDSGDASRGC
				ļ		WNLSQHAAVTSPESEERRIRTL
l						SCRSVGVCRRSTPDPVCLGISSG
1	1					GCRTVNIGEQQMLLPDRSSGSF
				1		VSEGYRPCEVSAPTGGCPPVRC
ŀ	1					LMINTVSLIGVKFTEVFDSINISE
						HLELACLQDHNSLLAREQNWT
	1					EDEFDELTEVGFRRWVITNSSE
						LKEEVQTHCKEVKNLETRLDE
		l			ĺ	WLTRITNAEKSLKDLMELKTM
						AGELRDACTRFSSRFNQLEERV
l		1		l		TEIEDQMNEMKQEEKFREKRIK
		1		[	ĺ	RNEQSLQEIWDYVKRPNLHWL
1				ŀ		GVPESDRENGTKLENTLQDIIQE
						NFPNLARQTNIQIQEMQRMP
15693	46061	В	15784	596	1414	

2016

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	eodon for last amino acid	*-Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
15694	46062	A	15785	610	2986	QTERNSININRNGHQHQNPICRS
						PSSKTKGSIKPQRSGRNQSRKA
i	ł				ļ	ENSKDORTSSPTKDCSSSPATE
į .				1		ORWMENDFDELTEV/VLOKPG
	ŀ					RDTT\KQKEKFRPISLMNIDVKI
i						LNKILANRIQQHIKKLIHHDQV
						GFISGMOGWFNICKSINVIHHIN
	ŀ					RTNDKNHMIISIDAEKAFDKIQ
	i					<b>QPFMLKTLKKLGIDGTYLKIIRA</b>
	ĺ					IYDKSTASIILNGQKLEAFPLKD
	ŀ				İ	RTRQGCPLSPLLFNIALEVLARA
	Ī					IRQEKDIKCIQLGKEKVRLSLFA
	ŀ					EDMIVYLENPIVSAPNLFKLISN
	l					FSKVSGYKINVQKSQVFLYINN
	l				1	RORESQIMNEFPFTIARRRIKYL
1	ľ		1			GIOLTROVKOLFKENYKPLLKE
						IKEDTNKWKNMPCSWIGRINIM
			ĺ			KMAILAKVIYRFNAIPIKLPMTF
						FTELEK\TTLKCI*NQKRAHIAK
	1					PILSOKNKAGGITLPDFKLHYK
			ĺ			AAVTKTAWYWYONRDIDORN
	ŀ		İ			RTEPTEIMLHIYNHLIFDKPDKN
						KKWGNDSLFNKWCWENWLAI
						CRKLKRDPFLTPYTKINSRWIE
						DLNIRPETIKTLEENLGNTIQDIA
						MGKDFMSKTPKAMATKAKIDK
				i		WDLIKLKNFCTAKETTIRVNRQ
				İ		PTEWEKIFAIYSSDKGIISRIYNE
	ĺ					LKQIYKKK\NNPIKKWAKDINR
1	ĺ					HFSKEDIQAASKHVKKHSTSRIF
	1					MQIKTTLGYHLTPVRMATIKKS
	i					KNNRCWCGCGEKGTLIHCW/M
15695	46063	A	15786	1	906	MVNQKRYHIPGGTAEISGTIKK
					i	LKNAGVVIPTTSPLNSPIWPVQ
					l	KTDGSWRMTMDYHKLNQVVT
						PIAVAVPYVVALLEQINTFSCT
i						WYAAIDLANTFFSFSVHKA/HK
1				ĺ		K*FAFSRQGQQYTFTVHP\YDN
						YSPFERQLLACYWASVETEHLT
1			1	l		MGYQVTIQLELPIMNWVLSDPS
1						SHKLGHAKQHSIIKWKWYIRD
						RARAGPEGTARIHRSRNQGVEV
						EVAPLTITPSDPLARFLLPVPTIL
	1					HSAGLEVLVPEGGTLPLGDTTT
						IPFNWKLRLPPGHFRLLLPLNQ
1						QAKKGVTVFAGVIEAIKMK
						·

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nuclcotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
15696	46064	Α	15787	1	909	MVLEVSVSDRDAVWRLWRAPI
						GESQQRSLGFWSKVLPYSADN
				i		YFPFERQLLACYWALLETDRLT
						VGHQVTLQPELPIMNWVLSDPS
						SHKVGHVHQHSIIKWKWYIRD
						QTRAGPEGTTTPVITQ/WDAHE
						QSGLSGRDG\KGQRFVLTGVDT
i						YSGYWFAYPAHNASAKTSIYG
						FTECLIHCHGIPHSIASDQGTLFT
				l		AKEVWQWAHAHGIHWSYHIP
						HHPIAAGLIEWWNGLLKSQLQ
		l				CQLGDNTLQGWGKDLQKAMY
				l		SLNQRLIYSTVSPISRIHGSRNQ
						RVEVEVAPLTITLSDPLAKFFFL
15697	46065	Α	15788	I	754	MQNNVDSFQEPPPTPLFSSRPIA
						RLKSKQAPRGEAESVTHEELESI
	l					RLRAKTSDKISSLTFRRGWGKV
					l	LQKAMYALNQHPIYGTVFPIPRI
						DGSRNQGVEVKVAPLTITLSDP
			1			LAKFLLPVLSALHSAGLEVLVP
			1			EGGILPPGAGDMRMIQLNWKL
						SLPPGYFGLLLPLSQQTKKGVT
						DLGGVIDLDYQDEISLLFHI\KV
			1	l		NGKLQQPNPDRTTSGPDPSGM
						KVWVTPPGK/EPQPAEGLAEGK
	10000		1.5000		1506	GNTEWVVEE
15698	46066	Α	15789	686	1506	VETVHLMLQIGEFKKTDVS/WK
						TVDYHKLNQVVTPTAAAVPDV VSLLEQINTYPGTWYAVIDLEN
			1			
					1	AFFSVPVHNAHQKGFAFSWQG QQYTFTVLPQGYINSPTLCHNLI
		l				
		i				RRDPGHFSYPQDITLVHYIDDI MLIGSSEKEVANTLDLLPIYOV
			l	i		TLKAANYEWGPEQEKAVQQV OAAVOAALPLGOHNPADPTVL
				i		
				l		EVSVADRDAIWNLWQAPIARIH
		1				GSRNQGVEVEVAPLTITPSDPL
			l			AKFLPPVPATFCSAGLEVLVPE
15500	14047	<u> </u>	15700	400	507	GGMLPPGEIETIPLK
15699	46067	A	15790	422	537	VNQFGVIFCAAIIN*YECLKQSF
15000	15050	<u>_</u>	15701		510	KTQTDYFPSPLNTSQ
15700	46068	В	15791	1	519	

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
		<u> </u>		ļ		
15701	46069	Α	15792	53	753	SLGTGTLRVLLGTAEAQMLQFS
i						HLYADYGGKPALEDINLTLESG
		l				ELLVVLG/PSGCGKTTLLNLIAG
1		l			1	FVPYQHGSIQLAGKRIEGPGAE
		l				RGVVFQNEGLLPWRNVQDTVA
	1	1				FGLQLAGIKKMQRLKFAHQML
						KKVGLEGADKRYIWQLSGGQR
						QRVGIARALAANPQLLLLDEPF
		l	ł			GALDAFTRDQMQTLLLNLWQE
		i			1	TGKOVLLITHDIEEAVFMATEL
						VLLSSAP\GRVLERLPHI
15702	46070	A	15793	2348	2760	LWLVCINCFIPAFLLMLRWLPR
						LKPLSQLSVPTYRLPSVPFLKPT
				į.		GMESPEAISRVSGKGIL*RDSDA
					1	YSVSLSYHYPIIRHPSSIIVDHRS
1						SIDP*PIVDHSSSIAKRSGTFPLG
		l				YWEVFVQLTFGQQRQASGILQ
15703	46071	A	15794	2	415	HPGLETTDLLSPLPAALEPQGQ
13703	40071	l^	13794	-	113	GRPSIQGAPRGSFTRIEAGTPHV
					1	PAPCPAAORNOGWGLVGAWL
			ĺ			GFMAP*EOSVASSWK*PLMKS
						QYSREVISHLPLVPMQQGRPVM
1						TOSMWGWLVWFPALFLVOIGH
1					1	
15004	44070		15705	400	005	LVMSSGHS
15704	46072	A	15795	428	885	GISMKLSRISAI/NWNKISDDKD
		i				LEVWNR/LTSNFWLPEKVPLSN
		l				DIGAWQTLTVVEQQLTMRVFT
					i	GLTLVDTLQNVIGAPSLMPDAL
1		ĺ				TPHEEAGLSNISFMEAGHARSY
I		ŀ			ı	SSIFSTLCQTKDVDAAYAWSEE
		l				NAPLQRKAQIIQQHYRGDDPLK
		L_				K
15705	46073	Α	15796	1	1125	
15706	46074	Α	15797	57	303	SHKHYADALLYPAPDVCTAC*
		l	1			LLRGNRRDQSKS\TAKRHLTAA
		1				HFRFVRMVRHGNH/SRLRPDSF
		<u></u>				R*PVSPDR*PPLRAAHFR
15707	46075	A	15798	3	430	
15708	46076	В	15799	I	1338	
15709	46077	Α	15800	380	1043	WTRWRASAADNLAHGRWGEQ
		1	l			KLVVTTGASGAPDRQAARCGC
		1	1			IWRKISWYRSKGSKHPLTPKEV
1		1				EKTGWGLKIRGMGKQQIA\ERV
1		l				KEAARILELDGLLKRRPRELSG
		I				GQRQRVAMARA1VRDPAVFLF
1		I				DEPLSNLDAKLRVOMRLELOO
		I				LHRRDQVEAMTLAQRVMVMN
1	1	1				GGVAEOIGTPVEVDGDDTLEIL
1	1	1	1	1		GADNLAHDAGRAEAGGDWRI
	1	1		1		RSARRSSTCAH
					1	TO LOCALI

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
15710	46078	A	15801	1	900	MAAIAFLITWFLSHDKKRIRILK
				ŀ		RLSGGGNMADEFPGGAVVFTV
						LNLTHWLEDWGLPVHWRSSC
				i		MPSGLEYLIVLIFKGVIVAVHLL
i				ł		IVDALNLIRRIHAV/QGSPCVET
	l					CQHALDQLIMHSQPTHAVAVF
						DDENRSSGWRHQGLPDYKAGR
	1					PPMPEELHDEMPALRAAFE\QR
		ĺ				GVPCWSTSGNEADDLAATLAV
						KVTQAGHQATIVSTDKGYCQL
l	1					LSPTLRIRDYFQKRWLDAPFID
l	1					KEFGVQPQQLPDYWGLAGISSS
	1					KVPGVAGIGPKSATQLLVEFQS
						LDGIYENL\D\AVAEKWRHKL
15711	46079	A	15802	1	1350	
15712	46080	Α	15803	1618	2082	
15713	46081	A	15804	1	803	MINLIGSDVNYDWLKLPLVHL
		1	I	ł		HWYDKEVRPGRKVGHLNLTDS
		1				DTSRLTATLEALIPLLPPEYASG
		1				VIWAQSLIRCVKHRIRHCAPIAG
Ì		1				CGTGCRPDKTRQASHQAQMSN
						AYDYSEIQGIGKQKAANRVAEP
		1	l			RTYHSFASITDRRADLLKPGNH
						AQDGRLTAARRADKHDELFIG
					İ	NFQKADNRGQVSDSVEGNSNC
						APVKPAPIPTERIPLALMASMPA
						CASSMPIHACGGTPSPAQAARK
						ISGSGFEFLSWEASAQKVKNSR
		1		Į.		SSSAAKIVGAFRETEASPTEICC
				[		ARRSASKERMPG*ARADPHRA
	1			[		HTAGVNGVNARLRIFNADTCL
			l	1		RRHAQPCTGGEKDFRVRFRVF
		1				KLGSIRAEGEKLAQLQRR

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SEQ ID	SEO ID NO	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1.00	09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
		1		sequence		
15714	46082	A	15805	1	1655	MRGHNWIDMDQARQQSTPHT
13/14	40082	l <sup>A</sup>	13803	1'	1033	DRKICHKNDRPRTTPLRKIDAH
		1				PHTLIILPAESTLSTTKYKLRAL
					ļ	LVENTNKDKSAVSVVFRGSVL
		1				
		1				HQQAANFPNLMLCFQLKNGVN
				l		ACNOFIMLEVODONAAGSIERAA
1		1		l .		SPCINEKQHAFSESVPAIAAVRG
				ı	i	LGSMIAVEFNDPQTGEPSAAIA
						QKIQQRALAQGLLLLTCGAYG
1		1				NACKRRIDYVCRIKHSRRIRQV VLLNFAKSGAFSTTRGTDDKLT
1						
				1	i	PVIQPRASGEYNEEFSLLPVVN
1		1		1	1	YLKDKLSNPVRLVKDYLDGVD
		1			l	VAEGELVVLENVRFNKGEKKD
						DETLSKKYAALCDVFVMDAFG
1						TAHLRAGFLLTGI\GKLRCSLRC
I		1				AGPLLAAELDALGKALKEPARF
		1		1		MVAIVGGSKVSTKLTVLDSLSK
		1		i		IADQLIVGGGIANTFIAAQGHD
		1				VGKSLYEADLVDEAKRLLTTC
				I		NIPVPSDVRVATEFSETAPANL
1				ì		KSVNDVKADEQILDIVRDLDAA
1			1	ł		NVVINAVFSYVTNVWGWAFE
			1			WYMVVMLFGWFWLVFGPYAK
16716	46002	١.	15906	ļ	1359	KRLGNEPPEFSTASWIFMMFAL
15715 15716	46083	A	15806	670	1008	
15717	46085	A	15808	455	1137	GTKPRDIDHILGTFITPGMPKGG
13717	10000	ľ	13000	1.55	1	KLDVYAAPELPLKLLGRPTEGE
1						YNEEF/SLLPVVNYLKDKLSNP
						V/RLDGVDVAEGEL/VVLENVR
				l .	į.	FNKGEKKDDE/HRAQASTHGIG
			i			K/FADVACAGPLLA/AVLDSLSK
		1			1	/IADQLIVGGGIANTFI/AAQGHD
						VGKSLYEADLV/DEAKRLLTTC
						NIPVPSD/VRVATEFSETAPATL
		1				KSVRHSDKISYISTGGGAFLEL
		1				WKVKYLPAVAMLEERG
16710	46086	A	15809	465	888	RGLVALSSERRCRLRRRNHPES
15718	40080	l <sup>A</sup>	13809	703	000	GTRSPDPAGAASLSRRFFYAPP
		1	1	I		
1				1		GTPETGCGYSSRSRSQRKR/LST WRCNS*ETPKSPPKACCRPARIP
				1	1	APRSSSVKKASACGPAAVMKK
1		1		1	1	RCRKASITPISKITCAIHRMRRW
				1	1	
1.0016	46007	١.	16010	417	707	TCTKRAAF
15719	46087	Α	15810	417	707	IQIHERSWRYLHWWSSVRRRA
1		1		1		A*YGAPL*RDGIQRGTRRISQV
1		1		1		YQ*SSVRQLRRDASASGSAPRV
					[	CREYAAACYLRHEHWSCDAVS
	46000	1	1.0011	<del> </del>	1250	PTPRMLKSFV
15720	46088	В	15811	1	4350	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
15721	46089	В	15812	1	2862	
15722	46090	A	15813	1	1471	MLHSRGFLAEVFGILARHNISV
						DLITTSEVSVALTLDTTGSTSTG
		l				DTLLTQSLLMELSALCRVEVEE
						GLALVALIGNDLSKACGVGKE
		l				VFGVLEPFNIRMICYGASSHNL
		1		1		CFLVPGEDAEQDGTGTSGIGAQ
		l				KKKMYANNGAIDRKLLFEATF
		ı				VTIEKCCDTNQKGDDTHALGQ
		1				PIRGHDKSLAGSFCYACRSEEG
		1				LSQYRAYDSRGQLIAVKDTQG
	ŀ					HETRYEYNIAGDLTAVIAPDGS
						RNGTQYDAWGKAVRTTQGG\L
						TRSMEYD\AAGRVIRLTSENGS
	į.					HTTFRYDVLDRLIQETGFDGRT
	i	1				QRYHHDLTGKLIRSEDEGLVTH
	i					WHYDEADRLTHRTVKGETAER
		1				WQYDERGWLTDISHISEGHRV
	i	1				AVHYRYDEKGRLTGEROTVHH
	i	l			l	POTEALLWOHETRHAYNAOGL
		l				ANRCIPDSLPAVEWLTYGSGYL
		l	İ		1	AGMKLGDTPLVEYTRDRLHRE
		l	İ			TLRSFGRYELTTAYTPAGQLQS
		1			}	QHLNSLLTYRHANFAL
15723	46091	Α	15814	1	1367	MSKLLERFRYFKQKGETFADG
					1	HGQVMHSNRDWEDSYRQRWQ
		l				FDKIVRSTHGVNCTGSCSWKIY
			İ			VKNGLVTWEIQQTDYPRTRPD
		l			İ	LPNHEPRGCPRGASYSWYLYSA
		l				NRLKYPLIRKRLIEL WREALKQ
	1	l			l	HSDPAADNDLIARFQSFTNQPFI
		l				ANRLTGNDRARFNLTFIVNNQH
		l				ATAITTTGTFLPEWSTTFIITLIL
		l	1			QSKVQAIDLTKEAIVTVGCNTIS
						TTVHEVVSASIGIATKFWQHIGF
		l				CFYVIYDTVVTTIVESRTTEYSP
		ł				DVVTGLITRITTPDGRASAFYN
		l				NHHSQLTSATGPDGLEIRREYD
	1	1	ĺ	l		EWGRLIQETAPDGDITRYRYDN
	1	1	ŀ			PHSDLPCATEDATGSRKTMTW
	1		İ	l		SRYGQLLSFTDCSGYVTRYDH
	1	1	l			DRFGQVTAVHREEGLSQYRAY
	1	1		1		DSRGQLIAVKDTQGHETRYEY
		1				NAA/GDIRQCESDLQSPSCSQYR
	1	1		l	1	AIDGESLSETARYSVHO

SEQ ID	SEQ ID NO:		SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	eodon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide sequence	of peptide sequence	deletion, \"possible nucleotide insertion)
15724	46092	Α	15815	357	1733	TADSPETLRCQTSGENARGAGT
						VERAGKSLWRSLR*SHRP*STR
	l	ŀ				TGDIHCQIQTNFSLFN*QHPGQH
						R\YGSGTAIINQSLITHDPEYPEN
						LPAAPLVRYGWTPRGELAVVY
						DRSGKQVRSFTYDDKYRGRMV
1						AHRHTGRPEIRYRYDSDGRVTE
					8	QLNPAGLSYTYQYEKDRITITD
						SLDRREVLHTQGEAGLKRVVK
						KEHADGSVTQSQFDAVGRLRA
1		1				QTDAAGRTTEYSPDVVTGLITR
						ITTPDGRASAFYYNHHNQLTSA
		ĺ				TGPDGLELRREYDELGRLIQET
						APDGDITRYRYDNPHSDLPCAT
						EDATGSRKTMTWSRYGQLLSF
	ľ					TDCSGYVTRYDHDRFGOMTAV
1				1		HREERLSQYRAFDRRGTVIAVK
1		l				ETOGLETGFEYHFPVPDGVIAP
1				Ì		KG/SRNGNSQSVGKRRSTEDIR
1		l				G*TRWRGYTADRRAAKTHARV
		1				E*HLRARPRVCALFFPKQCERH
15725	46093	A	15816	1595	3228	DNNAKLFRAGOMKVLKPYVDS
		1		1		GKIKVVGDQWVDGWLPENAL
		1		l		KIMENALTANNNKIDAVVASN
		1		1	1	DATAGGAIQALSAQGLSGKVAI
		ŀ		l		SGODADLAGIKRIAAGTOTMT
		ŀ				VYKPITLLANTAAEIAVELGNG
		ŀ	i e			QEPKADTTLNNGLKDVPSRLLT
		ŀ		l		PIDVNKNNIKDTNLPAAPLVRY
				l		GWTPRGELAVVYDRSGKQVRT
İ		1				FTYDDKYRGRMVAHRHTGRPE
1		l				IRYRYDSDGRVTEOLNPAGLSY
				l		TYOYEKDRITITDSLDRREVLH
i						TQGEAGLKRVVKKEHADGSVT
1				l		QSQFDAVGRLRAQTDAAGRTT
						EYSPDVVTGLITRITTPDGRASA
1		1				FYYNHHNOLTSATGPDGLELR
		l	l			REYDELGRLIQETAPDGDITRY
1		1	l	l		RYDNPHSDLPCATEDATGSRKT
1			1	1		MTWSRYGQLLSFTDCSGYVTR
1	1	1		i		YDHDRFGOMTAVHR\EEGL\SO
1		1				YRAYDSRGQLIAVKDTQGHET
				l		RYEYNIAGDLTAVIAPDGSRNG
1		1				TQYDAWGKAVRTTQGGLTRS
		1				MEYDAAGRVIRLTSENGSHTTF
				1		RYDVLEQYCGQVIKAHAVSRF
15726	46094	A	15817	1	627	KIDI DEQICOQVIKANAVSKI
	46095	A	15818	701	895	
15727	40093	I <sup>A</sup>	12919	/01	07.7	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
15728	46096	A	15819	1412	1705	LASISTSCAPPKVNCGVMAIFLA
		1				SDSRLWSGLRAQATSRSTLSLM
					l	TRSGLWLAIO*NALRSWLASHE
						TKRPPSTLGGNTVPS*ALRLGIL
						ASSRILL
15729	46097	Α	15820	344	547	
15730	46098	Α	15821	1	1518 '	
15731	46099	Α	15822	1693	2455	VLAAFTRSKQRYGAPRLTDELR
l						AQGYPFNVKTVAASMRRQGLR
						AKASRKFSPVSYRAHGLPVSEN
1		İ				LLEQDFYASSPNQKWAGDITYL
İ						RTDEGWLYLAVVIDLWSRAMA
						LLRRKSPGNVIVHTDRGGOYCS
						ADYOAOLKRHNLRGSMSAKG
	ļ.			l		CCYDNACVESFFHSLKVECIHG
						EHFISREIMRATVF\IISNVITIGG
						GGTVAARGGVP*AVKSNVNDV
				ŀ		RRNCLARSSNNGWIFPPVVVNG
l						WROOALTIVAGICC
15732	46100	В	15823	1	1407	
15733	46101	Α	15824	1	3252	
15734	46102	Α	15825	1	2409	
15735	46103	В	15826	1	2802	
15736	46104	Α	15827	1715	1824	
15737	46105	A	15828	410	720	PGSRAVIGWSMSPRMTAHWPA
						MPCRWRCGGVRTYAPEPTG*R
	ŀ					RWLQNCSACSS**LRKTSRKNR
1		1				TT*RTPARSSSAPPLMLKQPFTR
		1				QWPLNTPWKPPRLSPS
15738	46106	Α	15829	905	1008	SCDSYRLSSRAAAVTPMRSASF
						RASGFLLVILFVCRVSVVGCRV
						LAWSGGSVFRRGVPLAWTVLR
			l	l		WVRRRCGCGVGRCRGLSAVV
	1			l		YPSGIITVDSARSWRIMGRSGSP
l				1		LA\TVGLAGCWSOPRL*TDAFS
l				l		KLOGFRVFTGDTICM
15739	46107	В	15830	ī	3148	
15740	46108	Α	15831	1896	2062	SVCYPGRN*IPSG*N*PRIWSDP
1			1	l		VQRRERAGKKWLHENPGWRK
				1		**PDYHYRSEAD

SEQ ID NO:	SEQ ID NO: of peptide sequence		in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X-Unknown, *-Stop codon, /-possible nucleotide deletion, √-possible nucleotide insertion)
15741	46109	A	15832	1	1456	MSTEIARLKRQLADGMKSWLS SKRPRHTSRAPEMKYVFIEKHQ AEFASKQCAACSGWPATAGNV VSAADKDKHASAVPPHCDSVV LAAFTRSKQRLPLNVKTVAASL RRQGLRARPFGSSARSATAHTA CLVRKSVGAGFLRQWPEPKWA GDTTYLKTDEGWLYLAVVIDL WSRAVIGWSMSPRNTAQLACD LOGALGMALWRKFRENVIVIDL GGQFGDRWKALANALNIPLDQ LSARISANPKGGFUYLAREVNP MADYIKKLKPGHVYRESSR YYPSGEVTAHLIGFTNVDSQGI EGYGKSFGKWTGACGEGWKTGACGKWTG DRYGRVIEDISSTDSQAAHNLA LSIDERLQALVYRELNNAVAFN MSPSYNPNNLSGTPKEAMRNRT LDVFERGSTVKPMVWMTGLOR
						GVVRENSVLNTIPYRINGHEIKD VARITTEEDFNHASAARFVCAA AERALONHH
15742	46110	A	15833	2	929	
	46111	A	15834	1	472	
	46112	A	15835	1	513	
15745	46113	A	15836	ı	254	CDNLKTCHTSHGSVMAETAVI NHKKRKNSPRIVQSNDLTGAA YSLSRDQKRV/LRYEPVSQFRLS ETQKHQSVCHAFIRIPVSVS

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SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1.01	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1			sequence		
15746	46114	Α	15837	145	1929	VSGVIEIADGSRRRKAAALTES
						DYRVLVGELDDEQMAALSRLG
						NDYRPTSAYERGQRYASRLQN
ŀ						EFAGNISALADAECDNLKTCHT
						SHGSVMAETAVINHKKRKNSP
						RIVQSNDLTEAAYSLSRDQKRM
1						LYLFVDQIRKSDGTLQEHDGIC
1						EIHVAKYAEIFGLTSAEASKDIR
						QALKSFAGKEVVFYRPEEDAG
1			ŀ			DEKGYESFPWFIK/RPSRGLYSV
	l			ŀ		HINPYLIPFFIG\LQNRFTQFRLS
				l .		ETKEITNPYAMRLYESLCQYRK
						PDGSGIVSLKIDWHERYQLPQS
1				1		YORMPDFRRRFLOGFCRFRNH
1				ļ		HQTGFSPAGANQRGPLAATLSG
					1	PGGEGQSAVARLTGEKKNHPG
i i						AQYANRLSPRVGRFINAAGTTG
l	]	i				FPTWKAGSERNAINDDVTYAIK
l				l		PTCWPGLDIIPSCLALHRIETEL
1				l		MGKFDEGKLPTDPHLMLRLAIE
1				l		TVAHDYDVIVIDSAPNLGIGTIN
1			l	İ		VVCAADVLIVPTPAELFDYTSA
				l		LOFFDMLRDLLKNVDLKGNSN
1						GSQSPWMEEQIRDAWGSMVLK
				İ		NVVRETDEVGKGQIRMRTVFE
				1		QAIDQRSSTGAWRNALSIWEPE
				i		CNEISIGVSLDQDGGSNSVLRK
15747	461I5	В	15838	I	1734	<b></b>
15748	46116	Α	15839	1	97I	
15749	46117	Α	15840	1	1143	
15750	46118	Α	15841	1	556	
15751	46119	В	15842	8	1000	
15752	46120	Α	15843	1	1169	MLTLILLDLQFMAQLAGYQMS
				ĺ		FNSTKSKQTKNNFAVGYRTGD
				l		FQLHTNVNDGAEFGGSVYQKV
						CEELDALINLAWTSSTSCTRFG
						LAAKFQLKPIAFISTKVNHWLT
						GVSYTPPLEAGVKLNLSALCDN
				ŀ		LKTCHTSHGSVMAETAVINHK
						KRKNSPRIVQSNDLTEAAYSLS
				i .		RDQKRMLYLFVDQIRKSDGTL
				ļ		QEHDGICEIHVAKYAEIFGLTSA
						EASKDIRQALKSFAGKEVVFYR
				1		PEEDAGDEKGYESFPWFIKRAH
			1			SPSRGLYSVHINPYLIPFFIGLQN
1						RFTOFRLSETKEITNPYAMRLY
1			l			ESLCQYRKP\DGSGIVSLKIDWII
						ERYOLPO/TYORMPDFRRRFLO
		1	l	l		EEFESLNRQITGSEIVAMINSLST
						KKSPGPDGFTAEFYQ
15753	46121	Ā	15844	1	1509	

NO:	SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
15754   46122							
15754   46122				09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
15755   46123	1	1			sequence		
15755   46123	15754	46122	_	15945		1559	
15756   46124			-				
15757   46125							
WISAGAAPGGPIVKQLPSPVRT							MENT LOWLETT COTTOUR
EQLEQERPYTIGS.APSTPNIKLLL   SHSNCQLPRPLRSITNISACFSLE   LAIDHRGPPHSPCARSLYSNSVY	15757	46125	A	15848	11	812	
SHSNCQLPRPLRSITNISACFSLE   LAIDHRGPPHSPGARSLYSNSVF   GTYQLCDLCDNLKTCHTSHGS   VMAETAVINHKKRKNSPLIVQS   NDLTEAAYSLSRDQKRMLV_F   VDQIRKSDGTLQEHDGICGIHV   AKYAEIFGLTSAEASKDIRQAL   KSFAGKEVVFYRPEEDAGDEK   GYESPFWFIKRSPE*RRGKFPFT   QMGQD   1755		l	l		i	1	
LAIDHRGPHISPOARSI, SYNSVE GTYQLCDLCDNILKTCHTSHGS VMAETAVINHKKRKNSPLIVOZ NDLTEAAYSLSRDQKRMLYLF VDQIKKSDGTLQEHDGICEIHV AKYAEIFGLTSAEASKDIRQAL KSFAGKEVVFYRPEEDAGDEK GYESPFWFIKRSPE*RRGKFPFT QMGQD							
GTYOLCDLONI,KTCHTSHGS			1				
WAMETAVINHKKRKNSPLIVOS   NDLTEAAYSLSRDQKRMLYLF   VDQIRKSDGTLQEHDGICEHV   AKYAEIFGLTSAEASKDIRQAL   KSFAGKEVVFYFPEEDAGDEK   GYESFPWFIKRSPE*RGKFPFT   QMGQD   15758   46126   A   15849   1   1773   15750   46128   A   15851   1   726   MPASGNENDLNMPSGTIEIFVR   CYVEVERIMSAWTEQPNEHRT   MMWSVLLQPCDNLKTCHTSIG   SVMAETAVINHKKRKNSPRIVQ   SNDLTEAAYSLSRDQKRMLYL   FVDQIRKSDGTLQEHDGICEHW   AKYAEIFGLTSAEASKDIRQAL   KSFAGKEVVFYFPEEDAGDEK   GYESFPWFIKRAHSPSRG/LYSV   HINPYLIPFFIGLQNRT/PFRLSE   TKEITNPYAMRLYESLCQYRKS   15762   46132   A   15853   1   2121   15763   46131   B   15854   721   2739   MQEQQQASSLIRSGNGRLPGSG   AQRTPCHIRRDGSQRRVCDDCK   QQWWAKXYNIPSGLHACTATL   EETHILDSGAHVQYFYKGQLH   HGYWAETAVSLSRDQKRML   HGSWMAETAVINHKKRKNSPRIVQ   VMRVPCTDYFDTQKNPDLSHL   HGSWMAETAVINHKKRKNSPRIVQ   CQWWAKXYNIPSGLHACTATL   EETHILDSGAHVQYFYKGQLH   HGYWAETAVSLSRDQKRML   HGSWMAETAVINHKKRKNSPRIVQ   VMRVPCTDYFDTQKNPDLSHL   HGSWMAETAVINHKKRKNSPRIVQ   CQWWASAVNIPSGLHACTATL   EETHILDSGAHVQYFYKGQLH   HGYWAETAVSLAEASKDIRQG   LGGYGSFPWFIKRSAESKDIRQG   LGGYGSFPWFIKRSAESKDIRQG   LGGYGSFPWFIKRSAESKDIRQG   LGGYGSFPWFIKRSAESKDIRQG   LGGYGSFPWFIKRSAESKDIRQG   LGGYGSFPWFIKRSAESKDIRQG   LGGYGSFPWFIKRSAESKDIRQG   LGGYGSFPWFIKRAHSPSRGLY   SVHINPYLIPFFIGLQN   SVHINPYLIPFFI		1	ı				
NDLTEARYSLSRDOKRMLYLF	1		ŀ				
VDQIRKSIDGTLQEHDGICEIHV				l			
AKYAEJEGLTSAEASKDIRQAL   KSFAGKEVVYPYPEEDAGDEK   GYESPPWFIKRSP*RGKFPFT   QMGQD	1		ļ				NDLTEAAYSLSRDQKRMLYLF
IS758   46126   A   15849   1   1773			l				VDQIRKSDGTLQEHDGICEIHV
GYESFPW/FIKRSPE*RRGKFPFT			1				AKYAEIFGLTSAEASKDIRQAL
New York   State							KSFAGKEVVFYRPEEDAGDEK
15758   46126   A   15849   1   1773	ļ	1		ŀ			GYESFPW/FIKRSPE*RRGKFPFT
15759					l		QMGQD
15760   46128	15758	46126	Α	15849	1	1773	
CYVEVERIMSA WTEQPNEHRT   MMWSVLLQPCDNLKTCHTSHG   SVMAETAVINIKKRKNSPRIVQ   SNDLTEAAYSLSRDQKRMLYL   FVDQIRKSDGTLQEHDGICEHV   AKYAEHFGLTSAEASKDIRQAL   KSFAGKEVVFYRPEEDAGDEK   GYESPPWFIKRAHSPSRG/LYSY   HINPYLIPFFIGLQNRFTOFRLSE   TKEITNPYAMKLYESLCQYRKS   TKEITNPYAMKLYESLCQYRKS   15763   46131   B   15853   1   2121   15763   46131   B   15855   1   2529   MQEQQASSLIRSGNGRLPGSG   AQRTPCHIRRDGSQRRVCDDCK   QQWKAKYNIPSGLHACTATL   EFHILDSGAHVQYFYKGQLH   VMRVPCTDYFDTQKNPNLSHL   HGSVMAETAVINHKKRKNSPRI   VQSNDLTEAAYSLSRDQKRML   VLFVPQIRKSDGTLQEHDGICEI   HVAKYAEHFGLTSAEASKDIRQ   ALKSFAGKEVVFYRPEEDAGD   EKGYESPPWFIKRAHSPSRGLY   SVHINPYLIPFFIGLQN   SVHINPYLIPFFIGLQN   SVHINPYLIPFFIGLQN   SVHINPYLIPFFIGLQN   15765   46133   B   15856   537   1318   15856   46134   B   15857   1   411	15759	46127	В	15850	1		
MMWSULLOPCDNILXTCHTSHG   SVMAETAVINHKKRKSPRIVQ   SNDLTEA4YSLSRDQKRMLYL    FVDQIRKSDGTLQEHDGICEIHV    AKYABIFGLTSABASKDIRQAL    KSFAGKEVVFYRPEEDAGDEK   GYESFPWFIKRAHSPSRG/LYSV    HINPYLIPFFIGLQN    15762   46130	15760	46128	Α	15851	1	726	MPASGNENDLNMPSGTIEIFVR
SVMAETAVINHKRKRNSPRIVQ   SNDLTEAAYSLSRDQKRMLYL   FVDQIRKSDGTLQEHDGICEHV   AKYAEIFGLTSAEASKDIRQAL   KSFAGKEVVFYFPEEAGDEK   GYESPPWFIKRAHSPSRG/LYSV   HINPYLIPFFIGLQNRTOFFLSE   TKEITNPYAMRLYESLCQYRKS   15762   46130   A   15853   1   2121     15763   46131   B   15854   721   2739							CYVEVERIMSA WTEQPNEHRT
SNDLTEAAYSLSRDOKRMLYL   FVDQIRKSDGTLQEIDGICEIHV   AKYAEIFGLTSAEASKDIRQAL   KSFAGKEVVFYRPEEDAGDEK   GVESPPWFIKRAHSPSRG/LYSV   HINPYLIPFFIGLQNRFTQFRLSE   TKEITNPYAMRLYESLCQYRKS   TKEITNPYAMRLYESLCQYRKS   TKEITNPYAMRLYESLCQYRKS   TKEITNPYAMRLYESLCQYRKS   15763   46131	1		ļ				MMWSVLLQPCDNLKTCHTSHG
FVDORKSDGTLQEHDGICEHIV   AKYAEIFGLTSAEASKDIRQAL   KSFAGKEVVFYRPĒEDAGDEK GYESFPWFIKRAHSPSRGILYSV HINPYLIPFFIGLQNFTOFRLSE TKEITNPYAMRLYESLCQYRKS     15761   46129   B   15852   356   671							SVMAETAVINHKKRKNSPRIVQ
AKYAEJEGLTSAEASKDIRQAL   KSFAGKEVVFYRPEEDAGDEK   GYESPPWIKKRAHSPSRG/LYSY   HINPYLIPFFIGLQNRFTQFRLSE   TKEITNPYAMRLYESLCQYRKS   HINPYLIPFIGLQNRFTQFRLSE   TKEITNPYAMRLYESLCQYRKS   TKEITNPYAMRLYESLCQYRKS   15762   46130   A 15853   1 2121   15764   46132   A 15855   1 2529   MQEQQASSLIRSGNGRLPGSG   AQRTPCHIRRDGSQRRVCDDCK   QQWWAKYNIPSGLHACTATL   EETHILDSGAHVQVFYKGQLH   VMRVPCTDYEDTQKNPALSHL   HGSVMAETAVINHKKRKNSPRI   VQSNDLTEAAYSLSRDQKRML   VLFVDQIRKSDGTLQEHGGICE   HVAKYAEJFGLTSAEASKDJRQ   ALKSFAGKEVVFYRPEEDAGD   EKGYESPFWIKKRKHSPSRGLY   SVHINPYLIPFFIGLQN   15765   46133   B 15856   537   1318   15765   46134   B 15857   1 411							SNDLTEAAYSLSRDQKRMLYL
RSFAGKEVVFYRPEEDAGDEK   GYESFPWFIKRAHSPSRG/LYSY   HINPYLIPFFIGLQNRFTQFRLSE   TKEITNPYAMRLYESLCQYRKS   TKEITNPYAMRLYESLCQYRKS   TKEITNPYAMRLYESLCQYRKS   TKEITNPYAMRLYESLCQYRKS   TKEITNPYAMRLYESLCQYRKS   TKEITNPYAMRLYESLCQYRKS   TKEITNPYAMRLYESLCQYRKS   TSF02   46130   A 15853   1 2121   TSF02   46132   A 15855   TSF02   TSF			l				FVDQIRKSDGTLQEHDGICEIHV
GYESFPWFIKRAHSPSRG/LYSV     15761   46129   B   15852   356   671     15762   46130   A   15853   1   2121     15763   46131   B   15854   721   2739     15764   46132   A   15855   1   5828   MQEQQASSLIRSGNGRLPGSG AQRTPCHIRRDGSQRR VCDDCK QQWWAKXNIPSGLHACTATL EETHILDSGAHVOFFVKQQLH VMRVPCTDYFDTQKNPNLSHL HGSWMAETAWINHKKRKNSPR I VQSNDLTEAAYSLSRDQKRML YLFVDQIRKSDGTLQEHDGICEI HVAKYAEIFGLTSAEASKDIRG ALKSFAGKEVVFYRPEEDAGD EEGYESFPWFIKRAHSPSRGLY SVHINPYLIPFFIGLQN     15765   46133   B   15856   537   1318     15765   46134   B   15857   1   411			1			1	AKYAEIFGLTSAEASKDIRQAL
HINPYLIPFFIGLQNRFTQFRLSE     15761   46129   B   15852   356   671     15762   46130   A   15853   1   2121     15763   46131   B   15854   721   2739     15764   46132   A   15855   1   5828   MQEQQQASSLIRSGNGRLPGSG AQRTPCHIRRDGSQRRVCDDCK QQWKAKYNIPSGLHACTATL EFTHILDSGAHVQYFYKGQLH VMRVPCTDYFDTQKNPNLSHL HGSVMAETAVINHKKRKNSPRI VQSNDLTEAAYSLSRDQKRML VLFVPQHRSGSGTLQEHGGICE HVAKYAEIFGLTSAEASKDIRQ ALKSFAGKEVVFYRPEEDAGD EKGVESFPWIFKRKAHSPSRGLY SVHINPYLIPFFIGLQN     15765   46133   B   15856   537   1318							KSFAGKEVVFYRPEEDAGDEK
TKEITNPYAMRLYESLQYRKS			l				GYESFPWFIKRAHSPSRG/LYSV
15761   46129   B   15852   356   671     15762   46130   A   15853   1   2121     15763   46131   B   15854   721   2739     15764   46132   A   15855   I   5828   MQEQQASSLIRSGNGRLPGSG AQRTPCHIRRDGSQRRVCDDCK QQWWAKYNIPSGLHACTATL EETHILDSGAHVQYFYKGQLH YMRYPCTDYEDTQKNPMLSHL HGSVMAETAVINHKKRKNSPRI VQSNDLTEAAYSLSRDQKRML YLFVDQIRKSDGTLQEHDGICEI HVAKYAEIFGLTSAEASKDIRQ ALKSFAGKEVVFYRPEEDAGD EKGYESFPWIFKRKHSPSRGLY SVHINPYLIPFFIGLQN     15765   46133   B   15856   537   1318		·					HINPYLIPFFIGLQNRFTQFRLSE
15762   46130   A   15853   1   2121				_			TKEITNPYAMRLYESLCQYRKS
15765   46131   B   15854   721   2739   MQEQQQASSLIRSGNGRLPGSG AQRTPCHIRRDGSQRRVCDDCK QQWWAKXNIPSGLHACTATL EETHILDSGAHVCPYFKQQLH VMRVPCTDYFDTQKNPNLSHL HGSWMAETAVINHKKRKNSPRI VQSNDLTEAAYSLSRDQKRML YLFVDQIRKSDGTLQEHDGICEI HVAKYAEIFGLTSAEASKDIRQ ALKSFAGKEVVFYRPEEDAGD EKGVESFPWIFKRAHSPSRGLY SVHINPYLIPFFIGLQN   15765   46133   B   15856   537   1318   15765   46134   B   15857   1   411		46129	В	15852	356		
15764   46132   A   15855   1   5828   MQEQQQASSLIRSGNGRLPGSG AQRTPCHIRRDGSQRYCDDCK QQWKAKYNIPSGLHACTATL EETHILDSGAHVQVFYKGQLH VMRVPCTDYFDTQKNPNLSHL HGSVMAETAVINHKKRKNSPRI VQSNDLTEAAYSLSRDQKRML YLFVDQIRKSDGTLQEHDGICEI HVAKYAEIFGLTSAEASKDIRQ ALKSFAGKEVVFYRPEEDAGD EKGYESFPWIFKRAHSPSRGLY SVHINPYLIPFFIGLQN   15765   46133   B   15856   537   1318   15765   46134   B   15857   1   411							
AQRTPCHIRRDGSQRRVCDDCK   QQWWAKYNIPSGLHACTATL   EETHILDSGAHVQVFYKGQLH   VMRVPCTDYFDTQKNPNLSHL   HGSVMAETAVINHKKRKNSPRI   VQSNDLTEAAVSLSRDQKRML   YLFVDQIRKSDGTLQEHDGICEI   HVAKYAEIFIGTSAEASKDIRQ   ALKSFAGKEVVFYRPEEDAGD   EKGVESFPWFIKRAHSPSGLY   SVHINPYLIPFFIGLQN   SVHINPYLIPFFIGLQN   13765   46133   B   15856   537   1318   15856   46134   B   15857   1   411   411							
QQWWKAKYNIPSGLHACTATL   EETHILDSGAHVQVFYKQCJH   VMRVPCTDYFDTQKNPNLSHL   HGSVMAETAVINHKKRKNSPRI   VQSNDLTEAAYSLSRDQKRML   YLFVDQIRKSDGTLQEHDGICEI   HVAKYAEJIFGLTSAEASKDIRQ   ALKSFAGKEVVFYRPEEDAGD   EKGYESFPWFIKRAHSPSRGLY   SVHINPYLIPFFIGLQN   13765   46133   B   15856   537   1318   13766   46134   B   15857   I   411	15764	46132	Α	15855	1	5828	
EETHILDSGAHVQVFYKGGLH			l			\	
VMRVPCTDYFDTQKNPNLSHL	1		l				
HGSVMAETAVINHKKRKNSPRI   VQSNDLIEAAYSLSRDQKRML   YLFVDQIRKSDGTQLEDHOGICE    HVAKYAEJIGLITSAEASKDIRQ   ALKSFAGKEVVFYRFEEDAGD   EKGYESFPWIRKAHSPSRGLY   SVHINPYLIPFFIGLQN   15765   46133   B   15856   537   1318   13766   46134   B   15857   1   411		l	l				EETHILDSGAHVQVFYKGQLH
VQSNDLTEAAYSLSRDQKRML   YLFVDQIRKSDGTLQEHDGICEI   HVAKYAEIRGLTSAEASKDIRQ   ALKSFAGKEVVFYRPEEDAGD   EKGYESFPWFIKRAHSPSRGLY   SVHINPYLIPFFIGLQN   13765   46133   B   15856   537   1318   13766   46134   B   15857   1   411			l				VMRVPCTDYFDTQKNPNLSHL
YLFVDQIRKSDGTLQEHDGICEI   HVAKYAEIRGLTSAEASKDIRQ   ALKSFAGKEVVFYPEEDAGD   EKGYESFPWFIKRAHSPSRGLY   SVHINPYLIPFFIGLQN   15765   46133   B   15856   537   1318     15766   46134   B   15857   1   411	1		ı	1	l		HGSVMAETAVINHKKRKNSPRI
HVAKYAEIRGLTSAEASKDIRQ   ALKSFAGKEVVFYRFEEDAGD   EKGYESFPWFIKEAHSPSRGLY   SVHINPYLIPFFIGLQN   15765   46133   B   15856   537   1318     15766   46134   B   15857   1   411	1		l				VQSNDLTEAAYSLSRDQKRML
HVAKYAEIRGLTSAEASKDIRQ   ALKSFAGKEVVFYRFEEDAGD   EKGYESFPWFIKEAHSPSRGLY   SVHINPYLIPFFIGLQN   15765   46133   B   15856   537   1318     15766   46134   B   15857   1   411	1		l				YLFVDQIRKSDGTLQEHDGICEI
ALKSFAGKEVVFYRPEEDAGD EKGYESFPWFIKRAHSPSRGLY SVHINPYLIPFFIGLQN 15765 46133 B 15856 537 1518 15766 46134 B 15857 I 411	1	1	1		l		
EKGYESFPWFIKRAHSPSRGLY	1	1	1		l		
SVHINPYLIPFFIGLQN	1		l		l		
15765         46133         B         15856         537         1318           15766         46134         B         15857         I         411	1				l		
	15765	46133	В	15856	537	1318	1
15767 46135 A 15858 I 1356	15766	46134	В	15857	ı	411	
	15767	46135	Α	15858	1	1356	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
		_				
15768	46136	A	15859	1	1215	MPYDRPFTVMAAFPLCPACDK
						EYRDPLDRRFHAQPVACPECGP
						HLEWLKMGKIVAIKGIGGFHLA
					i	CDARNSNAVATLRARKHRPAK
						PLAVMLPVADGLPDAARQLLT
						TPAAPIVLVDKKYVPELCDDIA
						PDLNEVGVMLPANPLQHLLLQ
						ELQCPLVMTSGNLSGKPPAISN
						EQALADLQGIADGFLIHNRDIV
						QRMDDSVVRE\RRNAAPF/AGA
						VLSQHLGDLSDDGIQMQWRER
						YSLMQNIYDFTPQYVVHDAHP
						GYVSSQWAREMNLPTQTVLHH
						HAHAAACLAEHQWPLDGGDVI
						ALTLDGIAQPDERSRSEDVDRA
						HQRGHERDRRRRRSGTSHLTR
İ				l		VDLKEDGKGLKIVRQSLPYGTA
			ĺ			SGTHGLYFCAYCARLHNIEQQL
						LSMFGDTDGKRDAMLRSPNR
15769	46137	В	15860	74	2050	
15770	46138	Α	15861	2	703	LQARFPLSWRNFPITFACYAGL
						FCLSASIIYP/DHLCPVSVPRAFA
						GPRHRRHLLVLHRGCGLRH/TK
						RPGPGPGPARALAIWPPDPGC*
						RCRRPSLPASSLRSSATPTCTST
						QPALEWCVAVYAICFILAAIAIL
				l		LNLGECTNVLPIPFPSFLSALAL
						LSVLLYATALVLWPLYQFDEK
						YGGOPRRSRDVSCSRRHAYYV
1				l		GAWDRRLAEAILTAINLLTYVA
						DLMHSAHLDFSKV
15771	46139	A	15862	I	849	MAQPLAKQWTPVSPRALLVSIS
1		1				SMPPRPAADVTVCRHRNCTLRE
		l	1			LLYGFAYAAAQQLNLHGDVCN
1		l	l	I		DGDG/VEVRLREDPETFLVQLY/
		l	l	I		QHCPPLA\RTGGTMNTQIVPDA
		l	l			ATCPASLSEMNTPGERRYRYPF
	1	l				INCTHYGPSFPIIRAMPYDRPFT
	1	l				VMAAFPLCPAC/DKEYRDPLDR
		l	1			RFHAOP/VACPECGPHLE/WGIG
						GFHLAC/DARNSNAVATLRARK
		1	l			H/RPAKPLAVMLPVADGLPD/A
	1	l	l			
	1	l	l			ARQLLTTPAGAGLWLGGNGYP
		l				RAPDNANSTAMSCASHAHSFG
1.5770	16140	l .	1,6062	l	2688	GGHPRGR
15772	46140	В	15863	1	2688	
15773	46141	A	15864	1	1578	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
15774	46142	A	15865	1	877	MQAAHRLRRAYRIKTÖKPPAL ADYHPAYQEMI.SRKQDRVIDQ IDFGIKDTVEILHMGQIQSMGRE FALSLRFSIHGHNVHGNESPEM GPERSGFYDEWSPERIIQYYRP AREQLMNELVQILKNTROHLM TGVSHMIPFVVSGGILLAVSVM LYGKGAVPDAVADPINLKILFD IGVAGLTLMVPFLAAYIGYSIA ERSALAPCAIGAWVGNSFGAGF FGALIDAPFRISEEINPALPEAK VMACLEAVARQDNVDSPQELP PTPLFASRPITRLKSWWAPGGE VESGTHKK
15775	46143	Α	15866	3	423	
15776	46144	A	15867	633	771	NNRSHPALCTNRPPRTRLVFYP LLAPNA*LAALQKGWAYGAGH NA
15777	46145	Α	15868	1	4014	
15778	46146	Α	15869	1	180	SGHPFIPLKDLTQIAIGDVFNNN LILWANREIIHSVP*RY*HDANI QCFVVISSFVRSQQ
15779	46147	A	15870	815	1905	IFQEHINDHLPMPKFGPLAGLR VYPSEMWRAEVIWIENVAWA DTIRVQPNYPQLSRRNLHALSL NIFKDEGREAFLKLMETTDIFIE ASKGPAFARRGITDEVLWEDKP KLVIGHLSGFAHQVSQISTHQG SSNWVSPDQLQCNTQTNSPKQ LESTHCMQCKPNSTTNSRQFQS NPVNIHALNHQSKPHHPLVYAQ LKAKRAHRAKSITASRKQATTF QQVGAPAGGHTHTSSHPQTT KALEQVKHLTTRQAILSKAKPQ TASPIPROTIGELGRGPHALNPS TTVIGQPANQRIGQHGPGPKP KTPEWPQPKEKVPNRQCTSKTY NLKQOPLNPGKAKT
15780	46148	А	15871	1	361	QTTGISFQGRGGAGPGVPTRTQ/ CLRCHGGRHG/HPSHLCKPNKG DPRKIRLKMSWR*PWFAIGPRD WSSSRPKPTSPRGSCRSFIEASK MSAPVVWSTKTHSSRSMLSFSL MEDFVTALSIL
15781	46149	Α	15872	1	447	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
15782	46150	A	15873		1424	MLLEQLSQHKLDMIISDCPIDST QOEGLESVRIGECGYSFWCTINP PPEKPFPACLEERILLIPGRRSM LGRKLLNWFINSQGLONVEILGEF DDAALMKAFGAMHNAIFVAPT LYAYDPYADKTYVEIGRYENV MEEYHAIFAERMIQHPAVORIC UTDYSALFSPALLRRALYHDA TELHPACGKDFRQLYRRIQNQI QRHALWHKIFDVEIPHPILIAR YSANMPHTOCRIAIEWPGKVVE AILRLTNDAPEYLPIGFNIKSK MRSEGMNPYQROFMELALSNQ VLKCGEFTLNRGRKSPYFFNAG LENTGRDLALLARFYAEALVDS GIEFDLLLAPAYKGIPHATTTAV ALAEHHDLDLPYCFNRKEAKD HGEGGRLVGSALQGRYMLVD DVTTAGTAIRESMEIIQANGATL AGVLISLDROEBGR*CDHRRNG DSRYDGDYSGQWRDACWRVD FARSSGTRARRDFGSOWRDACWRVD FARSSGTRARRDFGSOS*A*L QLQSDLYHHPERPDCLPGREAG
15783	46151	В	15874	1	1086	110010000
15784	46152	A	15875	484	729	CTQFRKTCFTCKASNGFCFATS CNLIYTSEIICRGPTG*HNLIASL LQRIDNLRKFIVIPTLKYLTRCR LDDNIMIFYAQGI
15785	46153	A	15876	1717	1971	PANAWAEMWEYSAWQRRMYS MG*TSKVVVHBGATDRW*NTN GCYRIFWIAAPFVPAAVIHGNIL PTHGACVHKGFGRAPAGAAVE
15786	46154	В	15877	1	765	
15787	46155	A	15878	103	823	VPACAGLKKEARSLLASPPRLL TITKLQASCRALFSPPIOSRQTTG ISFQGRGGAOFQVPIRTQCLRC HGGRHG/HPSHLCKFPNKODPRK IRLKMSWR*PWFAIGPROWSS RPRTSPRGSCRSFIEASKMSAP VVWSTKTHSSRSMLSFSLMEM PARMPITSSMSPTELRQGSVMF PARMPITSMSPTELRQGSVMF DFVTALSILLRGTVHEKLRWTF NLYDINKDGYINQEEMMDIVK AIYDMMGKYTYPVLKEDTPRQ

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X-Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \-possible nucleotide insertion)
15788	46156	A	15879	1	2926	MVKDASQSQASLGLDAFLPAS
ĺ						GVQYTHERSPDSPLKSQECPSG
						VVNEDTFKQIYAQFFPHGGLMS
				1		ENGTGKKASVFGSTGSGALLLE
		l				EGERRREQPLIEMRKPPHVLIN
						YQAKVGGNSIPSPSLCKPAFPPL
				1		PSWAVDLASARQKEDASRSLQ
						NKEEDFYTSQPGFPALALGCCL
						RVNLLLGHRGISAGSSYRPITST
						PCHLCKLGQEVFAKPLNLQDQ
						CQQNLVMQVLKLVLNCLNFDF
1			ĺ			IGSSADESADDLCTV
15789	46157	A	15880	1	1521	
15790	46158	Α	15881	1	1182	MDKFLDTYTLPRLNQEEVESLN
						RPITGSEIVAIINSLPTKKSPGPD
				l		GFTAEFYQRYKEELVPFLLKLF
				l		QSIEKEGILPNSFYEASIILIPKPG
}				l		RDTTKKENFRPISLMNIDAKILY
}				l		KILAKRIQQHIKKLIHHDQVGFI
ł				l		PGMQGWFNIRKSINVIQHINRA
1				l		KDKNHMIISIDAEKAFDKIQQPF
		1				MLKTLNKLAQNLLKLISNFNKV
						SGYKINVQKSQAFLYTSNRQTE
						SQIMSELPFTIASKRIKYLGIQLT
		1	l			RDVKDLFKENYKPLLKEIKEDT
						NKWKNIPCSWVGRINIVKMAIL
						PKVIYRFNAIPIKLPMTFFTELE
	ŀ					KTTLKFIWNQKRAHIAKSILSQ
				İ		KNKAGGITLPDFKLYYKATVT
						KTAWYCYQNRHIDQWNR\PSEI
						TPHIYNYLIF
15791	46159	Α	15882	1	690	
15792	46160	В	15883	I	458	
15793	46161	Α	15884	1	719	
15794	46162	В	15885	I	3552	
15795	46163	Α	15886	1	321	
15796	46164	A	15887	I	362	
15797	46165	В	15888	1	489	
15798	46166	В	15889	1	1660	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
15799	46167	Α	15890	11	1593	MGKKQNRKTGNSKKQSTSPPP
						KERSSSPAMEOSWMENDFVEL
						REEGFRRSNYSELQEDIQTKGK
					Ì	EVENFEKNLEECMTRITNTEKC
						LKELMELKTKARELHEECRSLR
						SRCDQLEERVSAMEDEMNEMK
	ĺ					REGKFREKRIKRNEQSLQEIWD
1		l		ŀ		YVKRPNLHLMGVPESDGENGS
1						KLENTLQDIIQENFPNLARINKI
						DRPLARLIKKKREKNOIDTIKN
						DKGDITTNPTEIQTTIREYYKHL
						YANKLENLEEMDTFLDTYTLPR
		1				LNQEEVESLNRPITGAEIVAIINS
1		1				LPTKKSPGPDGSIAEFYQRYKE
						E/PADKQLQQSLSIQNQCTKITS1
						LIHQQQTNREPNHE*TPIHNCFK
1		l				ENKIPRNPTYKGCEGLLPGELQ
1						TTAQGNKRGYKQTEEHSMLM
		l				GRKNQYRENGHTAQGNF*IQC
l		l				HPHQATNAFLHRIGKNYFKVH
		l				MEPKKSPHRQVNPKPKEQSWR
		l				HHTT*LQTILQGYSNQNSMVLV
1		1				PKQGYRSMEQNRALRNNAAYL
		1				QLSDL*QT*EKHAMGK/EFPI**
15800	46168	Α	15891	1	1177	
15801	46169	Α	15892	1	3663	
15802	46170	Α	15893	1	1995	
15803	46171	Α	15894	1	4191	MVKGSIQQEELTILNTYAAHTG
						APRLIKQVLSDLQRDLDSHTIIM
		l				GDFNTPLSTLDRSTRQKVNKDT
1						QELKSALHQADLTDIYRTLHIIK
		l				STEYTFFSAPHHIYSKIDHILGSK
		l		l		ALLSKCKRTEIITNYLSDHSAIK
		l				LELWIKNLTQNHSTTWELNNLL
						LNDYWVHNEMKAEIKMFFETN
1	1	l				ENKDTTYHNLWDTFKAVCRGK
1	1	l		I	1	FIPLNAHKRKQERSKIDTLTSQL
1		l				KELEKQEQTHSKASRRQEITKIR
		L				AELKEIETQ

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
15804	46172	Α	15895	I	1659	MGDFNTPLSTLDRSTRQKVNK
					Ì	DTQELNSALHQADLIDIYRSLH
l						AKSTEYTFFSAPHHTYSKIDHIL
					ĺ	GSKALLSKCKRTEIITNYLSDHS
					ŀ	AIKLELRIKNLTQNRSTTWKLN
ŀ						NLLLNDYWIHDEMKAEIKMFF
					ŀ	ETNENKDTTYQNLWDAFKATA
						SKTNKEKEKNQIDTIKNDKGDI
1						TTDPTEIQTTIREYYKHLYANK
1	l .					LENLEEMDKFLDTYTLPRLNQE
1	1			1		EVESLNRPITGAEIVAIINSLPTK
						KSPGPDGFTAEFYQRYKEELHI
i	1					NRAKDKNHMIISIDAEKAFDKI
						QQPFMLKTLNKLGIDGTYFKIIR
	1					AIYDKPTANIILNGQKLEAFPLK
	1			1		TGTRQGCPLSPLLFNIVLEVLAR
						AIRQEKEIKGIQLGKEEVKLSLF
					1	ADDMTVYLENPIVSAQNLLKLI
			1			SNFSKVSGYKINVQKSQAFLYT
						NNRQTESQIMSELPFTIASKRIK
	1					YLGIQLTRDVKDLFKENYKPLL
						KEIKEDTNKWKNIPCSWVGRIN
						IMKMAILPKVIYRFNAIPIKLPM
						TFFTELEKTTLKFIWNQK\RARI
15805	46173	A	15896		1740	AKAILSQKNEAGGITLP
15806	46174	A	15897	1	880	
15807	46175	A	15898	í .	2777	MGKKQNRKTGNSKKQSTSPPP
		1	,			KERSSSPAMEQSWMENDFVEL
1						REEGFRRSNYSELQEDIQTKGK
l						EVENFEKNLEECMTRITNTEKC
						LKELMELKTKARELHEECRSLR
1						SRCDQLEERVSAMEDEMNEMK
						REGKFREKRIKRNEQSLQEIWD
						YVKRPNLHLMGVPESDGENGS
	l					KLENTLODIIQENFPNLASTLSD
						HSGIKLEINSKRNPONHANTWK
				1		LSNLLLNAHWVNNEIKMKVKN
						FFELNDNSDTIYQNFSD
15808	46176	Α	15899	326	3096	QTERTSTPKTHLYVTIIKDQK*I
	1					KPQRRGKNRGEKLETLKSRAP
						VLLQRNAVPQQQRNKAGRRM
				1		TLTS*EKKSSDNQTTPSYRRKF
l	1	1	1		1	KPMAKKLKTL/RKKLDECITRIT
						NAEKCLMELMELKAKARELRE
	1	1	1			ECKSLRSQCNQLEER\INKIDRP
	1		1			LARLIKRKREKNQIDAIKIDKGD
						ITTOPTEIQTTIREYYKHLYANK
				l		LENLEEMDKFLDTYTLPRLNQE
	1	1	1		l	EVESLNRPITGAEIVAIINSLPTK
				1		KSPGPDGFTA
		_				

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hed	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \*=possible nucleotide insertion)
15809	46177	Α	15900	li .	2047	MENDFEELREEGFRRSNYSELR
						EDIQTKGKEVENFEKNLEECITR
i		l				ITNTQKCLKELMELKTKARELR
l					1	EECRSLRSRCDQLEERVSAMED
l						EMNEMKREGKFREKRIQRNEQ
i						SLQEIWDYVKRPNLRLIGVPET
l						LHPRDEAHLKNLIDAIKNDKGD
l						ITTDPTEIQTTIREYYKHLYANK
İ	1	l				LENLEETDKFLDTYTLPRLNQE
l						EVESLNRPITGSEIVAIINSLPTK
l	1	ł				KSPGPDGFTAEFYQRYKEEL/PD
i	1					KQLQQSLRIQNQCTKITSILIHQ
i	İ	ĺ		1		QQTNREPNHE*TPIHNCFKENKI
	i					PRNPTYKGCEGPLQGELQTTAQ
ĺ	1					GNKRGYKQMEEHSMLMGRKN
ĺ	1					QYHENGHTAQGNLQIQCHPH*
	1	l				ATNAFLHRIGKNYFKVHMEPK
	1	ł		1		KSPHRQVNPKPKEQSWRHHTT
	1			ļ		*LQTILQGYSNQNSMVLVPKQR
	i					YRSMEQNRALRNNAAYLQLSD
	i	1				L*QT*EKQEMGKGFPI**MVLG
	İ	l		l		KLASHM*KAETGSLPYTLYKN
	l	1				QFKMD*RLKR*T*NHKNPRRKP
	1					RHYHSGHRHGQGLHV*NTKSN
						GNKSQN*QMGSN*TKELLHSK
i						KKKNY*QTEQATCKMGENFHN
						LLI*QRANIQNLQ*TQTNLQEKN
	1		1	ŀ		KQPHQKVGKGHEQTLLKRRHL
				l		CSQK\NHEKMVTITGHQRNAN
						QNHNEIPSHAS*NGNH*KVRKQ
				l		VLERMCRNRNTFTLLVGL*TSS
15810	46178	Α	15901	1	3285	
15811	46179	A	15902	1	3681	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nuclentide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	eodon for last amino acid	*=Stop codnn, /=possible nucleotide
	sequence	ı	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
15812	46180	Α	15903	1	1854	MKAEIKTFFETNENKDTTYONL
		1		ŀ		WDAFKAVCRGKFTALNAHKR
		l				KQERSKIDTLTSQLKELEKQEQ
		l				THSKASRRQEITKIRAELKEIET
		l				QKALQKINESRSWCFEKIHKID
		l				RPLARLIKKKREKNQIDAIKND
		l				KGDITTDPTEIQTTIREYYKHLY
		ı				ANKLENLEEMDKFLDTYTLPRL
						NQEEVESLNRPITGSEIVAIINSL
		1				PTKNSPGPDGFTAEFYQRYKEE/
		l				RENKIPRNPTYKGCEGPLQGEL
		ı				QTTAQGNKRGYKQMEEHSML
İ		1				MGRKNQYRENGHTAQGNLQIQ
		1				CHPHQATNDFLHRIGKNYFKV
		1		1		HMEPKKSPHRQVNPKPKEQSW
		1		l		RHHTT*LQTILQGYSNQNSMVL
1		1				VPKQRYRSTEQNRALRNNATY
		1		ļ		LQLSDL*QT*EKQAMEKGFPI**
		1				MVLGKLASHM*KAETGSLPYT
				ļ		LYKNQFKMD*RLKR*T*NHKN
		1				PRRKPRHYHSGHRHGQGLHV*
				l		NTKSNGNKSQN*QMGSN*TKE
		1				LLHSKRNYHQSEQATYKMGEN
		1				FRNLLI*QRANIQNLQ*TQTNLQ
		1		l		EKNKPPHQKVDEGHEQTLLKR
		1				RHLCSQKTHEKMLIITGHQRNA
		1				NQNHNEIPSHTS*NGNH*KVRK
		1		i		QQVLERMWRNRNTFTLLVGL*
15010	46101	<u></u>	15904		2718	TSSTIVEVSVV
15813	46181	B A	15904	1896	5031	TWKGTTSTSRCKIMPKYRSTRO
15814	40182	l <sup>A</sup>	13903	1890	3031	KVNKDTOELNSALHOADLIDIY
		1				RTLHTKSTEYTFFSAPHHTYSK
		1				TDHIVGSKALLSKCKRTEHTNY
		l				LSDHSAIKLELRIKNPTOSRSTT
		l		ŀ		WKLNNLLLNDYWVHNEMKAE
		1	1			IKMFFETNENKDTTYONLWDT
		l				FKAVCRGKFIALYAHKRKQERS
		l	i	İ		KIDTLTSQLKELEKQAQTHSKA
1		l	1	l		SRROEITKIRAELKEIETOKTL\Q
			ĺ	ĺ		KINE\SRSWFF\ERINKIDRPLAR
1		l	l			LIKKKREKNO
15815	46183	A	15906	4	133	LIGUIGERING
13013	C0101	I**	13300	<u> </u>	1.50	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	eodon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	İ	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
15816	46184	Α	15907	95	1875	PFFGRKNYRLPSKNMPRRCRSS
						PLPCSMKMTI*CVLTSTATITRL
						PAASAQW*LDGRTLVTKNSFR
				l		YLHTLHTMGPAPEPNLTILWSE
						ELPIAFKKYAAQVSIVTSSLQYE
				l		NDDLMRTDFNSDDYAIACCVS
	į	1		l		PMVIGKQMQFFGARANLAKTL
				l		LYAINGGVDEKLKIQVGPKTAP
		1		l		LMDDVLDYDKVMDSLDHFMD
		1				WLAVQYISALNIIHYMHDKYSY
		l		l		EASLMALHDRDVYRTMACGIA
		1			1	GLSVATDSLSAIKYARVKPIRD
		1				ENGLAKDIQGTTEPQFRNSHSR
1		1				TSGTVTLYLPVSTFVGTGFFIRV
		1		1		DPPKKPLKIRKIEFVEIYEPFSEG
						QAKAQADRCLSCGNPYCEWKC
		1				PVHNYIPNWLKLANEGRIFEAA
		1	İ	ŀ		ELSHQTNTLPEVCGRVCPQDRL
		l				CEGSCTLNDEFGAVTIGNIERYI
		l	İ			NDKAFEMGWRPDMSGVKQTG
		l	1	l		KKVAIIGAGPAGLACADVLTRN
l		1				GVKAVVFDRHPEIGGLLTFGIP
						AFKLEKEVMTRRREIFTGMGIE
						FKLNTEVGRDPRASSFYEEKQL
		ŀ				IARKALPFIDNKTTMAADSSST
						VMELLKLLQDRSGLTLLTNSAE
1						AIHVLAQSEIKVVSTGGELNKN
	1					TLSLQGRITKEIIRRYHVDIMWL
	1					PDELRVEKGFSPDTLKLLEAKG
						QKVALKEAMGSTQSIMVGPDE
	46105	_	1.5000	071	0110	RRTGFSYLRYQNLMIRVKF
15817	46185 46186	B A	15908	271 597	2118	
15819	46187	A	15910	573	1066	IRAQNGSPWLSFLVDSVCVLKA
13019	40107	1	13710	373	1000	CVDAVMRAGICSVS\YWQYQS
						GVGANSSALSGFSOGAIMMLES
i						IKAEPGLASRVIAFNGRYSSLPE
1		1			i	TASTATTIHLIHGGEDPVIDLAH
1		1				AVAAQEALISAGGDVTLDIVED
1		1				LGHAIDNRSMQFALDHLRYTIP
						KHYFDEALSG
15820	46188	A	15911	1	2652	
15821	46189	В	15912	1	1494	
	1	드	1	L		l

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
15822	46190	A	15913	li .	1733	MGVGSKGTIFGSTTTQHGSFIPY
			i			LTGYLTYTHGHSPANPKPAVG
1						GOILTAVLPAHDGYVSRIMTM
1						NTOLTTPLTTATHTAROTASLIS
						VIGRQLRCFRHSSQPSVLTHVR
						DDSTQYAQLDMANGQPTSHGY
				1		EHWAOLMYATDRRYGRHMSD
						AARQGCSDTGIVKFSHPEPEMS
				1		VRKFTSARSGCVRSGAWNVTV
						SAQTRVSQALTTLLRRVHKSPM
1						NALTVPAVMAEAPSOAHGRRO
1						TRRLSLHQTLRLLLTTPDWVGV
						IRRCVPVVWGCLEHLDTAGFPL
				1		PNSHTMPLPIGWNDTRKRLHHS
						AHNGQHDVAQGRRVLGRKVG
1						LTHPKVQQQLGVDGLSLFCVY
	1					LVWYIGLHLRRPFRLAYTICPSL
1					i	VYGADLRVIVRLFSDSHHFMAF
1				ł		GNPQPKHLDCQEYALFLLNSM
						PDNTAEHYRNKIAIYLHCLPED
			ĺ	ŀ		DRIKAINEIRMAIHQVSPFREEP
				ł		VDCVLWVKYSQLMPNDYNPN
				1		NVAPPEKKLLQKSIEIDGFTQPI
				į .		VVTHTDKNAMEIVDGFHRHEI
				ŀ		GKG/SHASLKLRLRGYLPVTCL
						EGTRNQRIAATISHNRARGRHH
					l	ITAMSEVTPELRLLGW
15823	46191	В	15914	I	273	
15824	46192	В	15915	169	292	
15825	46193	A	15916	2	844	KGGVYKTSVSVHLAQDLALKG
				ł		LRCLLWKGT\PPQGTPSMVSRE
				l		GDPALHN*CKTQLLCLSYLGEK
						DDVTYAIKPTCWPGLDIIPFCLA
						LDRIETEL\MGKFDEGKLPTDPH
	'			1		LMLRLAIETVAHDYDVIVI\DSA
				1		HNRG\IGTINVVCAADVLIVPTP
				ł		VE\MFDYTSALQFFDMLRDLLK
				1	1	NA\DLKGFEPDVRIFVTKYSNSN
		1		l		GSOFP\WMEEPIPECLPKHGSKK
				l		NNVRNANEVGKGQIRMRT\VFE
						OAIDORSSTGAWRNALSIWEPV
1		l	1	l		CN/EIFDRLIKPRWEIR
	L			L	L	CITIES DICIKI KWEIK

15826   46194   A   15917   I   681   MSIGGSGNSLCTRPKQQQGGT   LKQYEVSVPGTLRCLACPQAC   LKREHWHFAPKSNYDSCRYIE   EYFAYEASFMSVQTELVIKSS   EPLASLEMHIKKNPVSIPHTVW   YADDIRRGEREAADVLGLTLY   LMLRAGEAAPDVLGTLY   LARAWGIDDTLAGESDKPHF   HWLVLCGHGNNGGDGYVVAI   LARAWGIDDTLAGESDKPHF   LARAWGIDTLAGESDKPHF   LARAWGIDDTLAGESDKPHF   LARAWGIDTLAG	SEQ ID	SEQ ID NO:		SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
15826   46194   A   15917   I   681	NO:		hod			codon for last amino acid	
IS826   46194   A   IS917   I   681   MSIGGSGNSLCTRPKQQQGGT   LKQYEVSYPGTLRCLACPQAC   LKKEHWHFAPKSNYDSCRYIE   EYFAYEASHMSVQTELVIKSE   EPLASLEMHIKKNPVSIPHTVW   YADDIRRGEREAADVLGLTLY, LMLRAGEAAPDVLGTLY, LMLRAGEAAPDVLGTLY, LMLRAGEAAPDVLGTLY, LMLRAGEAAPDVLGTLY, LMLRAGEAAPDVLGTLY, LMLRAGEAAPDVLGTLY, LMLRAGEAAPDVLGTLY, LAMPASSEHLIAN   GWPESEHLIV		sequence		09/540,217		of peptide sequence	deletion, \"possible nucleotide insertion)
LKQYEVSVPGTLRCLACPQAC LEKREHWHFAPKSNYDSCRYIE EYFAYEASFMSVQTELVIKSI EDLASLEMHKKNPVSIPHTVW YADDIRRGGERADVLGLTLY LMLRAGEAAPQVCRSAYPDTR HWLVLCGHGNNGGDGYVVAF LAKAVGIDDTLAQESDKPJPE EAPLAHEAWVNAGGEHALNI GWPESEHLIV 15827 46195 A 15918 3 774 VKCSEKCLFLPLGQFSOFIQKL VIFLDPLFIRKQQGVTPTAFAM HLHEVISQGLESILGALDIEGSS DKQRITITATTPSVGALVLPVIN RAIKTHYPQLLLRIPPISDARM LSQFGTDLIDNMFCTNRTVQ-H HGLFAANMVLICREGNPLLSLI DDREAIANAAHVLLIPEQMPS GLRQRVQEMPFGRQINFTSYNI LTIAALVANDDMALIPSRLYNI PSRCWPLEKLPHPSLNEQIDF: HYNKFSLR 15828 46196 A 15919 I 741 MITVLLIATQFAPYFTEMALKC GFSFAGESAQISALSVGNMFGV SISELMSLGIGGVVAVGVIVASV VLFLRVLSMSWLKEVIGTEKA* IAMCHLRALPGOPSFDAQLGM NWVIDKAWDDLMALQNGGVI AMFINERSLPYLTKGLVPALV ARELLVRGMYVRGRMVAFLI CCVALAISAMYELIEWWAALA MGQGADPHLGTGQDQWDTGS GYVLRAAWRINDGDIPRSLSLF PATALWLDNRI MVIDKAWDDLMALQNGGVD VMFSNESLPYLTKGLVPALV MGQADPHLGTGQDQWDTGS GYVLRAAWRINDGDIPRSLSLF PATALWLDNRI MVIDKAWDDLMALQNGGVD VMFSNESLPYLTKGLGVPALV MGRINGFGGDGWDTGGGGVDVVMGGGVDV VMFSNESLPYLTKGLGVPALV MARIIGQLMSDIRIPFGVNVLW DPVASFDLAMATGAKFRIEFT MARIIGQLMSDIRIPFGVNVLW DPVASFDLAMATGAKFRIEFT GAYANDFGVWDTNVGETIRHET GAYANDFGVWDTNVGETIRHET GAYANDFGVWDTNVGETIRHET					sequence		
LEKEHWHIFAPKSNYDSCRVIE EYFAYEASFMSVQLTELVIKSL EDLASLEMIHKKNPVSIPHTYW YADDIRRGEREAADVLGITLY LMLRAGEAAFQVCRSAYPDTS HWLVLCGHGNNGGDGYVVAI LAKAVGIDDTLLAQESDKPLP EAPLAHEAWYNAGGEHALNI GWPESEHLIV VKCSEKCLFLPLGQPSQFIQKL NIFELDPLFIRRQQVTPTAFAM HILIEVISQGLESILGALDIEGSY DKQRTITIATTPSVGALVLPIVI RAIKTHYPQLLLRNPPISDAEN LSQFQTDLIIDNMFCTNRTVQH HGLFAANMVLLCREGONPLLSL DDREAIANAAHVLLPEQQNF GLRQVQEMFPGQNIFTSYN LTTIAALVANDMLAIPSELYNI PSRCWPLEKLPHPSLNEEQIDF: HYNKFSLR  15828 46196 A 15919 I 741 MITVLLIATQFAPYFTEMALKC GFSFAGESAQISALSVGNMFGO SISELMSLGIIGVVVAVGIVASV VLFLRVLSMSWLKEVIGTEKA IAMCHERALFOOPSFDAQLGM NWVIDKAWDDLMALONGGVI AVMFSNEESLPYLTKGLVPALA MGQADDFLGTQGQWDTTOS GTYLRAAWRINDGDIPRSLSLE PATALWLDNRI  15829 46197 A 15920 I 678 MCHLRALFGDPSFDAQLGMN WVIDKAWDDLMALONGGVI VMFSNESLPSTLTKUPFETTAA MARIIGGLMSDIRIPFGVNVLW DDVASFDELAMATGAKFIEIFT GAYASDFGVWDTNVGETIRRIET GAYASDFGVWDTNVGETIRRIEFT	15826	46194	Α	15917	1	681	MSIGGSGNSLCTRPKQQQGGTG
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DDREAIANAAHULLIPEGONFI GLRQRVQEMFPGRQINFTSYNI LTIAALVANSDMLAHIPSRLYNI LTIAALVANSDMLAHIPSRLYNI PSRCWPLEKLPHPSLNEEQIDF: HHYNKFSLR  15828 46196 A 15919 I 741 MITVLLIATQFAPYFTEMALKC GFSFAGESAQISALSYGNMFGV SISELMSLGHIGGVVAVGIVASS VLFLRVLSMSWLKEVIGTEKA IAMCHERALFGOPSFDAQLGM NWVIDKAWDDLMALONGGVI AVMFSNEFSLPYLTKGLVPALV AREILVRGMYVRGRKMVAFLI CCVALAISAMYELIEWWAALA MGQADDFLGTGGODWDTOS GYVLRAAWRINDGDIPRSLSLF PATALWLDNRI  15829 46197 A 15920 I 678 MCHLRALFGDPSFDAQLGMN WVIDKAWDDLMALONGGVD VMFSNEFSLPYLTKVRFETTAA MARIIGOLMSDIRIPFGVNVLW DDVANSTELABLYTKVRFETTAA MARIIGOLMSDIRIPFGVNVLW DDVANSTELABLYTKVRFETTAA MARIIGOLMSDIRIPFGVNVLW DDVANSDFSLAMATGAKFIREIFT GAYASDFGVWDTNVGETIRHEIFT GAYASDFGVWDTNVGETIRHEIFT	l		l				LSQFQTDLIIDNMFCTNRTVQH
GLRQRVQEMFPGRQINFTSYNI LTTAALVANSDMLAIIPSRLYNI			ĺ				HGLFAANMVLICREGNPLLSLE
15828 46196 A 15919 I 741 MITVLIATQFAPYFEMALKG GFSFAGESAQISALSVGNMGV SISELMSLGIIGVVVAVGIVASV VUFLRVLSMSWLKEVIGTEKA IAMCHERALFOOPSFDAQLGM NWVIDKAWDDLMALQNGGVI AVMFSNEESLPYLTKGLVPAL) AREILVRGMYVRGRKMVAFLA CCVALAISAMYELIEWWAALA MGQGADPLGTQGQWDTOS GYVLRA WEINDGDIPRSLSLE PATALWLDNII 15829 46197 A 15920 I 678 MCHLRALFGDPSFDAQLGMN WVIDKAWDDLMALQNGGVD VMFSNESLPYLTKUFVALA ARRIGQLMSDIRTPGVNVLW DVAFSTELSHYLTKVRFETTAA MARIGGLMSDIRTPGVNVLW DDVASFDLAMATGAKFREIFT GAYASDFGVWDTNVGETIRHEIFT GAYASDFGVWDTNVGETIRHEIFT	1		1				DDREAIANAAHVLLLPEEQNFS
FSRCWPLEKLPHPSLNEEQIDF:   IHYNKFSLR	1		1				GLRORVQEMFPGRQINFTSYNI
IHYNKFSLR	1		l				LTIAALVANSDMLAIIPSRLYNL
15828 46196 A 15919 I 74I MITVLILATOFAPYFTEMALKC GFSFAGESAQISALSYGNMFOV SISIELMSLGIIGGVVAVGIVASV VLFLRVLSMSWLKEVIGTEKA IAMCHERALFODFSFDAQLGM NWVIDKAWDDLMALONGGVI AVMFSNEFSLPYLTKGLVPALV AREILVRGMYVRGRKMVAFLI CCVALAISAMYELIEWWAALA MGGADPLGTGGDQWDTOS GYVLRAAWRINDGDIPRSLSLF PATALWLDNRI MCHLRALFGDPSFDAQLGMN WVIDKAWDDLMALONGGVD VMFSNEFSLPYLTKVRFETTAA MARIIGOLMSDIRIPFGVNVLW DPVASFDLAMATGAKFIREIFT GAYASDFGVWDTNVGETIRHEIFT GAYASDFGVWDTNVGETIRHEIFT GAYASDFGVWDTNVGETIRHEIFT GAYASDFGVWDTNVGETIRHEIFT	1		i		ļ		FSRCWPLEKLPHPSLNEEQIDFS
GFSFAGESAQISALSVGNMFGV SISELMSLGIIGVVVAVGVGVASV VLFLRVLSMSWLKEVIGTEKA* IAMCHLRALPGDPSFDAQLGM NWVIDKAWDDLMALQNGGVI AVMFSNEFSLPVLTKGLVPALJ AREILVRGMYVRGRKMYAFLI CCVALAISAMYELIEWWALAL MQGADDFLGTQGDQWDTQS GYVLRAAWRINDGDIPRSLSLF PATALWLDNRI 15829 46197 A 15920 I 678 MCHLRALPGDPSFDAQLGMN WVIDKAWDDLMALQNGGVD/ VMFSNEFSLPYLTKVRFETTAA MARIIGQLMSDIRIPFGVNVLW DPVASFDLAMATGAKFIREIFT GAYASDFGVWDTNVGETIRHEIFT GAYASDFGVWDTNVGETIRHEIFT			1				IHYNKFSLR
SISELMSLGIIGVVAVGIVASV VLFLRVLSMSWLKEVIGTEKA IAMCHLRALPGDPSPDAQLGM NWVIDKAWDDLMALQNGGVI AVMFSNEFSLPYLTIGLUPAL) AREILVRGMYVRGRKMVAFLV CCVALAISAMYELIEWWAALA MGGADPLGTGQDQWDTOS GYVLRAAWRINDGDIPRSLSLF PATALWLDNRI 15829 46197 A 15920 I 678 MCHLRALPGDPSFDAQLGMN WVIDKAWDDLMALQNGGVD VMFSNEFSLPYLTKVRFETTAA MARIIGGLMSDIRIPFGVNVLW DPVASFDLAMATGAKFIREIFT GAYASDFGVWDTNVGETIRHEIFT GAYASDFGVWDTNVGETIRHEIFT	15828	46196	Α	15919	I	741	MITVLLIATQFAPYFTEMALKG
VERRVLSMSWLKEVIGTEKA* IAMCHLRALPGDPSFDAQLGM NWVIDKAWDDLMALQNGGYU AVMFSNEFSLPYLTKGLVPALV AREILVRGMYVRGRKMVAFLI CCVALAISAMYELIEWWAALA MGGOADPLGTGODQWDTQS GYVLRAAWRINDGDIPRSLSLY PATALWLDNRI MCHLRALPGDPSFDAQLGMN WVIDKAWDDLMALQNGGVD VMFSNEFSLPYLTKVRFETTAA MARIIGQLMSDIRIPFGVNVLW DPVASFDLAMATGAKRIEIT GAYASDFGVWDTNVGETIRHET GAYASDFGVWDTNVGETIRHET			1		Į	1	GFSFAGESAQISALSVGNMFGW
IAMCHLRALPGDPSFDAQLGM NWVIDKAWDDLMALQNGGVI AVMFSNEFSLPYLTKGLVPAL) ARBILVRGMYVRGRKMYAFLI CCVALAISAMYELIEWWAALA MGGADDFLGTQGDQWDTGS GYYLRAAWRINDGDIPRSLSLF PATALWLDNRI 15829 46197 A 15920 I 678 MCHLRALPGDPSFDAQLGMN WVIDKAWDDLMALQNGGVD/ VMFSNEFSLPYLTKVRFETTAA MARIIGQLMSDIRIPFGVNVLW DPVASFDLAMATGAKFIREIFT GAYASDFGVWDTNVGETIRHEIFT GAYASDFGVWDTNVGETIRHEIFT			1				SISELMSLGIIGVVVAVGIVASV
NWVIDKAWDDLMALQNGGVI AVMFSNEFSLPYLTKGLVPALV AREILVRGMYVRGRKMVAFLI CCVALAISAMYELIEWWAALA MGGADDFLGTGGDQWDTGS GYVLRAAWRINDGDIPRSLSLF PATALWLDNRI  15829 46197 A 15920 I 678 MCHLRALPGDPSFDAQLGMN WVIDKAWDDLMALQNGGVD. VMFSNEFSLPYLTKVRFETTAA MARIIGOLMSDIRIPFGVNVLW DPVASFDLAMATGAKFIREIFT GAYASDFGVWDTNVGETIRHEIFT GAYASDFGVWDTNVGETIRHEIFT			1		Ì		VLFLRVLSMSWLKEVIGTEKAV
AVMFSNEFSLPYLTKGLVPALI AREILVRGMYVGRKWAFLI CCVALAISAMYELIEWWAALA MGGGADDFLGTQGDQWDTQS GYVLRAAWRINDGDIPRSLSLF PATALWLDNRI 15829 46197 A 15920 I 678 MCHLRALPGDPSFDAQLGMN WVIDKAWDDLMALQNGGVD, VMFSNEFSLPYLTKVRETTAA MARIIGQLMSDIRIPFGVNVLW DPVASFDLAMATGAKFIREIFT GAYASDFGVWDTNVGETIRHEI GAYASDFGVWDTNVGETIRHEI			1				IAMCHLRALPGDPSFDAQLGM
AREILVRGMYVRGRKMVAFL CCVALAISAMYELIEWWAALA MGQGADPIGTQGDQWDT0g GYVLRAAWRINDGDIPRSLSLF PATALWLDNRI 15829 46197 A 15920 I 678 MCHLRALPGDPSFDAQLGMN WVIDKAWDDLMALONGGVD VMFSNEFSLPYLTKVRFETTAA MARIIGQLMSDIRIPFGVNVLW DPVASFDLAMATGAKFIREIFT GAYASDFGVWDTNVGETIRHEIFT	i			i			NWVIDKAWDDLMALQNGGVD
CCVALAISAMYELIEWWAALA MGQGADDFLGTQGDQWDTQS GYVLRAAWRINDGDIPRSLSLF PATALWLDNRI  15829 46197 A 15920 I 678 MCHLRALPGDPSPDAQLGMN WVIDKAWDDLMALQNGGVDV VMFSNEFSLPYLTKVRPETTAA MARIIGQLMSDIRIPFGVNVLW DPVASFDLAMATGAKFIREIFT GAYASDFGVWDTNVGETTRIAF	l		1				AVMFSNEFSLPYLTKGLVPALV
MGQGADDFLGTQGDQWDTQS GYVLRAA WRINDGDIPRSLSLE PATAL WLDNRI 15829 46197 A 15920 I 678 MCHLRALPGDPSFDAQLGMN WVIDKA WDDLMALQNGGVD, VMFSNEFSLPYLTKVRFETTAA MARIIGQLMSDIRIPFGVNVLW DPVASFDLAMATGAKFIREIFT GAYASDFGVWDTNVGETIRHEI	1		1				AREILVRGMYVRGRKMVAFLV
GYÝLRAA WRINDGDIPRSLSLF PATALWLDNRI 15829 46197 A 15920 I 678 MCHLRALPGDPSFDAQLGMN WYIDKA WDDLMALONGGVD. VMFSNESLPLYLTKVRFETTAA MARIIGOLMSDIRIPFGVNVLW DDVASFDLAMATGAKFIREIFT GAYASDFGVWDTNVGETIRHÉ	1		1				CCVALAISAMYELIEWWAALA
PATALWLDNRI  15829 46197 A 15920 I 678 MCHLRALPGDPSFDAQLGMN WVUDKAWDDLMALQNGGVDV VMFSNEFSLPYLTKVRPETTAA MARIIGQLMSDIRIPFGVNVLW DPVASFDLAMATGAKFIREIFT GAYASDFGVWDTNVGETTRHE	1		1				MGQGADDFLGTQGDQWDTQS/
15829 46197 A 15920 I 678 MCHLRALPGDPSFDAQLGMN WYIDKAWDLMALONGGVD/ VMFSNESLPLYLEVRPETTAA MARIIGQLMSDIRIPFGVNVLW DPVASFDLAMATGAKFIREIFT GAYASDFGVWDTNVGETIRHE			ı		1		GYVLRAAWRINDGDIPRSLSLP
WVIDKAWDDLMALQNGGVD/ VMFSNEFSLPYLTKVREETTAA MARIIGQLMSDIRIPFGVNVLW DPVASFDLAMATGAKFIREIET GAYASDFGVWDTNVGETIRHQ	1		1				
VMFSNEFSLPYLTKV\\(\text{PETTAA}\) MARIIGQLMSDIRIPFGVNVLW\) DPVASFDLAMATGAKFIREIFI\(\text{GAYASDFGVWDTNVGETIRHG}\) GAYASDFGVWDTNVGETIRHG	15829	46197	Λ	15920	I	678	MCHLRALPGDPSFDAQLGMN
MARIGGLMSDIRIPFGYNVLW DPVASFDLAMATGAKFIREIFT GAYASDFGVWDTNVGETIRH			l				WVIDKAWDDLMALQNGGVDA
DPVASFDLAMATGAKFIREIFT GAYASDFGVWDTNVGETIRHO			l				VMFSNEFSLPYLTKVRPETTAA
GAYASDFGVWDTNVGETIRHQ	i		l				MARIIGQLMSDIRIPFGVNVLW
			l				DPVASFDLAMATGAKFIREIFT
HRIGAGEVKTLFNIVPEAAVYL	1		l		l		GAYASDFGVWDTNVGETIRHQ
	1		l				HRIGAGEVKTLFNIVPEAAVYL
GNRDICSIAKSTVFNNHPDALC	1		1	l	l		GNRDICSIAKSTVFNNHPDALC
VSGLTAGTRTDSALLKRVKET	1		1		l		VSGLTAGTRTDSALLKRVKETV
			1				PDT\VVLANTGVCLENVEEQLSI
ADGCVTATTF			_				
	15830	46198	Α	15921	624	734	TRTLRQIVDSRAIPFT*ERLHSPI
NOPKNDVDESV	1	I	I		l	1	NQPKNPYPPESV

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nuclcotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
					<u> </u>	
15831	46199	Α	15922	I	1923	MPFALGGGDLEETPRSDPGVTF
		ļ				ACSLAQPMRKPTGVLGNRFHD
1						TQEPPVPGGPGLRGFHLWHAPP
		1				LDRPAQFAAIRTDSELMSSANP
						KSFTASPLMTFTPARSRINYRY
1			İ			YPAGTRAKGENEAAFAARIHSF
1	i	l	ĺ			LPYRRPVFWATTMGQAKSAIK
1						PMSTAVTRDASVFQTEYERSRF
		l				GARPWPLRKAPEAMGRGFHEI
			1	ì		GVQCEAPTANTLEPSRRGAVM
		l		l	l	AAGLSFQRTPWREVLGRGEGSF
		1				LGAGSDPVLRALSLASTPFPGE
		1		ŀ	ŀ	KHVGSWGMGRIVLRSFALASSS
		1		l		LRHSGERIPGTVLPCDDIFACHQ
						RNYAEVFGIWRTTSSVLOPIEPV
		ľ		i		EPKCISQFLYIVLERRSSSSLISLS
				l		FNSASLCRSRHDARYVLQHALF
				i		CFTTNDFGQIFTTFFVSGGSGTR
1					1	MSLPAEFGVIAQSDQKVLFIDA
				i		DLAVVIRITCLPSTSMSWLKEVI
				1		GTEKAVI/AMCHLRALPGDPSF
						DAQ/LGMNWVIDKAWDDLMA
1		i				LKMVRPETTAAMARI/IGQLMS
1						DIRIPFGVNV/LWDPVASFDLA
1		1				MATGAK/FIREIFTGAYASDFGV
		i		1		/WDTNVARSRRIRASTVFRLAQ
		1				RCOPDASEYGFRMIARVFVDVR
		l				GDONSEASLRVGSGIGPRTCAP
						VAWQSRRFPRLLDRSDDVKRF
						QADTDSLVLH
15832	46200	A	15923	480	900	KTRYSCRGETWSNPQSSQLSAL
1.5552	1.0200	'		1.00	1	IAAVRHPATSNAVCRSARSCCIL
1		1		l		RALRAIOFHTGCSAGNVAPEW
	l			1		CQFAPCWRKPLK\EESDSVFMR
		1		1		VIKESLWOELADITDKTOLEWR
	1			l		EVFQDLNHHGVYHSGEVVGLG
				ŀ		NLVCEKCHFH
15833	46201	A	15924		431	SKVFAVAGCVVLMTTMPDSCN
13833	40201	Ι^	13924	l'	451	SWOKCRNKTMNKKIHSLALLV
				ł		,
1		1		I		NLGIYGVAQAQEPTDTQAPGVS
1		1		1		TITADEIRKNPVARDVSKIIRTM
1		ı	İ			PGVNLTGNSTSGQRGNNRQIDI
1						RGMGPENTLIL/IDGKPVSSRNS
		-			10.00	VRQGYRLECGDG
15834	46202	В	15925	1	1352	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
15835	46203	Α	15926	31	546	CYCILFVSFPSNRPLCCRSAGVC
						ORYTPDPFCLGITSRGCRRAKIT
		ŀ				ACSFLWKLHPRGALARCOPELS
		ŀ				CWRCLST\LLEGVSPSGGTGVR
				ļ.		DPYEEAVCPLAELKCCAGRSA
						VLFRAGROGRLSLLKLFPOLPF
		l				SPCVLCLSKLVPVSPNSTRTSKL
				•		LSIPYSRGPALLEVLS
15836	46204	A	15927	2	479	
15837	46205	Α	15928	1082	1386	ADPFQEREAEKYANPIPSREFIL
1				1		EHLTKREKPASRDELAVELHIE
			ŀ	l		GEEQLEGLRR/RQCYALPERLD
İ						LVKGTVIGHRDGYGFLRVEGR
				1		KDDLYLS\SEQMKTC
15838	46206	Α	15929	3	40I	
15839	46207	В	15930	1	3675	
15840	46208	Α	15931	1749	1941	SQIPTSEAQVMSNLMGTNGVLR
1					•	PARAYRNEAVLS*ALVSAMYS
						QTFRNASFGVPQMFSTTSGV
I584I	46209	Α	15932	5	1465	KRSTTAQIRWISPLTSLKPRSKR
						QSKSCATKPKKWYVAAPCCWC
						SPTGISLKTRLPVPAPMAVGAIQ
				l		TRLVDQSLRCDANIIVETASAR
				l		DPHHFAVLLGFGATAIYPYLAY
						ETLGRLVDTHAIAKDYRTVML
						NYRNGINKGLYKIMSKMGISTI
						ASYRCSKLFEAVGLHDDVVGL
ĺ						CFQGAVSRIGGASFEDFQQDLL
	t					NLSKRAWWRCRLSATIGCCDC
						TRGYLGGARITGQISSITVWGVI
						IPVVGLCIIGWFWFSPTLYVDS
						WNPHHAPFFSAVGSSIAMTLW
						AFLGLESACANTDVVENPERN
						VPIAVLGGTLGAAVIYIVSTNVI
						AGIVPNMELANSTAPFGLAFAQ
l		1				MFTPEVGKVIMA\LMEMSCAGS
		1				ILGGKFTIAQVFKSSSDEGYFLT
						IFSRVTKVDAPVQGMLTIVIIQS
		1	1			ELALMTISPSLNSQLKEMVNLA
						VVTNIIPYILSMAALVIIQKVAN
		乚				VPPSKAKVANFVAFVGARNSF
15842	46210	A	15933	I	3666	

SEQ ID NO:	SEQ ID NO: of peptide		SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
15843	46211	Α	15934	979	1626	FSATITPPFIALQRVRFHPLDAL
						LLFVISLWLQLGLPDELSRFTPF
						CLALPIIALAWHYGWQGALIAT
		1				LMNAIALIASQTGLLLGAGIQR
						LRELNQSLQKELARNQHLAERL
						LETEESVRRDVARELHDDIGQT
		1				ITAIRTQAGIVQRPGAGHPLTDA
						GNGAGRARYCQPSRMANR*IS
		l				VKRKVVEHRCFVDFTFTNDDG
						AVNVDRRAVRGVFIAAS
15844	46212	С	15935	1	666	\
15845	46213	Α	15936	I	1137	MGKFGHTEIGEVDVRDWSDAL
1						QAKELQKLPGHSRKLEDPPTSL
						FMLLNPHSDQFSSNAHHHLHA
						TAIDDDYTDPTKSTYALGLNWS
						NSILGGFNISGYKTYSYDGDND
						SSNLNINWNKAFKHATVSVNW
						QHQLSASENNEDDGDLFYVNIS
						IPFGRSNTATLYTRHDDHKTHY
		l		ļ		GTGVMGVVSDEMSYYVNAER
	İ					DHDEPTLPAQNKAQEVLLDVV
						LDEAKIGVASMLGSRVRVKTW
1				ŀ		SWFADDKQEIRQGGFAGWLTD
		l				GTPLWVTGSGTSKTVLTRYAT
ļ		1				VLNRVLPVPTQVASGQCVEVE
1		l		ŀ		LFARYPLKKITAEKSTTAVNPG
				ŀ		VLNGRYRVTFTNGNHITFVSHG
		l				ETTLLSEKGKLKLQSHLDREEY
		_				VARVLDREAK\STPP
15846	46214	Α	15937	323	695	FTGPRRSLEIEVAELKQRLDSLL
						AIGAGGSVCWTLQGAWSPTRA
						KAGELKTQLATAASLR/MDKH
	1		i			RSNSVGPHDLYFTLLDDYLHV
1		1				VDTALWLSGGKASLDGGTLLT NDAGEMLFAEHHFSAGPL
15847	46215	١.	15938	I	235	NDAGEMLFAEHHFSAGPL
15847	46215	A	15938	98	593	MSKVRLMRNLSPAPPNAVAKG
13848	46210	A	13939	98	393	ESKPGIMSGWVF*AEWAYLITG
						*AKKKVYGSS/ARIHLRALRYY
1		l				SNWROYFAGYTFGROYWOSPE
		l		ļ		DDHLPLLREFLARHEYMQKYL
		1				LGTESGIQGEELGASDGIKPEEV
		l	l	1		EWQTAAIEGKLDLLVTLDFRM
		1	1			SSTCLFSDIVLPTAT
15849	46217	A	15940	367	677	LSSCLRATQSAPAVRNWKARFL
13849	1021/	l^	13940	J**	l°′′	RCTVVVWQKRSSTGRNMYLPV
		1				RPTILKLRPTWHVTW*LSGASL
1						RNWVHCCTRKKKVKCSSAVA*
1		1				RKRNICPMKLHVSSTRK
			<u> </u>	L	l	KKKINICTIVIKLEI VOOTKK

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
15850	46218	Ā	15941	1	921	MEMSSLEFLHSICSHLKCHLLY
13030	10210	ľ.,	1.57	ľ	12.	YIASAYNYDWYTOPAKLSFISE
i		l				GEIKYFTDKOMLRDFVTTRPAL
İ			İ			KELLKEAVNMERRNRWVDIGP
						GTELDCISQAYAQFVASTAECC
						GEGGIKAWDYVRMGFLSRMG
						VLNNWLTRRRKLLWSARSRIH
						LRALRYYSNWROYFAGYTFGR
		l	İ			QYWQSPEDDHLPLLREFLARYE
						RPMKKLAGRSSIAILAFRGHDQ
		l				RDYEFPSKSALNIN*LRWALAS
						VK*TTACATGVFPVSVTGARRF
15851	46219	Α	15942	531	637	SIFARLNASRRC*TSALYALLVR
						LPIIQITAKGIL
15852	46220	В	15943	120	881	
15853	46221	Α	15944	1	1583	MADRVDSKCSRSRPGAVAHNY
		1				NPSTLGGRGGRITFWLLSANPSI
		1				NRGTLEKESRTVAQRLSVLHGI
						NAPEFFDKAVFSSLVLTLRDEG
						YISDSGDAEPAETMKVYQLLAE
		l				LITSDLMIFNISATVLYITAFIAC
						SAAVDLTSLRGTRPYNQRAAA
						SKEIEDLKKKLTEGEEISGCDVS
						GSDGDDNEEGKIGEDEEKRNT
						GGNKVFPERTVETPATADAER
						KALETKLDVEEETRLQLNSRNR
						KKDLKTRQEHQSLPEKFSGLQK
						NVLLEAVIDPALIAQLRQAYEE
						AL\RIAQAPAKSVWQPEEYEEA
						EHEILLAFRALLASDSERFLPSA
1						WQRFIQQLNYCSMEEIDELRWS
						LCTIAMNTAHLSFECVVLLAER
						LRWLQEENTGEIDEEELESFLY
						AIAKGNVFNFQTILHLPVAVQN
l		1	1	l		DTIDFYQMFARIWLPGAPGAYC
				i		DGLHTSKRTTCTTSTHQRQRKD
1		l		l		TPPALNPHTATCTPPHTWLGAP
				l		PPASMRSGPHNAPTPPFTGSTPR
L				L		HTHDHTNITNANIPHNVNSN

SEQ ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Uuknown,
NO:	of peptide	hod	in USSN	Incation of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
		_				
15854	46222	Α	15945	1	1228	MGVLNNWLSEEESLWIQSRIHL
		l		l		RALRYYSNWRQYFAGYTFGRQ
						YWQSPEDDHLPLLREFLARYER
ľ						PMKNCWKILDIEETTDVDIIRRA
				l		YLALLPSFHPETDPQDFKQLRQ
						AYEEALRI\AQSPAKSVWQPEE
						YEVAEHEIL\LAYRALLASDSER
						FLPSAWQRFIQQLNYCSMEEID
1		1			1	ELRWSLCTIAMNTAHLSFECVV
1		l				LLAERLRWLQEENTGEIDEEEL
						GSFLYAIAKGNVFNFQTILHLPV
	1					ARRPDICTOHNDOSRCEGYOIL
1		l				SDKRGHOHGGGITALYOCGNA
1		l				DPRAKGERLFFDAPAKDSTQTR
						AEDAHYAGSNNMSPPDQQGDG
		1				RKQIWESVRVHTPVRCQQRSLP
			1			VTSYLNGGEIFNLIGLICRTRRIA
		l				ARWVKSHRNRARSFECLKRHR
ı		1				FVVAFNRRKPGLV
15855	46223	A	15946	71	323	AAGAVVSAMPKAKGKTRROK
13833	40223	<u>۱</u> ^	13940	l''	323	FGYSVNRKRLNRNARRKAA\R
1		1			İ	GSNDLEAEASLPEKKGNTLSRD
1						LIDYVRYMVENHGEDYKVSGS
15856	46224	A	15947	48	627	AAGAVVSAMPKAKGKTRROK\
15856	46224	I <sup>A</sup>	13947	48	027	FGYSVNRKR\MSRNAKRKAAR\
1	1		1			
						GLECSHIRHAWDHAKSVRQNL
						AEMGLA\VDPNRA\VPSRKRKV
						KAME\VDIEEEA*KNLYRKPYV
						LNDLEAEASLSEKKGNTL\SRD
	1					LHLTMYRYMV\ENHGE\DYKAI
		l				A\RD\EKNYY\QDTPKQI\RS\KIN
i				i		VYKRFYPAEWQDFLDSLQKRK
	-					MEVE
15857	46225	Α	15948	796	1301	LTKKDYISPNARKAFVQRLPER
1				I		NLLTRGLKRQRQPCLSCWCGG
1		1				QARMPKAKG\KTRRQKFGYSV
						NRKRLNRNARRKAAPRIE/CVR
		1				GLGFRVAVGLGRDGPRDDGSA
1		1				MSLFAGSSHIRHAWDHAKSVR
1		1		1		QNLAEMGLAVDPNMAVPLRK
				I		RKVLTWQGLGPCLLYSSPAILT
15858	46226	Α	15949	512	675	SQDFGPPSAAPSPSGMP\PGPSG
		1				CSSHRQQEDPPDGAAAPPGHGL
						RPGRLQELLV
15859	46227	В	15950	1	717	· ·
11.000	1	_		L	L	L

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	coden for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
15860	46228	A	15951	587	1387	RARSRILGNPLRPLAPAPSNDV
						GVQRA\FRPIRCRKAQPVPGSV
						ANRRILROHTRPDPLGTNRSEP
						GWWDRSWSPDQAKSGQSCVA
						KIKNKNHMIISTDSEKAFDKIOH
						RFMIKTLSKISIQGTHF\KIIKAIC
						DKLTANIILNGEKLKAFPLRTE
						MROGCPRLSLLFNIVLEVLAKA
						IRQEKEIKDIQIAKEEVRLSLFA
						DDMIVYLENPKDSFRKLLELIK
						EFSKVSGYKIKNOYCENDHTA
						VSGVGSFQWICGLADVKNEAA
15861	46229	A	15952	3	3201 ·	SERGFRAGDLRYPTHFLSTNSV
13801	40229	l <sup>A</sup>	13932	3	3201	LASVTASLKEHPRGTLLSDGSP
1						ALSRNVGMTVSOKGGPOPTPSP
1				ļ		AGPGTOLGPITGEMDEADSAFL
				ł		KFKQTADDSLSLTSPNTESIFVE
						DPYTASLRSEIESDGHEFEAES
						WSLAVDAAYAKKQKREVVKR
				ļ		QDVLYELMQTEVHHVRTLKIM
						LKVYSRALQEVL\QFISTAIGRL
1						FPCADDLLETHSHFLARLKERR
						QESLEEGSDRNYVIQKIGDLLV
		_				QQFSGENGDRLIEK
15862	46230	В	15953	83	1969	
15863	46231	Α	15954	1	444	SSESAVEFSEPASGSSPSWELGS
						EGAIRDKKTSLGAHVGLSALGR
						ALENTIAFQGKETDVQKSYDSP
						QGDCL\QDVKGKRPTLE*PSLE
						NPETRRFLDASYAWRESCLSW
						HHHTAHDIFAGKPVDPLPGSTR
		_				GQDSAVCSQGQFLIVR
15864	46232	Α	15955	2	236	SEGAKRDKKTSLGAHVVLSAL
1		l	l	l		GRALEKTIAFQGSS/APSKGRKL
1						RSRKVMTRPKGIAWQDVKGKR
						PTLE*PSLENPEVR
15865	46233	Α	15956	1	459	KKVGNYYTTPIYRFRMKCHLC
1		l				VNYIEMQTDPANCDYVIVSGA
		l		l		QRKEERWDMADNEQVLTTGE
		l	1	l		RHPLTCLGAL/DPESALGPPKPS
1		l		l		RALIVAEHEKKQKLETDAMFR
				l		LEHGEADRSTLKKALAHT\DHI
				1		QEAQSAWKDDFALNSMLRRRF
		l		l		REKKKA

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
15866	46234	A	15957	564	1189	AAPKMGERKGVNKYYPPDFNP
15866	46234	Α.	13937	364	1189	EEAWLSSTDYHNSHPFRERASG
		l				SCSQGI\LIIRFEMPYNIWCEG\C
		j				
		1				RTNFGMGVRYNAEKKKVGNY
l				1		YTTPIYRFRMKCHLCVNYIEMQ
						TDPAN\FDYVIVSGAQRKEERL
1		1				GHWRTMNRLLTHRGIEEEAEA
1						WKTDAMFRAGTMGRPTAAHF
		l				KKALPKLEPHSGRPRAPWKDD
						FALNSMLRRRFRVPSKP
15867	46235	Α	15958	2	1047	FVDGKLHGRGSTDDIGPVAGWI
						NALEAYQKTGQETPVNVRFCL
		1		l		EGMEESGSEGLDELIFARKDTF
						FKDVDCVCISDNYWLGKKKPCI
ļ						TYGLRGICYFFIEVECSNKDLHS
						GVYGGSVHEAMTDLILLMGSL
ŀ		ł				VDKRGNILIPGINEAVAAVTEEE
1				İ		HKLYDDIDFDIKEFAKDVGAQI
						LLHSHKKDILMHRWRYPSLSLH
		l				GIEGAFSGSGAKTVIPRKVVGK
1		ı				FSIRLVPNMTPEVVGEQVTSYL
		l				TKKFAELRSPNEFKVYMGHGG
i						KPWVSDFSHP\HYLAGRRAMK
						TVFGVEPDLTREGGSIPVTLTFQ
		1		i		EATGKNVMLLPVGSADDGAHS
1		l		1		QNEKLNRYNYIEGTKMLAAYL
15868	46236	Α	15959	163	1388	RLVERWRPSGTLFKYIDENQDR
		l				YIKKLAKWVAIQSVSAWPEKR
		l				GEIRRMMEVAAADVKQLGGSV
		l				ELVDIGKOKLPDGSEIPLPPILL\
		İ				GRLGSDPOMKTVCIYGHLDVO
		l				PAALEDGWDSEPFTLVERDGLT
		1		1		WCSSCRGPYCRGSS/DRLSWKL
		1				PSVMWGDSREPHLARLD\HPSG
		1				LEPORPGSTWGGGDDRRGGRA
		1		1		LSROLPYAGYAAAOCKGEVRP
i		l				OVSSSRLVVECSNKDLHSGVY
		l				GGSVHEAMTDLILLMEEHKLY
		1		I		DDIDFDIEEFAKDVGAQILLHSH
		1		1	1	KSHLHLDLLPVVVRLLGQALFH
		l		1		TAHFPDNIPSSSKDILMHRWRY
				i		PSLSLHGIEGAFSGSGAKTVIPR
		1				KVVGKFSIRLVPNMTPEVVGEO
1		1				ACGAGTRESMSSLGYPSRAED
		1			1	
	<u> </u>				L	DSGLSALPSQPQPFILYAT

SEQ ID NO:	SEQ ID NO: nf peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
15869	46237	А	15960	3	433	FETLFSQVQLFISTCNGEHIRYA TDTFAGLCIQLTNALVERKQPL RGIGILKQAIDKMQMNTNQLTS IHADLCQAITTPAMAVSHIMLE SYKKYILVSLILLGKVQQLPKY TSP/QLVGRFIKPLSNA\YHELR HKLIVSTNNPC
15870	46238	A	15961	46	1481	TSGSDVAAREDLRWIAAAPPPR AAAFSRACCLRRSGRPGENMA SALEQFVMSVRLLLSQGGSCFP GQMTQLCELIMMSGELLAKNLS ALEQFVMSVRLLLSQGGSCFP GQMTQLCELIMMSGELLAKNLS LLDTVLGALDDVQEHSLGVLA VLEVKFSMPSVPDFETLFSQVQ LEISTCNGEHIRYATDTWQETV LLKSMVLVLVYJYQPLRGIGIL KQAIDKMQMNTNQLTSHADL CQLCLLAKCKFAALPYLDGDM MDICKENGAYDAKHFLCYYYYQ AITTPALMAVRHILWWESYKKY ILVSLILLGKVQQLPKIFHLKLY GMIYTGLKNFERALYFYGV GYPLSLLSNAYHELAQVYSTN NPSELRNLVNKHSETFTRDNN NGLVKQCLSSLYKKNIQRLTKT FLTLSLQDMASRVQLSGPQEAE KYYLHMIEDGEIFSNIQKDGM VSYFHDNPEKYNNPAMLHNIDQ EMLKCIELDERLKAMQGITVN
15871	46239	В	15962	1	3411	
15872	46240	Α	15963	689	925	
15873	46241	Α	15964	I	244	GSAPQSCASPAPVSRSAAPGTA EAAEPWAIVPGVEQKNYYVCV PLGLIGNCTVTSSG\\SLDCADW CLKWKSILMESLEVP
15874	46242	Α	15965	469	604	
15875	46243	A	15966	286	433	
15876	46244	A	15967	4356	4643	DCPLARNKSKPQTVCLKARQTF QAINFSRALRITGYLTSFPSLSRS TLPSSAGDFRASAWA*SGPTV* TLTSVPSVGINSSYIYEPVFRTLL SGE
15877	46245	В	15968	1	1472	L

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
15878	46246	A	15969	918	1619	KITHULSWGSPKSTWKAGWLQ KOKTTOEKKAESKAPIEEPAG AGLNKDKETEERSDGERVAEV APEERENVAVAKLQESQFONA VSCSGGRRKEDEREDWGKRTQ RTHPPAAAQAPGQCPPGSTEVG AGGGLRWTPSPGRQPAGVAAD MGITVLTVPLQRCLQNSWAKE PVLVVSFVIGSLTVILPPLSPYTK YSIMINEATPHYPYPVPHDDON
		l				M/PDMCSHPQGPQGPSLEWL
15879	46247	В	15970	183	459	
15880	46248	A	15971	864	1197	GSFRLGHGRIPPFHLRGMKESL GPDFGDPCPVCPLNSGPGPP\GV SAGGAGAGCGGMGRRDAWVP TGPVAESPGGHLAPISPGRQGA PWGGPCGQLGAGTLGQAVCG MTQDP
15881	46249	Α	15972	1	441	
15882	46250	Α	15973	3	182	
15883	46251	Α	15974	23	475	PLEKGRQFYPQYEDQITIFTDYL EEYPDTDELVWILWKQHLLKT EKSKLLSDISARLWFTYRRKFSP /ILGGTGPSSDAG\WGCMLRCG QMMLA\QAL\ICRHLGRDWSW EKQIEQPQEYQRILQCFLNRKD CCYSIHQMAQMGVGEGKSIGE
15884	46252	Α	15975	224	418	
15885	46253	A	15976	743	1220	WCWGHRVRLVLAAGPSSRGVL LLLVVLPSWASFLVRVCAWVG VLGDDGVLGGFLLWLGVVGRP LAVLRADLAVCVGVVCACVPF VVLPICAALVRVGCSLVEAALG \LGARPLKTFFAVVVPLTKGGV VAGSMLVFVPAVGEFVIPELLG GPDSIVIGRV
15886	46254	A	15977	3	3492	RKHKVGILYCKPÖQSSEEMSN NEEAGPAFEKFLSLIGEKVCLK GTTKYAAQLDVKTDSTGTHSL YTMYQDYEIMFHVSTLLPYTFN NROQULRKRHIGHDIVTILPOEP GALPFTPKNIRSHFQHVFIIVRV HNPCTDNVCYSMAVTRSKDAP PFGPIPPSGTTFKSDVFRADLA AKVI*RLRNAAEQVPTSFTPWA TRTRQEYLKDLAENCVSNTPID STGKFNLISLTSKKKEKTKARA GAEQHSAGAIA
15887	46255	В	15978	402	2884	

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	ol peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \*possible nucleotide insertion)
15888	46256	Α	15979	294	1721	AVRPGRHDPSAGLRSAAAASQ*
				l		VRGHPGGLCA*GSIQGPGASAA
	i i	1		l		EGPPAHSRAA*SKGGAELRTR*
		l		1		AGGRRPAGPHAQRP*LP*GPRV
		l		l		PLRPPSGTFLLP/PPACTPITSRPS
		l		l		*KSCSRASTPPTWSS*IPASGTSF
	l		1	1	i	GMVRTPGEA\PGEPGEPVPVPG
		1				PGAARVLPPGVE/PRPCLWARK
	1			1		SPGVFFRPSSGGRRPPS*KTKWS
	1	l		Ì		KPTSTAPPR\P*T*LRCTGLAFPL
		1		l		PPREGEPALGRGALEWTCAPLP
	1				LPAAAGPRGRRLGCGAAPPPPR	
					GRVDQEEK\PGPRVEGPPQANR	
	l				NHPALPLSPPLPSPT/*PPPAWVP	
						TPALAAAPAPVPTA\$SSHSPSPG
	İ	1				NAPVPTGSPRCLFFLRPYFPVGS
					ILLPFRCPLISPCRFLRRRQFYG	
					WSSAAYALLPHTPLSAACPSGP	
		1		1		TTALHGQPQSSCSCCQEATFTV
	1	l				KSGVVQSGRPSLRQFYVHDFCK
	1	l				IQPQQLLVSHATTKATTDRYST
		1				ASCVAR
15889	46257	В	15980	35	314	
15890	46258	A	15981	1	197	
15891	46259	A	15982	3	3889	
15892	46260	В	15983	172	287	
15893	46261	Α	15984	8	166	
15894	46262	Α	15985	250	1095	
15895	46263	A	15986	366	870	NHSLAKKGTAHGLGMEKCCGR
	i			I		SPFFSFFPSWIAKPTLRSSSSWPH
				l		SSSSPSMSSPLQRAVGDT\KRAL
						SASSSSSASLPFDDRDSNHPSEA
						CTTPGGGWEVADGNTDSLLAD
						EGSDFEDSFNRNVKKKAAKRPF
						KTTPV/AKQPKKGSRVVHRHSR
		L_				KQSEPPANDLFNAV
15896	46264	Α	15987	30	229	ALETNIGSSYNYGSEDQAEFLC
		1	1	l		VVSKELHSTPNGLSSESSRKTK\
						CYKPEAPGCEAPDHLQGLGVPI
15897	46265	С	15988	1	930	
15898	46266	Α	15989	1	609	

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence	1	09/540,217	sequence	or peptide sequence	decidon, (-possible nucleotide insertion)
15899	46267	Α	15990	1	875	MRMEAGEAAPPAGAGGRAAG
						GWGKWVRLNVGGTVFLTTRQ
						TLCREQKSFLSRLCQGEELOSD
				Ì		RDETGAYLIDRDPTYFGPILNFL
		ŀ		}		RHGKLVLDKDMAEEGVLEEAE
		l		İ		FYNIGPLIRIIKDRMEEKDYTVT
1						Q\VPPKHVYRVL\QCQEEELTQ
1		l		l .		MVSTMSDGWRFEQLVNIGSSY
İ				ł		NYGSEDQAEFLCVVSKELHSTP
				[	i	NGLSSESSRKTKSTEEQLEEQQ
		l		Ì		QQEEEVEEVEVEQVQVEADAQ
		l l				EKGSRPHPLRPEAELAVRASPR
		1		Į.		PLARPQSCHPCCYKPEEPGCEA
		1				PDHLQGLGVPI
15900	46268	Α	15991	1	2448	MRRGETRSRRPPQCWAFAHVV
		l				SRSSRRGEFFSFDRWKKHRSEV
1				l		RESAQVPTTKREPVLFQHKINIK
1		l				IVIALVDILFALGLGNLVCVSPV
1		l		1		QLFSVQTDSRATGDQRLPSWT
		1				AQRYGTRTLGPDGFTERCPYGP
	1	l		Ì		SPESLLCSALPWLRDLGMPVAE
İ		l				APQVAGGQGDGGDGEEAEPEG
İ		l				MFKACEDSKRKARGYLRLVPL
		ļ				FVLLALLVLASAGLEMLSDPGS
1		1		İ	i	RSYGSGLLPAWAKCPKAPHQR
		1		l		SLIPPDYAPGVNHPPPQERCSM
1		1		ŀ		GLRTQGTLGRHRVLSAQQVAF
				1		SVSLLMAKIAFAKQKSDDIIPDF
		1		l		KLFMVTLVHRPNRLSARVLTM
		l		ł		VPVLPAPCPMLLPLLEGYKAEV
		1		l .		MVSQVYSGSLRVLNRHFSQDL
1		1		i		TRRESSAFRSETAKAQKMLKEL
1		l	ł	l		ITSTRLGTYYNSSSVYSFGEGPL
		l	l	l		TCFFWFILQIPEHRRLMLSPEVV
		l		l .		QALLVEELLSTVNSSAAVPYRA
		l				EYEVDPEGLVILGQYCEWKPPG
1		l				RRMQTPRPAMRMEAGEAAPPA
			l			GAGGRAAGGWGKWVRLNVG
1		l		1		GTVFLTTRQTLCREQKSFLSRL
		l	l			CQGEELQSDRDETGAYLIDRDP TYFGPILNFLRHGKLVLDKDMA
1		l				
		1	1	l		EEGSQVWTVTSGGWGDRNAV
						LTGMGRALSLFLWLIQYLKFCL
		1	l	1		VRAWVLEEAEFYNIGPLIRIIKD
						RMEEKDYTVTQVPPKHVYRVL
		L_			l	QCQEEELTQMVSTMSDGWRFE

SEO ID	SEO ID NO:	Mct	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last aminu acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
15901	46269	Α	15992	li -	573	MPGLLSRPRRGSLRARPCGGGE
		ŀ				ALPEHVAIDVCPGPIRPIQQISG
						YFPHFPRDLPHDAPARPATASA
			ŀ		i	GRRRPSDGARDHDKDGDHLFG
		1				SLTIQHRPW/PAPSPDFPFTPFAV
			ŀ			LYPG\LKPMDHNGLADPCVKL
		l				HLRPGARKVPEACQLAPDLQD
			l			SSCLTAITKAHDVLTVFLPAAL
l	i					KIQGNKYLTFIECQKLF
15902	46270	Α	15993	500	2022	WTREKEPPGVETHGKASRTTL
		l			i	GLSLWCCLHLSEIQSSFISDCAR
			l			PRCSGRLPGSGPMLLATPHVLA
l						TVVASSCSKQLWWLPPKVATD
						QQQMKLKGLFIAGAPPGSPR/G
						VQPHLQPIRNMSVSRTMEDSCE
						LDLVYVTERIIAVSFPSTANEEN
İ						FRSNLREVAQMLKSKHGGNYL
l						LFNLSERRPDITKLHAKVLEFG
						WPDLHTPALEKICSICKAMDTW
		l				LNADPHNVVVLHNKGNRGRIG
		l				VVIAAYMHYSNISASADQALD
						RFAMKRFYEDKIVPIGQPSQRR
		ł	1			YVHYFSGLLSGSIKMNNKPLFL
						HHVIMHGIPNFESKGGCRPFLRI
						YQAMQPVYTSGIYNIPGDSQTS
ĺ		l				VCITIEPGLLLKGDILNSEILFGV
						DELSLTGFGLKCYHKKFRSPAR
		l				DVIFRVQFHTCAIHDLGVVFGK
						EDLDDAFKDDRFPEYGKVEFVF
						SYGPEKIQGMEHLENGPSVSVD
				1		YNTSDPLIRWDSYDNFSGHRDD
						GMEGAQHPQIGQDTPPGPSDPP
15903	46271	Α	15994	171	720	LSGSSÄGKVAAPCVPPSNHELV
					1	PITTENAPKNVLDKGERPSRGG
		l				NTRKSLE\TTASTGSPR/GVQPH
ŀ		l				LQPIINMNVSRTMEDSCELGPV
		l				YRTERNIAVSFPSTANEENFRSN
l		1	1			LREVAQMLKSKHGGNYLQRN
i		1	l	l	1	VSL/RRLSPSLRHPGPWPPSQEP
				l		GMCQGEPGPPATLWPMPCGPT
		_				VLESPGGPGP
15904	46272	В	15995	145	972	

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1			sequenee		
15905	46273	A	15996	2	1096	WPVLTAAGCWLQDPAGHRGG
13903	40273	^	13990	1	1090	RAGGAGRAVLFQLQAGRAELR
1	1	1	1			
						GLRARGWARSWAPAPGCQRTG
						RDAAAAGRRAGRAGALLGFTC
				1		LLLAALCGHLGPSWRGGLAPG
						GEWIWLRASETRGPSGPRPALM
ļ.						GSQKIRNITRTRHGPLHWLHSG
					·	CTTATPFCLTRSCSDAACSLKG
						LPCLCPCGLSVLIRVRLELRRHQ
ŀ						RAGHTIPRIFQAVVQRQPERLA
			ļ			LVDAGTGECWTFAQLDAYSNA
1			1			VANLFRQLGFAPGDVVAIFL/E
						GRPEFVGLWLGLAKAG/MEAA
						LLNVNLRREPLAF/CLGTSGAK
l						ALIFGGEMVRAPPPNAQAPPLT
						PVSPADRLFYIYTSGTTGLPKA
		1				AIVVHSSARPSCPSSRTLRAAHR
15906	46274	Α	15997	397	597	SIKSPEIHSPSTRIRMGCSSLPTE
1						EAHAEGVIELSRIKCVEIVKSD/
1	ł					DRIPCHYKYPFQVSPSGGSSP
15907	46275	Α	15998	1922	3886	EGDNKLRPRIRRKLFPLVVLRG
1			l			DAQGAPPFKNWIMNNFILLEEQ
		l				LIKKSQQKRRTSPSNFKVRFFVL
						TKASLAYFEDRHGKKRT\RKGS
		1				IELSRIKCVEIVKSDISIPCHYKY
1		1				PFQVVHDNYLLYVFAPDRESR
1	1					QRWVLALKEETRNNNSLVPKY
1	İ	1		i i		HPNFWMDGKWRCCSQLEKLA
ı						TGCAQYDPTKNASKKPLPPTPE
	1					DNRRPLWEPEETVVIALYDYQT
		ı				NDPOELALRRNEEYCLLDSSEI
	1					HWWRVQDRNGHEGYVPSSYL
	İ					VEKSPNNLETYEWYNKSISRDK
						AEKLLLDTGKEGAFMVRDSRT
1						AGTYTVSVFTKAVVSENNPCIK
1						HYHIKETNDNPKRYYVAEKYV
1						FDSIPLLINYHQHNGGGLVTRL
1						RYPVCFGRQKAPVTAGLRYGK
						WVIDPSELTFVQEIGSGQFGLV
		ı				HLGYWLNKDKVAIKTIREGAM
ľ	1	ł				SEEDFIEEAEVMMKLSHPKLVQ
Į.		ļ				LYGVCLEQAPICLVFEFMEHGC
		1				LSDYLRTQRGLFAAETLLGMCL
1		1		ŀ		DVCEGMAYLEEACVIHRDLAA
		1				RNCLVGENQVIKVSDFGMTRF
1		1				VLDDQYTSSTGTKFPVKWASPE
		1				VFSFSRYSSKSDVWSFGVLMW
1		1		1		
		1		1		EVFSEGKIPYENRSNSEVVEDIS
		1				TGFRLYKPRLASTHVYQIMNHC
15005	14000	1	1.5000	-	1506	WKERPEDRPAFSRLLRQLAEIA
15908	46276	В	15999	58	1526	

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				Sequence		
15909	46277	Α	16000	3	378	GASPDLGGRVLGAGASAESPR
						GRPFGPSPLGGPPVPGCQCAAP
						SLRDPWGLWAPVLQMTGSYEF
	į	l		ŀ		KLNQPPEDGISSVKLSPHTLPSP
						GLSPSWET\SVRLYDV\PGNFM
						AVKYQ\HTGARPGNGPF
15910	46278	В	16001	83	2851	
15911	46279	Α	16002	296	1186	AENHPGP\LVVEGKMTAPERM
						KHESNYLRGTIAE\NLNDGLTG
						GFKGANFLLIRFHGMYQQDDR
						DIRAERAEQKLEPRHAMLLRCR
		ļ				LPGGVITTKQWQAIDKFAGENT
						IYGSIRLTNRQTFQFHGILKKNV
						KPVHQMLHSVGLDALATAND
		1				MNRNVLCTSNPYESQLHAEAY
		l				EWAKKISKQLLPRTRAYAEIWL
		i		1		DQEKVATTDEEPILGQTYLPRK
		l				FKTTVVIPPQNDIDLHANDMNF
		1				VAIAENGKLVGFNLLVGGGLSI
		1	l			EHGNKKTYARTASEFGYLPLEH
						TLAVAEAVVTTQRDWG
15912	46280	Α	16003	225	386	GLCIPVVRSPCQLWGQKGPCM
		1				LRDEGRVFT*LSTKKNCPGNMR
						RKYETVDCRR
15913	46281	A	16004	386	739	PLLIHWRFATIEEADDHRLAAG
						ARTFQ/PLCGPPQAQAVWR*AQ
ļ.						*FQFADRFPASRWRRASSGRRF
		l	1			SRSGRARRCQSVAKRRRQIHEC
		ı				GRSTPDCRCRMRQQYRCCRDA
						RRYQNRAPRR
15914	46282	В	16005	10	1468	
15915	46283	Α	16006	3	1267	GRSRR**PPSAVPHD\PAVQRER
		1				DTQSLSVII*MQIYNFSNTTHLT
		l				NHNTFLTFHKTFTAETFQHIGP
	1	1				QPTTDTPYHTAEAYCCQLVKLI
						RRQALRRCWQGAAILKCNSKP
l	l	l			l	TNHCTS

sequence 09/540,217 eulon for peptide of peptide sequence deteiton, \square period of peptide sequence deteitor, \square period of peptide sequence deteitor, \square period of peptide sequence deteitor, \square period of peptide sequence deteitor, \square period of peptide sequence deteitor, \square period of peptide sequence deteitor, \square period of peptide sequence deteitor, \square period of peptide sequence deteitor, \square period of peptide sequence deteitor, \square period of perio	n, /=possible nucleotide sssible nucleotide insertion)  FRALSRLPDLWHRSI
sequence 09/540,217 culon for peptide of peptide sequence deterion, \( \sigma_p \)  15916 46284 A 16007 I 1673 MTPICTV. GTLTEAL SYSGLVE.  SYSGLVE ESGGLVEFI	
15916   46284   A   16007   I   1673   MTPICTVI GTLTEAL SYSGLYG ESGIWFFI	FRALSRLPDLWHRSI
GTLTEAL SYSGLYG ESGIWPFI	FRALSRLPDLWHRSI
GTLTEAL SYSGLYG ESGIWPFI	
SYSGLYG ESGIWPFI	POTDKROEOIAVALT
ESGIWPFI	LGYGSKEIOLTYSGT
	PYSPNATHKGCGRHR
I I I I I I I I I I I I I I I I I I I	IFLVIEPOSALGSCPSP
	CVFGAIRLLVLRDAP
SFSRLLN°	TLASGESLOGGPGFV
	AFLVVRNPTGTPMFT
	VPTFPIPPVFGRLGSF
VLOLOGE	RSPGQCEYDRELVSG
	LLVLGTLHLLSYKDA
GVDIDAC	NALVGRIKGVVKKT
	GGLGGFGALCALPOK
	SGTDGVGTRRRLAL
	IGIDLVAMCGNDLVV
	FLDYYATGKLDVDT
	IAEEKSEILDGSKVSD
	GSSGLHSNGYSLVRQ
	AADDVLSDADAVSW
	SGLRKKINQGAVSFV
	AOMVNYGFFGDIDV
	LAPDGRVWLTSGIRN
	AKKVIIELNHYHDPR
	VIPGAASRRNNGSIFH
AMDRLG!	NPHVQIDPEK\IVAVV
15917 46285 A 16008 425 595	
15918 46286 A 16009 315 721 QCFRALG	GHRRIADRGENIQV
	NDLLKWLNALDEKY
RSRLVW.	ARSSKNSLCASEANW
LEMNNRI	LSKGDLPCIRPILIIMLI
R*TCSYG	FTALR*TQNAAGGGD
SLAGGIG	IFTLVFFTLPAYAIRW
LPR	
15919 46287 B 16010 652 858	
15920   46288   A   16011   238   2526	
	KTSGAGLSITSEQRR
AAVSRIS	VTSSLLASAG/VRYRQ
	/RERPVDKL/PR**TPC
	GPSR*WW/MARVLIF
	RIVTVSPMRIGFSNRII
RPEIKLAN	KISCKPKPRPTPSAAT
SHCNFDH	ISIPIIEKPTSPPISISRY
LVMVVM	Α
15922 46290 A 16013 2 527	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			i	sequence		
15923	46291	A	16014	1	1734	MVNGCDSTNASSYANVNGCDS
13723	40271	^	10014	ľ	1734	TNASSYANGERCDSTNASSYA
		l				NGQRVRSTNASSYANGERVRL
				l		DNASSYAIGERVRLDERTSYAN
		l		l		GERVRLDERILLANGDRVRHHE
				l		RILERKATENNSGTTCCRAVYS
						RVSAMTAPDKAFTPHRQRCRLP
						DATLARLIRPOIPAPSVGRIRRL
				1		RRIGNSANCLMRRLRVLSGHKF
				ļ		PHHPSMPNVSANGYRSFPFMAS
						YMTPFFGYLTAWSYCLCGCRW
				l		GSLKSPPLALCPVLVPGDGAVD
						TRIDAVALVALANLAAVRLYA
						KSSSAAGIINFVVLTAALLAVT
				1		AACTVATYALRTGKNROYRA
						MOSFRESSIDNEVDTFFKGTGA
		1				LGISVTVIAVTCKSRLVYPIPVY
						TGLSLPORPAVVKVNEGSMET
						KDLIVI/GAGINGAGIAADAAGR
	ļ					
						G/LSVLMLEAQDLACATSS/ASS KLIHGGLRYLEHYESACEALAE
				}		
						REVLLK/MAPHIAFPMRFRLPH
		l				RP/HLRPAWMIRIAENIS/DFVEP
		l				KLCLPRMGTRESVLPGVCRNY
						ESTITSVISVSPCERDMANYVPR
		l			•	HSAGYRRRFYPMTQPIKDAVEP
		<u> </u>				VDQDWKAGKEMAASRS
15924	46292	A	16015	1	5895	
15925	46293	Α	16016	170	371	
15926	46294	A	16017	216	477	
15927	46295	Α	16018	2	263	
15928	46296	A	16019	11	2862	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
15929	46297	Α	16020	1	1567	MKLNKAGFNVPESYSLLKMPP
				l		VGCLISALKKAEDRQEVILRLF
	i					NPAESATCDATVAFSREVISCSE
				l		TMMDEHITTEENQGSNLSGPFL
	Į.					RVRAGESIKFFNVLLADTPGLD
İ				l		DTMDKDVAHDSRSIQLAMLRD
						DEILTHPVFNRYHSETEMMRY
				l		MHSLERKDLALNQAMIPLGSCT
				l		MKLNAAAEMIPITWPEFAELHP
				l		FCPPEQAEGYQQMIAQLADWL
		1		l		VKLTGYDAVCMQPNSGAQGE
						YAGLLAIRHYHESRNEGHRDIC
				l		LIPASAHGTNPASAHMAGMQS
l				l		RKTAGICCVHLWAGFGKVAIIG
				ŀ		AGPAGLQASVTLTTQGYDVTIY
	i	ŀ		l		EKEAHPGGWLRNGIPQFRLPQS
1					l	VLDAEIARIEKMGVP\IKCTTEV
1						G\NTLTLEQVKAENRAVLVTVG
				l	1	LSSGSGLPLFEHSDVEIAVDFLQ
						RARQAQGDISIPQSALIIGGGDV
		1		l		AMDVASTLKVLGCQAVTCVAR
		1		l		EELDEFPASEKEFTSARELGVSII
						DGFTPVAVEGNKVTFKHGDLR
1						TAPFLGVADKRNKSAGNHP
15930	46298	A	16021	62	329	
15931	46299	В	16022	289	334	
15932	46300	Α	16023	1	2991	
15933	46301	Α	16024	418	3156	
15934	46302	Α	16025	1	2169	

2055

SEQ ID	SEQ ID NO:	Met	ISEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		l		sequence		
1.502.5	146000	<del> </del>	114004	lana	10.404	CORPA (FREE LAND LAND LAND LAND LAND LAND LAND LAND
15935	46303	A	16026	800	2406	SSRRMFPPAIRLLLICLPARRWK
		l		1		SAL/GEEQLQNLQHISQEMGISP
		l		l	1	SLFSTQPLWQIAMVLQATQAQ
		l				KLGLRAEYGIDYQLLQAAKQQ
	1	l		l		HKPVIELEGAENQIAMLLQLPD
	l	l		l		KGLALLDDTLTHWHTNARLLQ
		1		i		QMMSWWLECEGGERERIFPVS
		1		l		KRMGKKLDAVFGDNHTASLTE
		1				TEEYRKSQVHFCICDKRERSSG
						NYQSIQGCRSAAFFIPSNSTRTK
1	1	l				RGESMYRMDKLTTGAAYGAS
	l			ŀ		AGSILNGMLNAYSPEQWNAIG
						VLTTAAAGAEMNPTLRNKLVG
	1				İ	AIVGGSGAITIAAVMLGNADGL
	1	İ		l	ľ	EGRRYYAYQDVVGVWTVCDG
					ŀ	HTGTDIRRGHRYTDKECDNLL
	l					KADLRKAIIYISGYSGTNGIRDS
	l					LLFSSLWLIPVFLFPKRIKIIAAVI
1	l					GVAFSRFIASHLAVAFESDPEAE
1						IRQLNSRRVELERALSNHENDN
						QQQRIQFEQAKEGVTALNRILP
						RLNLLADDSLADRVDEIRERLD
				ì		EAQEAARFVQQFGNQLAKLEPI
						VSVLQSDPEQFEQLKEDYAYSQ
1						QMQRDARQPGVCP
15936	46304	Α	16027	2336	3105	HGNAIALIASQTWRDHPVDLLL
				l		SLLVQSLT/GRLRELNQSLQKEL
		l				ARNOHLAERLLETEESVRRDV
				l		ARELHDDIGQTITAIRTQAGIVQ
ŀ		l		l		RLAADNASVKQSGQLIEQLSLG
Į.						VYDAVRRLLGRLRPROLDDLT
						LEQAIRSLMREMELEGRGIVSH
		1				LEWRIDESALSENORVTLFRVC
				[		QEGLNNIVKHADASAVTLQGW
						QQDERLMLVIEDDGSGLPPGSG
				l		OOGFGLTGMRERVTALGGAFH
				1		ISCLHGTRVSVSLAORHV
15937	46305	c	16028	l	1374	
	10000				1071	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nueleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop eodon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		į.
		_				
15938	46306	A	16029	1298	2896	GAFTCCATAGGCMNIRRKNRL
						WIACAVLAGLALTIGLVLYALR
						SNIDLFYTPGEILYGKRETQQM
		l				PEVGQRLRVGGMVMPGSVQR
						DPNSLKVTFTIYDAEGSVDVSY
						EGILPDLFREGQGVVVQGELEK
		i				GNHILAKEVLAKHDENYTPPEV
						EKAMEANHRRPARPSIMMPEIG
						NGLLCLALGIALLLSVYPLWGV
						ARGDARMMASSRLFA WLLFMS
		l				VAGAFLVLVNAFVVNDFTVTY
						VASNSNTQLPVWYRVAATWG
					1	AHEGSLLLWVLLMSGWTFAVA
			Ì			IFSQRIPLDIVARVLAIMGMVSV
		i				GFLLFILFTSNPFSRTLHLAYPN
						RCQPINWRGRHLVWYLLLFVIS
1		1				LWLQLGLPDELSRFTPFCLALPI
		l				IALAWHYGWQGALIATLMNAI
		ł				ALIASOTWRDHPVDLLLSLLVQ
						SLTGLLLGAGIORLRELNOSLO
		l l				KELARNOHLAERVLETEOSVR
						RDVARELHYDIGOTITAIRTHA
l		l				GIVORLAADNASVKOSGOLIEO
				ŀ		LSLGVYDAVRPLLGRLRPAOLD
		l		ŀ		DLT\LEQAIPLT
15939	46307	A	16030	15	277	KIGOKAPLGEARGGERT\SRTA
1		1		I		KNFGYEEMLSELEA/HRRG/WL
		1		İ		KRV*PRMKLPPEALVETFIAOLF
		1			1	DAPSQIMPLTSPIILLIAIEMGS
15940	46308	A	16031	1	2916	
15941	46309	A	16032	i	2862	
15942	46310	A	16033	i	3099	
13742	170310	111	110000	l <u>'</u>	12077	L

SEQ ID	ISEO ID NO:	Mar	SEQ ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1.0.	sequence		09/540,217	codon for peptide	of peptide sequence	delction, \=possible nucleotide insertion)
	l .			sequence		
15943	146211	-	16034	li -	1567	MKLNKAGFNVPESYSLLKMPP
15943	46311	A	10034	l'	1367	
	1	l	l			VGCLISALKKAEDRQEVILRLF
1		l				NPAESATCDATVAFSREVISCSE
		1				TMMDEHITTEENQGSNLSGPFL
		1				RVRAGESIKFFNVLLADTPGLDI
			İ			DTMDKDVAHDSRSIQLAMLRD
		1		l		DEILTHPVFNRYHSETEMMRY
		1		ľ		MHSLERKDLALNQAMIPLGSCT
						MKLNAAAEMIPITWPEFAELHP
		ļ		l		FCPPEQAEGYQQMIAQLADWL
		1				VKLTGYDAVCMQPNSGAQGE
		1		l		YAGLLAIRHYHESRNEGHRDIC
		1				LIPASAHGTNPASAHMAGMQS
		1	ļ			RKTAGICCVHLWAGFGKVAIIG
		1				AGPAGLQASVTLTTQGYDVTIY
		1				EKEAHPGGWLRNGIPQFRLPQS
		1		ł	\	VLDAEIARIEKMGVP\IKCTTEV
	1					G\ntltleqvkaenravlvtvg
		1		ŀ		LSSGSGLPLFEHSDVEIAVDFLQ
1				ŀ		RARQAQGDISIPQSALIIGGGDV
		1				AMDVASTLKVLGCQAVTCVAR
1		l		1		EELDEFPASEKEFTSARELGVSII
		1		ļ		DGFTPVAVEGNKVTFKHGDLR
		1		1		TAPFLGVADKRNKSAGNHP
15944	46312	Α	16035	367	849	NNFCSTTSHHGQHHHTDHRCG
1		1				EQNVCHRDAICQTLFRTTKDDS
						NFICLIEAQSACHKDVNYNHDS
}		l		1		QKNAADHHDKQQ*SPANFMPD
		1				TINDGFAERCINHQQNGRLVSF
	1		l	[		RNPFFIARHPVTNPRPGKMPQH
1		i				KRQQQLQHNFTDLLKAAPCTV
						NIHHQTNQQW
15945	46313	A	16036	1	1066	MHQRPRTRNAVEQHRFSRQLY
1						YALHAFEITIPPLRMRRGSIPAL
1		1		1	1	VNNKLRSLEKRFSTRLKIDDDA
		1	1	l		LARLVSCAWPGNDFELYSVIEN
		1	l	l		LALSSONGRIRVSDLPEHLFTEQ
1		1				ATDDVSATRLSTSLSFAEVEKE
		1		1		AIINAAQVTGAFPWWLGDVKL
1		1	l	l		TIPLTLGMVAAALTDLDDRLAG
				ł		RLRNLIITLFCFFIASASVELLFP
						WPWLFAIGLTLSTSGFILLGGLG
1		1		l		QRYATI\AFGA\LLNAIYTMLGT
1		1		l		SLYEHWYQQPMYLLAGAVWY
1		1		l		NVLTLIGHLLFPVRPLQDNLAR
		1		l		CYEQLARYLELKSRMFDPDIED
1		l	l	l		QSQAPLYDLALANGLLMATLN
		1	1	l		QTKLSLLTRLRGDRGQRGTRRT
		1		l		GIL
15946	46314	A	16037	<del></del>	951	OIL .
15946	46314	A	16037	576	669	
13947	40313	I'M	10038	270	007	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
15948	46316	Α	16039	jı .	1047	
15949	46317	Α	16040	2	425	
15950	46318	Α	16041	148	1052	RARRGVSVKAKKQETAATMK
						DVALKAKVSTATVSRALMNPD
						KVSQATRNRVEKAAREVGYFP
						QPMGRNVKRNESRTILVIVPDIC
						DPFFSEIIRGIEVTAANHGYLVLI
		l				GDCALQIQQEKPFIDLIITKQIDG
						MLLLGSRLPFDASIEEQRNLPP
						MVMANEFAPELELPTVHIDNLT
						AAFDAVNYLYEQGHKRIGCIA
						GPEEMT\LCHYRLQGYVQALRR
						CGIMFCRFTAEGVQEIDYKDIA
						TLKNYITESGGVTELIHFFIAEY
		l				SDNQRANAGGGVEDEDIEVLES
		l				LRLNENHAIKERCRS
15951	46319	Α	16042	3	741	
15952	46320	A	16043	237	1542	FHRLWTGRFLPSPPSRRGTDNA
		l				AGRTKMPPSPVIF/WFALAQFV
	l	1			Į.	GVKHSRSIPFAAVRSHKARIRSI
		1				SRSDVATSILPQLS*RMPF*SQK
	ł	l				ALVARFPARQNCAFRLPGV*/L
	ļ					DPGMDHAAVVARLVTGRGGIV
		1				WFGRDFYRSVDDIHFGAWGDL
		]				AKECFDIVIPQTNTARTYPHAN
		1				AEIGVRTMKQINAAIGRQTNRM
	l	1				MAHWVIRSSRHYRRQLNSLCFI
		l				TGADVCRWFPQHIVPGRDSVA
		1				HVVVQHVITYRLLRGLLHFAG
						DGGVNAITVFIGTFAITVIHLLA
		1		l		HHFAQVRRRESNLRRVIVSVNR
						LSACLIELLLGDIPFIQHPRQHD
	ŀ	l			ł	VTPRDGTIHRVERVEGGRRFRQ
		1				PGYHRHFVQRQLVDRFSEIDLC
		1				RSTDTIGAVTKVNLVQIKLEDL
		1				VFRQQLFNANREEDFLNLTHQR
		_				AFWTEEEVSRQLLGNGTCPL
15953	46321	Α	16044	1	1059	
15954	46322	A	16045	104	349	RSAASPWKTRKALVCCSAVVIS
				l		PALKISMIVTISVQAHG*LRKGS
	1	1	İ	l		GVKAALSWWKFQPTMKPTITS
l		_				SLTGRRISCRSRVKR

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown,
15955	46323	A	16046	1056	2373	GPRLVORSDHRPHDANYROYL AGLSVHODPLHGLAENTIPPDL YEASAMDGAGPFQNFFKITLPL LIKPLTPLMIASFAFNNFVLI LUNYTYRIAFEGGGGDFGLA AAIATLIFLLIRPRATTALGOTDL LUNYTYRIAFEGGGGDFGLA AAIATLIFLIRIPRATTALGOTTDL LUNYTYRIAFEGGGDFGLA KILMESSRWARANRILKAIN TILSLITITOSCETYLIQNTRPELI TOTTREFFDTPTVETAQDVHKQL KRLRRVIAWTGEBETPVTIYSW VAAATRYQLLKRGVISNTKAIA TEEEILQGEPEVKVESAERHHA MVNFWRTTLSCLIGTLFWLWT GGRBYAVGVFYGGCYCTRDG LTRAPPPNAAPTAARYGPRTTP RTLRKGITDVRCEKRHIRGRQA RNAGYGTVFSSLDRLRHPALR

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \≔possible nucleotide insertion)
15956	46324	A	16047		2581	MVLMGLAQNIWOFLILRALLG LLGGFVPNANALIATQVPRNKS GWALGTLSTGGVSGALLGPMA GGLLADSYGLRPVFFTTASVLIL GFVTLECIREKFOPVSKEML HMREVVTSLKNPKLVLSLEVTT LIIQVATGSIAPILTLYVRELAG NYSNVAFISGMIASVPGVAALL SAPRLGKLGDRIGPRKILITALI SAPRLGKLGDRIGPRKILITALI SAPRLGKLGDRIGPRKILITALI NKSNVAFISGMIASVPGVAALL SAPRLGKLGDRIGPRKILITALI NKSNVAFISGMIASVPGVAALL SAPRLGKLGDRIGPRKILITALI THOMINAY WTPDOLPEPKEM NKYTITTSRDEDKLHAPDNAW VQQTRSTGDVKQSNLIRQPDG TIAFVVDFTCAGMKKLPGDTY TAQTSIGDNGEIVESTVRYNPV TKGWRLVMRKVKADAKTITE KGWRLVMRKVKADAKTITE KGWRLVMRKVKADAKTITE KGWYLYGPLDSNWAFGLDANYVKQ RDWRSAKDMMKFTDYSVKTG HLTATWTFSFAQDVLKASVG QVLAGDKGTLEIAKREDSGV VVGGYATITNYSKEEVGEODFI KGYVYSVPLDSSGPTRSRAA IGWTPLTRDGGQLGPGYTDLL VNYTYRIAFEGGGQLGPGYTDLL VNYTYRIAFEGGGGQFGLAA IATLIFLLVAIMPPLLMVVAIS LRAGFSVEROAGRITPPFPVLL WLWNSVKVAGISAIGIVALSTT
		ļ.		ļ	2/4	CAYAFARMRFPGKATLLKGML
15957 15958	46325 46326	A	16048 16049	869	765 1012	MAISFMMSCFVT*VAANSAILL SMSWRA*SNSNGP*LANSILLS AAC

SEQ ID	ISEO ID NO-	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /=possible nucleotide
1	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1			sequence		
	<u> </u>	<u> </u>			1	New contame and the contame
15959	46327	A	16050	1	1854	MTLSCNSTDFEKTVTSVPALPD
1		1			ĺ	VVSDSDMSLNALSVTLADNVQ
		1			<b>!</b>	LSFRRDSYSGQPSVIYTTPQRPT
			1			AGSEDAPVWPEAFTEDVRHNR
	1	ı				PPYPVIPRATRPACLARERMAM
	1	i				YMRPQIKTIGKAPAEEALSNPR
		1				MQGPQLSSASTIPVTPFHWLFG
		1				SHAAGHFSQHAHRTALTGHFS
į.		1				HLATTLKGLALEGNAIFTITRFT
	i	1				RPYGHKNTTPHSPLCSAPHSPIF
		İ				NSRRKVYGQHGPQWWAFIHSH
		1				RPGGSSHSSILHCFALVCPGLVV
		1				QRDTPHPIIRPALCPPIAIAFSLSL
		1				WLGNPSFPSGTQHLQGPKTFQC
1						OASPSSKVCPKRLICTVIPOORV
1		1	1			ASHHHFHGHNRYYQLGLPVQH
l .		1				CTLOGVIRATHFIPRTARNOISH
		ì	1			VSWGAGPAHSDSQGKQDLE/H
		1				EPIKPLDNSEKASKV/SOALETV
						TTTAEKVQRQ/PVIAHLIRATER
		l				FNDR/LGNQFGGFVLAS/HPMLL
1						QDIFDKILQNIS/DPTLAATLKNT
			1			INTAVHSHLVPAGADGIFLLLRI
						FDAVCAAWIATAEYKDYPGMP
	]			i		GKTHLKIRLMRRERLIGIRFYSG
1	1					LLPGTKAPYSRTLAFKRVLHTA
1						
1						LSLHLGLGKTCTTGFELCSLTLI EYASNAFTYWPDWHINRIKNK
						N PROPERTY WEDWHINKIKNK
15960	46328	A	16051	249	724	EKVKKTQRKEIENVTNITGVRQ
13900	40328	^	10051	-77	1/27	IELWRRDDLQHPRLDEVAEEVE
		1				VALVYNGISHVVMMASPKDLE
1						YFALGFSLSEGD/IIESPRDIFGM
						DVGVPCACNGLEERRRALDG/R
						TVAGCGVCGVEQ/LLNDIGKPV
		i	1	1		QPL\PFTQT/FDLNKLDDALRHL
1		1		1		NDFOPVGN
15061	46329	A	16052	71	408	RYLSTASQTNSIQIGAGLSRSRA
15961	40329	I <sup>A</sup>	10052	<b> </b> ''	1400	
		i				FTTFGSKGILLSHTSVFIPRDRCT
1		1				SFSMMPTCSASLTSHCPFQMTS
1	1	1	1	1		LLSSHHP/FKKKKFGT\KTGHCL
L	ļ	1				CPSLNCLPCCFSQIMVIKQVIL
15962	46330	Α	16053	668	905	CLHVLHHLTSHCPFQMTKPYST
	1	1				IHFLPRMTSLLSSHHP/FKKKKF
		1	1	1		GT\KTGHCLCPSLNCLPCCFSQI
L	L	$\bot$				MVIKQVILEKKKK
15963	46331	Α	16054	834	1057	ARLLFMDLLDERTLVAVERPL\
		1				VTSLLSSHHP/FKKKKFGT\KTG
		1				HCLCPSLNCLPCCFSQIMVIKQV
		١.				ILEKKKKTK
15964	46332	Α	16055	1	1011	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	ı	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
15965	46333	Α	16056	191	631	NLLRGNKMATQSSPVITDMKVI
		1			\	PVAGHDSMLLNIGGAHNAYFT
						RNIVVLTDNAGHTGIGETPGGD
		l				VIYQTLVDA\IPMVLGQEVARL
		l				NKMVPOVHKGNOAADFDTFG
						KGAWTFELRVEAGAGLEARLL
		l		ļ		DLLGKALNVSGCELLGHGS
15966	46334	Α	16057	2	335	GARQQOKFVLIAGGFP*QLL*T
		1				NAVIGREFRNVOECIGLHTAGF
		ı				ANAVTKHFGKCAIALHNMAFR
						IEDNHRSVEMVNGNNOLSGLFF
		1			1	LRHFYAGIPYOROVINFPLGAH
15967	46335	Α	16058	736	910	RVSTPRATGTVPQRDYPLSVVA
						TG*PDSFHTYLFVRTY*K*V*VL
						AYLNTRQNDGDFP
15968	46336	В	16059	17	1699	
15969	46337	Α	16060	3	440	
15970	46338	A	16061	1	564	
15971	46339	A	16062	1	1062	
15972	46340	Α	16063	203	425	LNNWIISWLLHMMCLMKVAN
						CFRS*DRRELAVSAFFVLL*AM
		l				RLRRSSSGFLANLAHLQKMKL
			L			NSSTYVPPTKH
15973	46341	Α	16064	402	713	RGVAISLGQSKSHGYIHFQVAQ
						REPEILG\DSIKAVRWCSLHGRL
		l	ļ.			M***M*RDLKQWFSAPEA*VSL
		l				GTLCVIGQKAVGSLALMSWEP
						TPRPMGLLSTSRTLYS
15974	46342	Α	16065	944	1305	LPLWFISALRLAGIAVWCVLST
		l		l	1	GFEQIRMIKAFGLEDRQSAL/FA
				l		ADAEDTGKKNMRVAR/IDARF
	1			l		DPTIGWPSSLGLLFSNRTPWVPF
				l		PFFFQVPQ\LHTFIRGILIWKTFP
		ı	1	l		FWIFPFPASSW
15975	46343	Α	16066	1	756	

15976	SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
15976							*=Stop codon, /=possible nucleotide
IS976   46344   A   16067   S0   III91   CLTIAVFFPAPQCPEMFSIP ARDGERAASMIQDYIFCFFF MKLKPERMISHERAQTSD DCRRHLPIGILMAGGMFAW KHQGQTFIERPRISLTCMLP ATTH-WIFTRIGQVLYTCLLI ECTVNEVQVJATVVSVNPQ PDIVAMIGASAALSLSGIPF GAARVGVINDQVJANPTQI KESKLDLVVAGTEAAVLM EAQLLSEDQMLGAVVFGHI MRISDHIBISCIVYACLSLFA LVLVVIAVSVVNPCLLEVTI MASINSQPNLNISDTWGIGA GAYTCSCLDPHEMMSSGF SHSCVEK LILFMST/ALLDAVVKKNR PYMLALYVLAFLDRSNIGL TYQIDTGLSNEAYALGAGI VYAFLGVPANLLMRKLGAI GTTTLLWGFLSAAMAWAI AKFLIVATLIRAAEAGFFPC YLTSQWFPQRNRASIMGLF GAPLALTLGSPLSGALLEM MGHPGWFWMYPUFGLLAV GVFTFFWLDTPFQAFFLS KTLLINQLASEQQKVTSRI ALRNGRVWQLAITYLTIQV GLIFFLPTQVAALLGTKVG SVVTAIPWVAALGTVALITYTIQU GLIFFLPTQVAALLGTKVG SVVTAIPWVAALGTVALITYTIQU GLIFFLPTQVAALLGTKVG SVVTAIPWVAALGTVALITYTIQU GLIFFLPTQVAALLGTKVG SVVTAIPWVAALGTVALITYTIQU GLIFFLPTQVAALLGTKVG SVVTAIPWVAALGTVALITYTIQU GLIFFLPTQVAALLGTKVG SVVTAIPWVAALGTVALITYTIQU GLIFFLPTQVAALLGTKVG SVVTAIPWVAALGTVALITYTIQU GLIFFLPTQVAALLGTKVG SVVTAIPWVAALGTVALITYTIQU GLIFFLPTQVAALLGTKVG SVVTAIPWVAALGGTVLIPU DKSAAKRYTRPHRECGYS IIPPKKVNNAPHSGPGPTCI RVRVRNLGIGVVKHOSPP		sequence	1	09/540,217		of peptide sequence	deletion, \=possible nucleotide insertion)
ARDGERAASMIQDYIFCFFS MKLKPERMISHERAQTSDI DCRRHLPIGILMAGGMFAV KHQQGTIFERRISLTCMLP ATPLWLFTRIGQVLYTCLLI ECFVNEVQVIATVVSVNPC PDIVAMIGASAALSLSGIPFI GAARVGVINDQVJNPTQI KESKLDLVVAGTEAAVLM EAQLLSEDQMLGAVYGFH QVDSRGSPIKGNNTCDNYT LIDYVNDMIENVSEEAFCVI IMRRISDHIISCIVYCCLSLFA LVLVVIAVSVVNPCLLEVTI AASIVSQPNLNISDTWGIGA GAYTCSCIADPHKMMSSGF SHSCVEK 15977 46345 A 16068 401 1518 LILFMST/ALLDAVVKKNR PYMLALYVLAFLDRSNIGL TYQIDTGLSNEAVALGAGII VYAFLGSNEAVALGAGII GTTTILWGFLSAAMAWAI AKFLIVRTILRAAEAGFFPC YLTSQWFPQRNRASIMGLF GAPLALTLGSPLSGALLEM MGHPGWFWMFVIEGLLAV GVFTFFWLDDTPEQAFLSI KTLLINQLASEEQGKVTSRI ALRNGRVWQLAITYLTIQV GLIFFLFTQVAALLGTKVGF SVVTAIPWVAALGGTWLPI DKSAAKRYTRPHRECGYSE IIPPKKVRNNAPHSGPGPFICI RVRVRNLGIEVYKHDSPP			l		sequence		
ARDGERAASMIQDYIFCFFS MKLKPERMISHERAQTSDI DCRRHLPIGILMAGGMFAV KHQQOTTERERRISLTCMLP ATPLWLFTRIGQVLYTCLLI ECFVNEVQVIATVVSVNPC PDIVAMIGASAALSLSGIPFI GAARVGVINDQVJVNPTQI KESKLDLVVAGTEAAVLM EAQLLSEDQMLGAVVFGH QVDSROSPIKGNNTCDNYT LIDYVNDMIENVSEEAFCVI IMRRISDHISICTVYCCLSLF LVLVVIAVSVVNPCLLEVT AASIVSQPNLNISDTWGIGA GAYTCSCIADPHKMMSSG SHSCVEK TYQIDTGISNEAVALGAGII TYQIDTGISNEAVALGAGII TYQIDTGISNEAVALGAGII TYQIDTGISNEAVALGAGII TYQIDTGISNEAVALGAGII GTTTLLWGFLSAAMAWAI AKFLLYRTLRAAEAGFFPC YLTSQWFPQRNRASIMGLF GAPLALTLGSPLSGALLEM MGHPGWFWMFVIEGILAV GVFTFFWLDDTPEQAFLSI KTLLINQLASEEQGKVTSRI ALRNGRVWQLAITYLTIQV GLIFFLFTQVAALLGTKVG SVVTAIPWVAALGTVAIPL DKSAAKRYTRPHRECGYSE IIPPKKVRNNAPHSGPGPICI RVRNRNLGIEVYKHDSPP	15076	46244		16067	160	1101	CLTIA VEEDA DOCDEMENDOUT
MKLKPERMISHERAOTSD DCRRHLPIGILMAGGMFAV KHQQQTTELERRISLTCMLP ATFLWLFTRIGQVLVTCLLL ECFVNEZVQVLATVSVNPC PDIVAMIGASAALSLSGIPF GAARVGYINDQYVLNPTQI KESKLDLVVAGTEAAVLM EAQLLSEDQMLGAVVCGHI QVDSRGSPIIGNRTCDNYI LIDYVNDMIENVSEEAFCV. IMRHSDHIISCIVVRCLSLFA LVLVVIAVSVVNPCLLEVTI AASIVSQPNLNISDTWGIGA GAYTCSCIADPHKMMSSG SHSCVEK LILFNST/ALLDAVVKNRN PYMLALYVLAFLDRSNIGL TYQIDTGLSNEAYALGAGII VYAFLGVPANLJMRKLGAI IGTTTLLWGFLSAAMAWAL AKFLIVRTLRAAEAGFFC YLTSQWFQRYRASIMGLF GAPLALTLGSPLSGALLEMM MGHPGWFWMFVIGGLAV GVFTFWLDDTPEQAFFLSI KTLLINQLASEQQVKTTSM ALRNGRVWQLAITYLTIQV GLIFFLFTQVAALLGTKVG SVVTAIPWVAALGTVAIPL DKSAAKRYTRPHRECGYFS IIPPKKVNNAPHSGCIPGI RVRVRNLAIGVVKNNEPISPCIPG RVRVRNLAIGVVKNNEPISPCIPG RVRVRNLAIGVVKNSPSPP	13976	46344	l^	10007	30	1191	
DCRRHLPIGILMAGGMFAY KHQQTFIERPRISTCMLP ATFLWLFTRIGQVLVTCLLI ECFVNEZVQVIATVVSVNPP PDIVAMIGASAALSLSGIPFI GAARVGVINDQYVLNPTQI KESKLDLVVAGTEAAVLM EAQLLSEDQMLGAVVFGHI QVDSRGSPIKGNRTCDNYTI LIDYVNDMIENVSEEAFCVI IMRRISDHIISCIVVRCLSLF, LVLVVIAVSVVNPCLLEVTI AASIVSQPNLNISDTWGIGA GAYTCSCIADPHRMMSSGF SHSCVEK  I5977 46345 A 16068 401 1518 LILFMSTALLDAVVKNRN PYMLALYVLAFLDRSNIGL TYQIDTGLSNEAVALGAGI UYAFLGVPANLLMRKLGAI VYAFLGVPANLLMRKLGAI GTTTLLWGFLSAAMAWAI AKFLIVRTLRAAEAGFPFP YLTSQWFPORNASIMGLF GAPLALTLGSPLSGALLEM MGHPOWFWMFVIEGLLAV GVFTFFWLDDTFEQARFLSI KTLLINQLASEEQOKVTSRI ALRRIGWWQLAIJVLTIOV GLIFFLFTQVAALLGTKVG SVVTAIPWVAALGTWLPI DKSAAKRYTRPHRECGYFS HPPKKVRNAPHSGCPGIC RVRKPNLGIEVKHOSPP							
KHQGOTTERRRISLTCMLP ATFLWLFTRIGQVLVTCLLI ECTYNEVQVIATVVSVNPC PDIVAMIGASAALSLSGIPF GAARVGYINDQVJVAPTQI KESKLDLVVAGTEAAVLM EAQLLSEDQMLGAVVFGHI QVDSRGSPIKGNRTCDNYT LIDYVNDMIENVSEEAFCV IMRISDHISICIVYCLSLFA LVLVVIAVSVVNPCLLEVTI AASINSQPILNISDTWGIGA GAYTCSCLADPHEMMSSGF SHSCVEK  ILLEMSTJALLDAVVKKNR PYMLALYVLAFLDRSNIGL TYQIDTGLSNEAYALGAGI UYAFLGVPANLLMRKLGAI GTTTLLWGFLSAAMAWAI AKFLIVRTLLRAEAGFFPC YLTSQWFPQRNRASIMGLF GAPLALTLGSPLSGALLEM MGHPGWFWMYEIGLLAV GVFTFFWLDDTPEQAFLSI KTLLINQLASEQGVTSRI ALRNGRVWQLAITYLTIQV GLIFFLFTQVAALLGTKVG SVVTAIPWVAALGTWLPILD DKSAAKRYTRPHRSCGYFS IIPPKKVNNAPHSGPGPICI RVRVRNLGIEVYKHDSPP	l		l				
ATELWIFTRIGOVLYTCLLI ECFVNEVQVIATVVSVNP DDIVAMIGASAALSLSGIPFI GAARVGYINDQYVLNPTQI KESKIDLVVAGTEAVLM EAQLLSEDQMLGAVVCFHI QVDSRGSPIKGNRTCDNYV LIDYVNDMIENVSEEAFCVI IMRRISDIHISCIVVRCLSLF, LVLVVIAVSVVNPCLLEVT AASIVSQPNLNISDTWGIGA GAYTCSCIADPIKMMSSGF SHSCVEK  IS977 46345 A 16068 401 1518 LILFMSTALLDAVVKKINA ILFMSTALLDAVVKKINA VAFIGVPANLAMRKLGAI IGTTTLLWGFLSAAMAWAI AKFLIVRTLRAAEAGFFPP YLTSQWFPQNRVASIMGLF GAPLALTLGSPLSGALLEM MGHPGWFWMFVIGGLAV GVFTFFWLDDTPEQARFLSI KTLLINQLASEGQVETNSI KTLLINQLASEGQVETNSI ALRINGRVWQLAITYLTIQV GLIFFLFTQVAALLGTKYG SVVTAIPWVAALGTWLIPI DKSAAKRYTRPHRECGYFS IIPPKKVRNAPHISGPGIC RVRKVRNADIEGGYVKHDSPP			l				
ECFVNEZ/QVIATVVSNING BCFVNEZ/QVIATVVSNING PDIVAMIGASALSLSGIPF GAARVGYINDQYVLNPTQI KESKLDLVVAGTEAVLM EQULSEDQMLGAVVFCH QVDSRGSPIKGNRTCDNYI LIDYVNDMIENVSEEAFCVI IMRISDHIISCIVYCLGLEF LVLVVIAVSVVNPCLLEVT AASIVSQPNLNISDTWGIGA GAYTCSCIADPHKMMSSGF SHSCVEK SHSCVEK LILPNST/ALLDAVVKKNR PYMLALYVLAFLDRSNIGL TYQIDTGLSNEAYALGAGI VYAFLGVPANLLMRRLGAI IGTTTLLWGFLSAAMAWAI AKFLIYRTLRAARAGFFPC YLTSQWFPQRNRASIMGLF GAPLALTLGSFLSGALEM MGHPGWFWMFVIEGLLAV GVFTFFWLDDTPEQAFFLS KTLLINQLASEEQKVTSRI ALRNGRVWGLAITYLTIQV GLIFFLFTGVAALLGTKVGF SVVTAIPWVAALGTWLIPI DKSAAKRYTRPHRECGYFS IHPKKVRNNAPHSGPGPICI RVRVRPNLGIEVYKHDSPP							
PDIVAMIGASAALSILSIGIPE    GARRYGYINDQYVLNPTQ    KESKLDLVVAGTEAAVLM    EAQLLSEDQMLGAVYCHI    QVDSRGSPIIGNRTCDNYI    LIDYVNDMIENVSEEAFCV    IMRHSDHIISCIVVRCLSLFA   LVLVVIAVSVVNPCLLEVTI   AASIVSQPNLNISDTWGIGA   GAYTCSCIAPPHKMMSSG   SHSCVEK    LILFMSTJALLDAVVKKNR   PYMLALYVLAFLDRSNIGL    TYQIDTGLSNEAYALGAGII    UYAFLGYANLAMIARKLGAI    GTTTLLWGFLSAAMAWAI    AKFLIVRTLRAAEAGFFPC    YLTSQWFPQRYRASIMGLF    GAPLALTLGSPLSGALLEMI    MGHPGWFWMFVIGGLAV    GVFTFWLDDTPEQARFLSI   KTLLINQLASEEQQKVTSI   KTLLINQLASEEQGKTSI   KTLLINQLASEEQGKTSI   ALRNGRVWQLAITYLTIQV   GLIFFLFTQVAALLGTKVG    SVVTAIPWVAALGTVAIPU   DKSAAKRYTRPHRECGYFS    IIPPKRVRNAPHSGPGIPE    RYRVRNLGIEVYKHDSPP    RYRVRNAPHSGFGOYFS    IIPPKRVRNAPHSGFOYFS    IIPPKRVRNAPHSGFOYFS    IIPPKRVRNAPHSGFOYFS    IIPPKRVRNAPHSGFOYFS    IIPPKRVRNAPHSGFOYFS    IIPPKRVRNAPHSGFOYFS    IIPPKRVRNAPHSGFOYFS    IIPPKRVRNAPHSGFOYFS    IIPPKRVRNAPHSGFOYFS    IIPPKRVRNAPHSGFOYFS    IIPPKRVRNAPHSGFOYFS    IIPPKRVRNAPHSGFOYFS    IIPPKRVRNAPHSGFOYFS    IIPPKRVRNAPHSGFOYFS    IIPPKRVRNAPHSGFOYFS    IIP			l				
GAARVGYINDQYVLNPTQI KESKLDLVVAGTEAAVLM EAQLLSEDQMLGAVVFGHI QVDSRGSPIKGNRTCDNYYI LIDYVJADMENSVESEAFCVI IMRISDHIISCIVVRCLSLFA LVLVVIAVSVVNPCLLEVTI AASIVSQPNLNISDTWGIGA GAYTCSCIADPHIKMMSSGE SHSCVEK  LILFMST/ALLDAVVKKNR PYMLALYVLAFLDRSNIGL TYQIDTGLSNEAYALGAGI VYAFLGVPANILMRKLGAI IGTTILLWGFLSAAMAWAI AKFLIVRTLRAAEAGFPFP YLTSQWFPQNTRASIMGLF GAPLALTLGSPLSGALLEM MGHPQWFWMFVIEGLLAV GVFTFWLDDTPEQARFLSI KTLLINQLASEEQQKVTSRI ALRNGRWQGLAHJVTIQV GLIFFLFTQVAALLGTKVG SVVTAFPWVAALGTWLPI DKSAAKRYTRPHRECGYFS HIPPKKVRNNAPHSGOPGIC RVRWRNLGIEVYKHDSPP	1		1				
RESKLDLVVAGTEAAVLM EAQLLSEDQMLGAVVFGH QVDSRGSPIKGNRTCDNYI LIDYVNDMIENVSEEAFCVI IMRISDHIISCIVYCLGLEF LVLVVIAVSVVNPCLLELFI AASIVSQPNLNISDTWGIGA GAYTCSCIADPHKMMSSG SHSCVEK  IS977 46345 A 16068 401 1518 LILFMST/ALLDAVVKKNR PYMLALYVLAFLDRSNIGL TYQIDTGLSNEAVALGAGII VYAFLGENBAVALGAGII VYAFLGENBAVALGAGII GTITLLWGFLSAAMAWAI AKFLIVRTLRAAEAGFFPC YLTSQWFPQRNRASIMGLF GAPLALTLGSPLSGALLEM MGHPGWFWHVEIGLAV GVFTFFWLDDTPEQAFLSI KTLLINQLASEQQKVTSRI ALRNGRVWGLAITYLTIQV GLIFFLFTQVAALLGTKVGF SVVTAIPWVAALGTKVIG SVTAIPWVAALGTKVIG SVTAIPWVAALGTKVIG FURNRAPHSGCYFSF IIPPKKVRNNAPHSGFQFPICI RVRVRPNLGIEVYKHDSPP	ŀ		l				
EAQLLSEDOMLGAVVEGH   QVDSRGSPIKGNRTCDNYY    LIDYVNDMIENNSEEAFCVI     IMRRISDHIISCUVYRCLSLF    LVLVVIAVSVVNPCLLEVT     AASIVSQPNLNISDTWGIGA     GAYTCSCIADPIKMMSSGF     SHSCVEK     LILFMSTJALLDAVVKKMSK     TYQIDTGLSNEAYALGAGI     TYQIDTGLSNEAYALG			ĺ				
QVĎSRGSPIKGNRTCDNYT LIDYVNDMENVSEEAFCVI IMRHSDHISCIVVRCLSLFA LVLVVIAVSVVNPCLLEVT AASIVSQPNLNISDTWGIGA GAYTCSCIADPIKMMSSGP SHSCVEK  I5977 46345 A 16068 401 1518 LILFMST/ALLDAVVKKNR PYMLAL VVLAFLDRSNIGL TYQIDTGLSNEAYALGAGI VYAFLGVPANLLMRKLGAI IGTTTLL WGFLSAAMA WAI AKFLIVRTLLRAAEAGFPFC YLTSQWFPQRNRASIMGLF GAPLALTLGSPLSGALLEM MGHBGWFWMFVUEGLLAV GVFTFFWLDDTPEQAFFLS KTLLINQLASEEGQK VTSRI ALRNGRVWQLAIIYLTIQV GLIFFLFTQVAALLGTKVGF SVVTAIPWVAALGTWLIPU DKSAAKRYTRPHREGCYSE IIPPKKVRNNAPHSGPGPICI RVRVRPNLGIEVVKHDSPP							
LIDYYNDMIENVSECAFCV IMRHSDHIISCIVVRCLSLFA LVLVVIAVSVVNPCLLEVTI AASIVSQPNLNISDTWGIGA GAYTCSCIADPHIKMISGG SHSCVEK  IS977 46345 A 16068 401 1518 LILFMST/ALLDAVVKKNN PYMLALYVLAFLDRSNIGL TYQIDTGLSNEAYALGAGII VYAFLGYPANLLMRKLGAI IGTTTLLWGFLSAAMAWAI AKFLIVRTLRAAEAGFFPC YLTSQWFPQRYRASIMGLF GAPLALTLGSPLSGALLEMI MGHPGWFWMYEIGLAV GVFTFEWLDDTPEQAFFLSI KTLLINQLASEEQOKVTSI ALRNGRVWQLAITYLTIQV GLIFFLFTQVAALLGTKVG SVVTAIPWVAALGTWLPI DKSAAKRYTRPHRECGYFS IIPPKKVRNNAPHSGPGIPE RVRVRNLGIEVYKHDSPP			ı				
IMRHSDIHISCIVVRCLSEA LVLVVIAVSVNPCLLEVT AASIVSQPNLNISDTWGIGA GAYTCSCIADPHKMMSSG SHSCVEK  15977 46345 A 16068 401 1518 LILFMST/ALLDAVVKKNR PYMLALYVLAFLDRSNIGL TYQIDTGLSNEAYALGAGII VYAFLGVPANLLMRKLGAI IGTTILLWGFLSAAMAWAI AKFLIVRTLRAARAGFFP YLTSQWFPQRNRASIMGLF GAPLALTLGSPLSGALLEMI MGHPGWFWMFVIEGLLAV GVFTFWLDDTPEQARFLSI KTLILNQLASEEGOK VTSRI ALRNGRVWQLAIIYLTIQV, GLIFFLFTQVAALLGTKVG SVVTAFWVAALGTWLIPU DKSAAKRYTRPHREGCYFS IHPKKVRNNAPHSGPGPICI RVRVRPNLGIEVYKHDSPP			l				
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SHSCVEK							AASIVSQPNLNISDTWGIGAILY
IS977 46345 A 16068 401 IS18 LILFMST/ALLDAVVKKNRN PYMLALYVLAFLORSND TYQUDTGLSNEAYALGAGII VYAFLGYPANLLMRKLGAI IGTTILLWGFLSAAMA WAI AKFLIVRTLLRAAEAGFFPC YLTSQWFPQNRVASIMGLF GAPLALTLGSPLSGALLEMI MGHPGWFWMFVIEGLLAV GVFTFFWLDDTPEQARFLSI KTLLINQLASEEGOKVTSRI ALRNGRVWQLAIIYLTIQV, GLIFFLFTQVAALLGTKVG SVVTAFPWVAALGTKVG SVYTAFPWVAALGTKVG SVYTAFPWVAALGTKVG FUPKKVRNNAPHSGPGPICI RVRVRPNLGIEVYKHDSPP							GAYTCSCIADPHKMMSSGPMY
PYMLALYVLAFLDRSNIGL TYQIDTGISNEAYALGAGII VYAFLGUSNEAYALGAGII VYAFLGUSNEAVALGAGII VYAFLGUSNEAVALGAGII VYAFLGUSNEAVALGAGII IGTTILLWGLSAAMAWAI AKFLIVRTLLRAARAGFFPC YLTSQWFPQRNRASIMGLF GAPLALTLGSPLSGALLEM MGHPGWFWMFVLGGLAV GVFTFFWLDDTPEQAFFLSI KTLLINQLASEEQKVTSRI ALRNGRVWQLAIIYLTIQV GLIFFLFTQVAALLGTKVGF SVVTAIPWVAALGTKVGF SVVTAIPWVAALGTKVGF FUNGAGIIFLFTGVAGIIGTWLIPI DKSAAKRYTRPHRECGYFS IIPPKKVRNNAPHSGPGPICI RVRVRPNLGIEVYKHDSPP							
TYQIDTGLSNEAYALGAGI VYAFLGVPANLLMRKLGAI IGTTTLLWGFLSAAMAWAI AKFLIVRTLRAAEAGFFPP YLTSQWFPORTNASIMGLF GAPLALTLGSPLSGALLEMI MGHPOWFWMFVIGGLAV GVFTFFWLDDTPEQARFLSI KTLLINQLASEEQOKVTSRII ALRNGRWQULAHIYLTIQV GLIFFLFTQVAALLGTKVG SVVTAIPWVAALGTKVG FVFTFWLDTFEQARFLSI HPFKTVRNAFHSGFØFIC RVRVRNLGIEVYKHOSPP	15977	46345	Α	16068	401	1518	LILFMST/ALLDAVVKKNRVRLI
VYÄFLGYPANLLMRKLGAI IGTTILLWGLSAAMAWAI AKFLIVETLERAAGGFPE YLTSQWFPORNRASIMGLE GAPLALTLGSPLSGALLEMI MGHPGWFWMFVIEGLLAV GVFTFFWLDDTPEQARFLSI KTLLINQLASEEGOK VTSRI ALRNGRVWQLAIIYLTIQV, GLIFFLPTQVAALLGTKVG SVVTAIPWVAALGTKVG FYVTAIPWVARLGTWLPI DKSAAKRYTRPHREGGYPS IIPPKKVRNNAPHSGPGPICI RVRVRPNLGIEVYKHDSPP							PYMLALYVLAFLDRSNIGLAKQ
IGTTILLWGFLSAAMAWAI AKFLIVRTLRAAEAGFFFC YLTSQWFPQRYRASIMGLF GAPLALTLGSPLSGALLEM MGHPGWFWMFVIGGLAV GVFTFWLDDTPEQARFLSI KTLLINQLASEQQKVTDIST ALRNGRVWQLAIIYLTIQV GLIFFLFTQVAALLGTKVG SVVTAIPWVAALGTKVG FVFTFWLDTPEQCFS IIPPKRVRNAFHSGFQFS IIPFKRVRNAFHSGFGTE IPFKRVRNAFHSGFGTE RVRVRPNLGIEVYKHDSPP							TYQIDTGLSNEAYALGAGIFFV
AKFLIVRTLLRAAEAGFFPC YLTSQWFPQRYRASIMGLE GAPLALTLGSPLSGALLEM MGHPOWFWMFVIEGLLAV GVFTFWLDDTPEQARFLS KTLLINQLASEEQOKVTSRI ALRNGRVWQLAIIYLTIQV GLIFFLPTQVAALLGTKVGF SVVTAIPWVAALFGTWLIPI DKSAAKRYTRPHRECGYFS IIPPKKVRNNAPHSGPGPICI RVRVRPNLGIEVYKHDSPP			1				VYAFLGVPANLLMRKLGARTW
YLTSQWFPQRNRASIMGLF GAPLALTLGSPLSGALLEM MGHPGWFWMFVLGGLAV GVFTFFWLDDTPEQAFFLS KTLLINQLASEEQK VTSRI ALRNGRVWQLAHYLTIQV, GLIFFLFTQVAALLGTKVG SVVTAIPWVAALGTKVGF FOXATAPWAALGTKVGF HPPKKVRNNAPHSGPGFIC RVRVRPNLGIEVYKHDSPP			l				IGTTTLLWGFLSAAMAWADTE
GAPLÄLTLÖSPLSGALLEM MGHPOWFWMFVIEGLLAV GVFTFFWLDDTPEQARFLSI KTLLINQLASEEQQKVTMIN ALRINGRVWQLAIFYLTIQV GLIFFLFTQVAALLGTKVG SVVTAIPWVAALGTKVG DKSAAKRYTRPHRECGYFS HIPPKKVRNNAPHSGPÖPICL RVRVRNLGIEVYKHDSPP							AKFLIVRTLLRAAEAGFFPGMI
MGHPGWFWMFVIEGLLAV GVFTFWLDDTPEQARELS; KTLLINQLASEEGORVTSRI ALRNGRVWQLAIIYLTIQV, GLIFFLPTQVAALLGTKVG SVVTAIPWVAALIGTWLIPI DKSAAKRYTRPHRECGYFS IIPPKKVRNNAPHSGPGPICI RVRVRPNLGIEVYKHDSPP			1				YLTSQWFPQRNRASIMGLFYM
GVFTFEWLDDTPEQAEFLS KTLLINQLASEQOKVTSRI ALRNGRVWQLAIIYLTIQV. GLIFFLDTQVAALLGTRVG SVVTAIPWVAALGTRVG DKSAAKRYTRPHRECGYFS IIPPKKVRNNAPHSGFQDIC RVRVRPNLGIEVYKHDSPP							GAPLALTLGSPLSGALLEMHGF
KTLLINQLASEQQKVTSRI ALRNGRVWQLAITYLTIQV/ GLIFFLFTQVAALLGTKVG SVVTAIPWVAALFGTWLIPI DKSAAKRYTRPHRECGYFS IIPPKKVRNNAPISGPGPICI RVRVRPNLGIEVYKHDSPP							MGHPGWFWMFVIEGLLAVGA
ALRAGRVWQLAITV.TIQV. GLIFFLPTQVAALLGTKVG SVVTAIPWVAALFGTWLIPI DKSAAKRYTRPHRECGYFS IIPPKKVRNNAPHSGPGPICI RVRVRPNLGIEVYKHDSPP							GVFTFFWLDDTPEQARFLSKQE
GLIFFLPTQVAALLGTKVGF SVVTAIPWVAALFGTWLIPI DKSAAKRYTRPHRECGYFS HIPPKKVRNNAPHSGPGPICI RVRVRPNLGIEVYKHDSPPI							KTLLINQLASEEQQKVTSRLSD
SVVTAIPWVAALFGTWLIPI DKSAAKRYTRPHRECGYFS IIPPKKVRNNAPISGOPFICI RVRVRPNLGIEVYKHDSPP							ALRNGRVWQLAIIYLTIQVAVY
DKSAAKTYRPHRECGYFS HIPPKKVRNNAPHSGPDIC RVRVRPNLGIEVYKHDSPP	i		l		1		GLIFFLPTQVAALLGTKVGFTA
HPPKKVRNNAPHSGPGPICI RVRVRPNLGIEVYKHDSPPI	l		ĺ		1		SVVTAIPWVAALFGTWLIPRYS
RVRVRPNLGIEVYKHDSPP			l		1		DKSAAKRYTRPHRECGYFSAPY
			l		1		HPPKKVRNNAPHSGPGPICLIRL
	l						RVRVRPNLGIEVYKHDSPPNNA
15978  46346  A  16069  283  822	15978	46346	A	16069	283	822	

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
15979	46347	IA	16070	II	1400	MTDLIQRPRRLRKSPALRAMFE
13979	46347	A	10070	1	1400	ETTLSLNDLVLPIFVEEEIDDYK
		l				
			1			AVEAMPGVMRIPEKHLAREIER
		l			l	IANAGIRSVMTFGISHHTDETGS
					1	DAWREDGLVARMSRICKQTVP
		ļ				EMIVMSDTCFCEYTSHGHCGV
					l	LCEHGVDNDATLENLGKQAVV
					ŀ	AAAAGADFIAPSGAMDGQYDV
						FVRNENYWGEKPAIKKITFNVI
						PDPTTRAVAFETGDIDLLYGNE
		l				GLLPLDTFARFSQNPAYHTQLS
		l		Ì	İ	QPIETVMLALNTAKAPTNELAV
		1			ŀ	REALNYAVNKKSLIDNALYGT
		l				QQVADTLFAPSVPYANLGLKPS
		l				QYDPQKAKALLEKAGWTLPAG
		l			<u> </u>	KDIREKNGQPLRIELSFIGTDAL
1		l				SKSMAEIIQADMRQIGADVSLI
			l		i	GEEESSIYARQRDGRFGMIFHR
		l				TWGAPYDQRPSQSKRVRQR*F
		l				QAQQD*MKKPTQSKWNRATR
		l	ŀ			VRGGREILTKFVLTAPLKWLKR
		1			İ	SNSRRVSFAG
15980	46348	Α	16071	592	1427	IPIGVTPCFSTLRRTLFALLACAS
		1				FIVHAAAPDEITT\AWPVNVGPL
		1				NPHLYTLNQMFAQSMVYEP\LV
		i i				KYQADGSVIPWLAKSWTHSED
1		1				GKTWTFTLRDDVKFSNGEPV\D
		l				AEAAAENFRAVLDNRQRHAW
		l	ļ			LELANQIVDVKALSKTELQITL
		l				KSAYYPFLQELALPRPFRFIAPS
		l				QFKNHETMNGIKAPIGT\QPWN
		l	1			LQESKLNQYHGFGRNENYWGE
		l				KPAIKKITFNVIPDPTTRAVAFE
		l				TGDIDLLYGNORLLPLDTFARF
		1				SQNPVYHTQLSQIWNQ
15981	46349	Α	16072	I	1071	
15982	46350	Α	16073	585	1072	RPARDVPLPIRGLQPSLRGPQQL
		l				PEKPAVEVRLDKWLWAARFYK
		1		1		TRALA\REMIEGGKVHYNGQRS
	1	1				KPSKIVELNATLTLRQGNDERT
						VIVKAITEORRPASEAALLYEET
						AESVEKREK\MSPRGPPFVGAP
1		1				KNPRGFLKLNALTMPHPDRRP
1						DKKERRDLLR
15983	46351	A	16074	36	356	ASHTLARKSC*S/PSLLYQENQA
1		Γ.		F-	[ · · ·	HNQMPASELKASEIPFHPSIKTQ
						DPKAEEKSPRSKR*L*QRQVLP
1		l	l			DPAADLSVKPPGPLMLPLCYLS
						GPADITVLKASQDGLIIA
		Ц_	L	L		OI ADII YERASQUOLIIA

15984 46352 A 16075 I 2111 MNTPLQSAHTHLT	
SDSPFPAASTLSLP  KLGAGTMPPAAC PPAAYPHRNKVRA PPAAYPHRNKVRA PVREYEAGDEASG KSVQNARADRGM VRGGENTVVVFAA QIVLRDIAREMY TQMDAKKPRKCDI RKKQRFTSAKHLW VEDHADWQQQIW EGQGINLTGAFNR GPALNALEIDSSY QGWQGLFPPLG VQIQKPPSNIKNSR TSVTSLPFVDTKGR SKKVLLKSSLLYQ KAGERQFSPKVI TVAAEEENQAHNC SEIPFHSSIKTQOFK QKVTLTAAEALKL QSEILGYPELWFLC APEKFSKTSPOED DHIAYRYEVLETIG KCLOHKNNELVAL HQQALMELKLAL HQQALMELKLAL LGSEILGYPELWFLC APEKFSKTSPOED LGREYPELWFLC APEKFSTEN LGREYPELWFLC APEKFSTEN LGREYPELWFLC APEKFSTEN LGRE	ICNFDPCPT IGORIPOPCPT IGORIPOPCPT IGORIPOPCPT ICON ICON ICON ICON ICON ICON ICON ICON

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
15985	46353	IA	16076	28	1327	CVKMBUITI BDGGGBUVBUAV
15985	46353	I <sup>A</sup>	16076	28	1327	GYKMPVITLPDGSQRHYDHAV
		1		1		SPMDVALDIGPGLAKKPLVIRQ
ļ ·		1				GAAGLMAKLVDACDLIENDAQ
				1		LSIITAKDEEGLEIIRHSCAHLLG
		1				HAIKQLWPHTKMAIGPVIDNGF
		1		1		YYDVDLDRTLTQEDVEALEKR
		1				MHELAEKNYDVIKKKVSWHEA
		1				RETFANRGESYTV\SIVEENSAD
		1				DDKPGLYFHEEYVDMCRGPHV
				ŀ		PNMRFCHHFKLMKTAGAYWR
		1				GDSNNKMLQRIYGTAWPDKKA
		1		1		LNAYLQRLEEAAKRDHRKIGK
						QLDLYHMQEEAPGMVFWHND
						GWTIFRELEVFVRSKLKEYQYQ
		1		l		EVKGPFMMDRVLWEKTGHWD
		1				NYKDAMFTTSSENREYCIKPM
		1		l		NCPGHVQIFNQGLKSYRDLPLR
		1				MAEFGSCHRNEPSGSLHGLMR
		1		Į.		VRGFTQDDAHIFCTEEQIRDEV
		ı		1		NGCIRLVYDMYSTF\GFEKIVV
15986	46354	Α	16077	1692	1776	
15987	46355	C	16078	I	1341	
15988	46356	В	16079	83	373	
15989	46357	Α	16080	2	64	
15990	46358	Α	16081	1695	2293	EMISNPFIPSSILPLAKIRNIGIMA
		1			İ	HIDAGKTTTTERILYYSGYTRSL
		1				GDVDDGDTVTDFMAQERERGI
		1				TIQSAAATFEWKGYRVNLIDTP
		1				GHVDFTLEVERCLRVLDGAVA
	,	1				VFDASAGVEAQTLTVWRQADK
	•	1		1		HNIPRI\VFLNKMDKTGASFKYE
	ľ	1				VITISSLOKSGITKLCFFCVLKLV
		1		1		SQERCQASKCNKIEGQRFNQ
15991	46359	A	16082	1	2901	
15992	46360	Α	16083	1196	1740	FWLKAMPTIVTASPRWFSC/LR
		1				EIRSAASAIASTAIQQAIARPSTV
				1		IATTLLSNSHGNSSDSTSVEMK
		1	1	1		AIINKLRILRGRSRPORTRGPTPS
	1	1				SSANGTISQVNMVLKNGSPIEIL
		1				PSPSCLCTNGSSVPSNTTSIAAT
		1				SKTLFANSKDSRDHSALFTRER
		1				TLCPRAANSSSEPANHQHHKGE
						D
15993	46361	В	16084	49	398	
15994	46362	Α	16085	378	566	
15995	46363	Α	16086	1	2184	
15996	46364	В	16087	311	4963	
15997	46365	Α	16088	12	335	
15998	46366	Α	16089	1034	1400	
	1.3000	1	1	1		

SEO ID	ICEO ID NO.	Mar	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1,0.	sequence	""	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
15999	46367	A	16090	1767	2973	SGARRLAG*KPGNAVSAAPFYF
13377	40307	ľ`	10050	1707	2,7,3	YARPV/SMISPMLIPC*CWKC/D
		l				PAAKROFRERTAVRCVAOFVD
		1				VGKLIPFWGLCVGIYATNSAET
		l				
l		l				FLHRVVQLLNDSVEHTLQDAIT
						IRDEDFTATPSPADEVAYIQLSG
		1				GTTGTPKLIPRTHNDYYYSVRR
						SVEICQFTQQTRYLCAIPAAHN
		1		i .		YAMSSPGSLGVFLAGGTVVLA
1		l		i		ADPSATLCFPLIEKHQVNVTAL
1						VPPAVSLWLQALIEGESRAQLA
l .						SLKLLQVGGARLSATLAARIPA
		1		1		EIGCQLQQVFGMAEGLVNYTR
						LDDSAEKIIHTQGYPMCPDDEV
		l		i		WVADAEGNPLPQGEVGRLMTR
1		l		1		GPYTFRGYYKRSSVLGKGSDCS
ļ						FGVFLPGLLPSASSVRRDSNVSI
				1		RNVVSLINSSRWKSGFTWHDN
						VLQLDGSFPLT
16000	46368	Α	16091	845	1920	YPMMRK/RLMKLWREAKALHS
ŀ					1	DPFEPWASIIEDADKAKSSKQA
		1				RGRGGFVRSSWQEVNELIAASN
		1				VYTIKNYGPDRVAGFSPIPAMS
		l				MVSYASGARYLSLIGGTCLSFY
i						DWYCDLPPASPQTWGEQTDVP
1						ESADWYNSSYIIAWGSNVPQTR
		1		l		TPDAHFFTEVRYKGTKTVAVTP
						DYAEIAKLCDLWLAPKQGTDA
1						AMALAMGHPPERESGRYRLIPV
1	l	1				PASGYPPDPAPEWDQFPHVHEL
ł		l		l .		CDTANGCPLPELASPAGYTSSIN
						RVSTCVSTLAKSSYRSRVRVKR
1						LRRRFNGGVHFRRVVAVVIDQ
1	i	1		1		HCRTAFTIHWLQREFTEEIKTAT
	i					SPLEAFKRPONSLVVNALFRSN
						RNAAAAFSAL
16001	46369	A	16092	1	209	VSFMIIAALMMMGIDTGWLLV
	1	1				AAGFVGAIVIAS/ARPGRNSKRL
		1				IALISAIGMSIFLQNYVSLTEGSR
1		1				DVA
16002	46370	A	16093	194	657	CLDHILRAVOSLRLPLSVPAAM
10002	1.03,0	ľ.	10075	1	100,	RPGAAIGYTMVYGIIGMIN/FAH
				1		GEVYMIGSYVSFMIIAALMMM
				1		GIDTGWLLVAAGFVGAIVIA/S/
						AYGWSIER/VAYRPVRNSKRLI
1		1	1	1		
	l			1		ALISAIGMSIFLQNYVSLTEGSR
16002	46271	-	16004	1,	2202	GLATEMFLEKGDNGTEDGRAR
16003	46371	A	16094	3	3303	
16004	46372	A		144		
16005	46373	В	16096	1144	326	L

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide inscrtion)
16006	46374	Α	16097	282	599	IPVSISGCHLAGAGTQTASGVP
						VHPHGHLAHQRQSFIGNTKTEC
			l	l .		WPISSVPPHHW*A**TDIGAGSG
				l		DDQRVLDVWWNWRTKE*P*W
						W*PTNGLCRKVANRQAAR
16007	46375	В	16098	1	276	
16008	46376	Α	16099	812	1084	
16009	46377	c	16100	1	1608	
16010	46378	Α	16101	173	504	SADSKPVLPRTSASLVSASCSTR
				1		CGLRQASMESNNLTMVFGFSIG
	1	1				KVWMRS*NSATSLAKSRISFGT
	1	1				RRRWHSCSTN/SNTRRAMTMM
		l		l		TRPEFWRRQPCGLSIAAIESVIK
						v
16011	46379	Α	16102	ì	816	
16012	46380	Α	16103	742	1182	PAFIECSKAQENNHKGNCYQSG
	1					SLVSR*AFLIRHTRPVITNARR*F
		ļ				*RKVFHQRHGIAGTGSWRGFPL
		1			1	NLH*RQTVVAFQSRRAIHPM*S
						GKGREWHHFAVGAADIKFIDIF
		İ				WQHTEFGIRLNTRRAMTMMTR
		ĺ				PEFWRRQPFTEIVA
16013	4638I	Α	16104	550	884	KRYGMAASFHSGEITTHRTPAP
						WRMVVMSPARSMAHDLAQTA
	1					WRG/APRPLPDTLATMTPQAY/
						NSIQYDAEKSLWHNVE/NRQLD
						AQFFHMGMGFRRRTLWAGITN
	l					AQVCGWTA

SEQ ID   SEQ ID NO:   Met   SEQ ID NO:   Nucleotide   N	VAASSV SPQVDV ELWPRH QRLRVP HTFPM
	VAASSV SPQVDV ELWPRH QRLRVP HTFPM
16014   46382   A   16105   2363   2856   MLTLWSSPTTTRWRV ANTLA*MTLSMAAMLS RFATLCHDLGKGLTPPI	SPQVDV ELWPRH QRLRVP HTFPM
ANTLA*MTLSMAAMLS RFATLCHDLGKGLTPPF	SPQVDV ELWPRH QRLRVP HTFPM
RFATLCHDLGKGLTPPF	ELWPRH QRLRVP HTFPM
1 1 1 1 1 1 1 1	QRLRVP HTFPM
HGHGPAGVKLVEOLCO	НТРРМ
NEIRDLARLVAEFHDLI	KDODV
LNPKTIVKLFDSIDAWR	NA VICE
EQLALTSEADVRGRTG	FESADY
PQGRWLREAWEVAQS*	VPTKAV
VEAGFKGVEIREELTRE	RIAAA
SDTIPQLNEHDIHRRRH	NKAIN
GERDQRNALNQLQEGF	NRYQR
HHKSGDQPNGKHRDIA	ACQEA
PALVEIERRCAHHHRHI	RQQERK
SEQHAARFGIANGDLV	RVWNK
RGQILTGAVVTDGIKKO	3VVCV
HEGAWPDLENGLCKNO	<b>JSANVL</b>
TADIPSSQLANACAGNS	SALVYI
EKYTGNAPKLTAFDQP	AVQAN
TRPLRLARNQHRAFRC	RITFHR
FTRIMWVEEIGQRFGN	HPFGRV
RIQDSLCVCGALRYISA	TFNVW
RKRAVTCVRSFGSDFTG	<b>JSPPLR</b>
APKGESIRRLLALREAG	IIHILAL
GEDYKMEINESRTVLK'	TEDNSY
SFDVFIDARGQRPLKVK	DIPFPG
LREQLQKTGDEIPDVGI	EDYTLQ
QPEDIRGRVAFGALPW	LMHDQ
PFVQGLTACAEIAAACC	GPFDKD
RIEGGIVVRMAKEGETI	LVLLDG
TEAKLNADTLVIADHN	KALAM
GGIFGGEHSGVNDETQ	NVLLEC
AFFSPLSITGRARRHGL	HTDAS
16015 46383 A 16106 390 636 KFLSFRPDRVCVACAE	ARAGL
CLRQCITGHPEACLAIP	VLVCVE
CWGGTDADQPVAVFPS	RFSQV
SPDRGT*QWLCWKFL	
16016 46384 B 16107 1 520	
16017   46385   A   16108   142   243	
16018 46386 B 16109 275 919	
16019 46387 A 16110 1 693	
16020 46388 A 16111 522 714	



SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
16021	46389	A	16112	1	900	STCSSRSHLHLIQASPILPNYVA
						TAVAARIIADVQGISDTCVIAQP
						SPPHPGALRTLVFTTDEPETPOP
						PGAAGFOLVOKKOVOLHNVLY
1						VMTPHAFAOGTVTIYLPGEOOT
						LSVAPLKNVVQLVTQQHLRDR
l		i				LWWPGAFLTDFAAKVKALKD/
1						YPNHVMAORASGEAEADDDV
		1				AATIKSVRQQLLNLNITGRLPV
		1				KLDPDFVRVDENSNPPLVGDYT
						LYTVQRPGTEQGSFKVKRARA
						RVROTRAPLFGPKSPAPEHMES
		1				ELEFELIGPSKSTSGNPRGLRSE
						RPVLFCLYPEMPTAAAR
16022	46390	Α	16113	150	649	NALLGTCPGTARFPGTGSAPTL
		ļ				HPDASRSGRGRAACPRSAQWS
		1				PRPWQSVAGLAWLGAHWGSR
1						STSRTAETTASKRGHPRSPAAQ
į.						LPPGPRPPRAPQLQRALQSVHP
i						LSPRPAPLA/EPKLTAACWAEA
	}					VKITTVRYSDSCSRLLTDLGKP
						VQSMLLKDIRKVYNWQ
16023	46391	Α	16114	153	740	THQLFLPPHHQEISQTTWLSAA
						WPRHTCAHSLSPLQPPVPFSRP
1						HVPLPGPSKTWSDGPRLQSLPG/
		1				RPSERTPRR/CRSASGQPPHLGG
		1				EERLCLAAPSGRICHCEGDDES
		l			1	PLITPCHCTGSLHFVHQACLQQ
		1			1	WIKSSDTRCCELCKYEFIMETK
		1				LKPLRKWEKLQMTSSERRKIM
		<u> </u>				CFSDIPRHCRPMCGLVLVCAH
16024	46392	Α	16115	1	1194	
16025	46393	Α	16116	323	642	TGYARQKPVPALGWWTNVSAS
		l		1	1	TAPPIILPSITGSRLAVIKWLTVS
						AGKLSALLCASCQKGG/VGEM
						ANGNGERNHKQIGDTVLTPPQ
l		l				HYRKIYQPIAARSCIRCVCGS

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hed	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
16026	46394	Α	16117	ī	1782	MAGIRSTLIKEKNMITNYEATV
				ŀ		VTTDDIVHEVNLEGKRIGYVIK
						TENKETPFTVVDIDGPSGNVKT
1					LDEGLSLLLSLVSIVVIMKLFYO	
						YEQRFGMRSTSLLNVIGSNTIAI
		1				YTTHRILVEIFSLTLLAQMNAA
		1				RWSPOVELTLLLVYPFVSLFICT
						VAGLLNLTTVMPEQYRYTLPV
				1		KAGEORLLGELTGAPCATLVA
				i		EIAERHAGPVVLIAPDMONALR
		ĺ		l		LHDEISKFTDOMVMNLADWET
			ĺ			LPYDSF\SLHQDNYLLVAFQPFY
						QLTDDAAVGVLIVPVNTLMQR
					1	VCPHSFLHGHALVMKKGORLS
				ŀ		RDALRTQLDSAGYRHVDQVME
						HGEYATRGALLDLFPMGSELPY
						RLAIGVNVAQAEVLNLESGAK
						QVLQETFGYQQFRPGQEEIIDT
						VLSGRDCLVVMPTGGGKSLCY
				l		OIPALLLNGLTVVVSPLISLMKD
						OVDOLOANGVAAACLNSTOTR
						EQQLEVMTRPRIGDGTGALRK
						RVAQLAFKNQPMMVGNWAQS
						ILHGGVIASALDVAAGLVCVGS
						TLTRHETISEDELRQRYRGWGP
						LIFALIICAQAGASVLLLLVACC
						VQAIKSPSPALNYTMKNSFILPV
16027	46395	Α	16118	380	1431	TALLIRDMPPYVEAYPNENLTT
						VMPEQYRYTLPVKAGEQRLLG
						ELTGAACATLVAEIAERHAGPV
				ĺ		VLIAPDMQNALRLHDEISQFTD
						OMVMNLADWET\LPYDSFSPH
						QDIISSRLSTLYQLPT\IQGGVLI
						VPVNTLMQRVCPHSFLHGHAL
						VMKKGORLSRDALRTOLDRAR
				l		YRHVDQPAHAGGKVLEMIVVG
						IATWLGFLLFGLNYSLLLAVLV
						GFSVLIPYIGAFVVTIPVVGVAL
						FOFGAGTEFWSCFAVYLIIOAL
						DGNLLVPVLFSEAVNLHPLHHR
						EQIGGNKMADRQCRKIVCATV
						RQLPEGGRGEMANGNGERNHK
						OIGDTVLKATGSKOGDGONHG
16020	46206	-	16110	1	940	QIGDT VLKA IGSKQGDGQNHG
16028	46396	Α	16119	1	940	

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
16029	46397	A	16120	114	1380	NRVHCRRCSGGDTGVSHLKGI
10029	40377	^	10120	1114	1500	NVKYRYELTDSVGVMASLGFA
						ASKKSSTVMTGEDTFHYESLRG
						RYVSVMAGPVLOISKOVSAYA
		1				MAGVAHSRWSGSTMDYRKTEI
		1				TPGYMKETTTARDESAMRHTS
						VAWSAGIOINPAASVVVDIAYE
						GSGSGDWRTDGFIVGISGVLKD
						GTGKPVQNCTIQLKARRNSTTV
				1		VVNTVGSENPDEAGRYSMDVE
		ŀ				
		l				YGQYSVILQVDGFPPSHAGTIT
						VYEDSQPGTLNDFLCAMTEDD
						ARPEVLRRLELM\VEEVARNAS
		ŀ				VVAQSTADAKKSAGDASASAA
		l				QVAALVTDATDSARAASTSAG
		-				QAASSAQEASSGAEAASAKAT
				1		EAEKSAAAAESSKNAAATSAG
						AAKTSETNAAASQQSAATSAST
						AATKASEAATSARDAVASKEA
						AKSSETNASSSADYAAS
16030	46398	Α	16121	165	299	GILPISEPPSNRIFACWGKPAWT
						ACCNSLRARR*RAISCCPSHW
16031	46399	Α	16122	1	388	MGSKSWVTQKGPAKAQSSQV
						GRVKQATATDTGRTRDSHMER
						PKCSKGYLCLPYMALQQHHLL
				ļ		SDVTVRGFVAGATNILFRQQKH
		l		i		LSDAIVEVRLCGSDLVLYGTST
						PKNLIWVMVHVVGHRPDRR*C
		l				CCNA/SVRQTQISLRAFGSFHM
				1		AVSGSSSVSGCSLFHSAHLTAL
			ļ			CFSWPLLCYPTLGPH
16032	46400	A	16123	130	414	
16033	46401	Α	16124	1	387	
16034	46402	С	16125	1	1611	
16035	46403	A	16126	318	401	
16036	46404	A	16127	519	658	YPGSQLLASKGTKLDGE*V*RS
				l		RLQKVGNNKLLQAKGACSNPT
		1		l		QES

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		i i		sequence		
16037	46405	A	16128	<u> </u>	1837	FRPRQLVAAKPSVFADVQSMES
10037	40403	^	10120	1'	1637	VGTGGGAEAEGGVRSRGLCPT
		1				RMLPGLAAAAAHRCSWSSLCR
		1				
		1				LRLRCRAAACNPSDRQEWQNL
		1				VTFGSF\SNVVPCTHPYIGTLSQ
						EKLYSTNVHKEGQGSHTLREE
		1				KVPSFVTAEGVGAKLISPLKQE
		1				PLQVRVKAVLKKREYGSKYTQ
		1				NNFITGVRAINEFCLKSSDLEQL
						RKIRRRSPHQDTESFTVYLRSD
		1				VDAKSLEVWGSPEALAREKKL
		1				RKDAEIEYRERLFRNQKILREY
1		1				RDFLGNTKPRSRTASVFFKGPG
		1				KVVMVAICINGLNCFFKFLAWI
	İ	1				YTGSASMFSEAIHSLSDTCNQG
		1				LLALGISKSVQTPDPSHPYGFSN
		1				MRYISSLISGVGIFMMGAGLSW
		1				YHGVMGLLHPQPIESLLWAYCI
1		1				LAGSLVSEGATLLVAVNELRRN
		1				ARAKGMSFYKYVMESRDPSTN
1		1				VILLEDTAAVLGVIIAATCMGL
		1				TSITGNPLYDSLGSLGVGTLLG
		1				MVSAFLIYTNTEALLGRSIQPEQ
		1				VQRLTELLENDPSVRAIHDVKA
	İ	1				TDLGLGKVRFKAEVDFDGRVV
1		1				TRSYLEKQDFDQMLQEIQEVKT
		1		i		PEELETFMLKHGENIIDTLGAEV
						DRLEKELKKRNPEVRHVDLEIL
16038	46406	В	16129	1	1065	
16039	46407	Α	16130	1248	1658	PLALPEFISKSWKERLTDTTVLF
i						LKARRQSLCLQIGGDPLES/ILQ
t						AFCVLSVAKESQLYTYLHAIMR
1						TLKSSIARGARTFQSTSDGTVKS
1						RPSKIIFLPRLHDRFRFSALRHL
						DPKKLDLGDGSRSAHRPDRRFF
16040	46408	В	16131	969	1026	
16041	46409	A	16132	339	432	RYMVLSEFRSMQTGITKWKERI
		L				L*NCRKRE
16042	46410	Α	16133	3	443	HTWNSDRTMYLQRRHIFFKNC
		1		1		FWLQAGYSLGAPSWRSLVTVW
		1				QIIFSDFYRKTLCNSNSPLF*SLC
		1				QRQSTLLGTLLIFCSYASSPEAI
						NSAAPRVRSPRTDPRKARSPRG
						VGGAEGNGSRDTEPKGGRPLA
		L				TPSQGERLMAGTVTK
16043	46411	В	16134	34	1426	
16044	46412	С	16135	62	217	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
16045	46413	Α	16136	1	609	MIPVSEKSKIGQLNLMLKGKKT
		i				KGKKVALVPAAVKKQEAKKV
						VNLLFEKRPKNVGIG/QDIQPKR
		l				DLH\RFVKWPRYIRLQQQTAIL
		İ				D/QFIQALDQQTATQLLKLAHK
						YRPETKQKNKQRLLA\RAEKKA
						ASKGDIPNKRPPVLQAGVKTVT
						NLVENKKAQLVVIAHDVDPVE
						LVVFLPVLHCKMGVPYCIIKGK
						ARLGHLVHRKT
16046	46414	Α	16137	1	824	GTRPKMPKGKKAKGKKVAPAP
						AVVKKQEAKKVVNPLFEKR\PK
		l			1	NFGIGQDIQPKRDLTRFVKWPR
						YIRLQRQRAILYKRLKVPPAINQ
		l				FTQAL\DRQTATQLLKLAHKYR
		1				PETKQEKKQRL\LARAE\KKAA
		1				WPKGTFPTKRPPV\LRAGVNTV
		i				TTLVENKKAQLVVIAHDVDPIE
		1				LVVFLPAL\CRKMGVPYCIIKGK
1		1				ASLGRIVHRKTCTTVAFTQVNS
ł		1				EDKG\ALAKLVEAIRSNYNARY
1		1				DEIRRHWGGNVLGPKSVARIA
		<u> </u>				KLEKAKAKDLATKLG
16047	46415	A	16138	1	799	
16048	46416	Α	16139	1	344	MHQTTAKTPHTSYPNNYEEHN
		1				RRANRSKNYDRIRHTTIILKRTN
1			i	1	,	PAQTITNLLKSRFNRYNYVQPR
					İ	SCRSIFIHIPGERDLNLCIAPNPP
		1				AIFPTSIGYLGPDLNNLPTYAPFI
						TTNLTGPAPTTTHPVGNLGTTG
						NPEPGGCGILIVWCCVNWACL
l		1				WDSVVAAPREPYMPAGLLRHR
		l				RHYRHRREDLIAVPAARQTDE
		ı				NRRPALCHEYAVGHRKIKTNV
		l				EHTEPYILPLITHSQPLNRGAFF
		1				CPGVRFLVVSVLDFEKRLAFAS
						*SCGVQLRIRGKVQGVGFRPFV
		1	l	I		WQLAQQLNLHGDVCNDGDGV
	ļ	_				EVRLAYRVLVGQPQHYPRGRP
16049	46417	В	16140	1	1323	
16050	46418	A	16141	I	1356	
1605 I	46419	A	16142	I	1524	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
16052	46420	A	16143	173	2310	QQWASRTRRWRSLITTLCVDA
						RSQHDYIALSRLFHTVMLFDVP
						VMTRLMESEARRFIALVDEFYE
						RHVKLVVSAEVPLYEIYQGDRL
						KFEFQRCLSRLQEMQSEEYLKR
						EHLAAKPETVKRDWYVVDAT
						GKTLGRLATELARRLRGKHKA
	İ					EYTPHVDTGDYIIVLNADKVAV
			ŀ	ľ		TGNKRTDKVYYHHTGHIGGIK
						QATFEEMIARRPERVIDNRRGS
				İ		LRQAGYAIHDGGNNSMAKNTS
						CGVQLRIRGKVQGVGFRPFVW
				l		QLAQQLNLHGDVCNDGDGVE
İ				ł		VRLREDPETFLVQLYQHCPPLA
		l		l		RIDSVEREPFIWSQLPTEFTIRQS
				1		TGGTMNTQIVPDAATCPACLAE
		i		l		MNTPGERRYRYPFINCTHCGPR
						FTIIRAMPYDRPFTVMAAFPLCP
			i			ACDKEYRDPLDRRFHAQPVAC
						PECGPHLEWVSHGEHAEQEAA
				l		LQAAIAQLKMGKIVAIKGIGGF
			1			HLACDARNSNAVATLRARKHR
						PAKPLAVMLPVADGLPDAARQ
						LLTTPA\AP\IVLVDKKYVPELC
1			l			DDIAPDLNEVGVMLPANPLQH
						LLLQELQCPLVMTSGNLSGKPP
					1	AISNEQALADLQGIADGFLIHN
1						RDIVQRMDDSVVRESGEMLRR
1		l				SRGYVPDALALPPGFKNVPPVL
1			1	l		CLGADLKNTFCLVRGEQAVLS
1		1		l		QHLGELSDDGVQMQWGQRLC
						RMGTQVLPPTFNIEKKVQSARY
16053	46421	С	16144	1	184	
16054	46422	A	16145	85	416	
16055	46423	A	16146	96	570	L

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown.
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
16056	46424	Α	16147	2	1690	CCCCPCCCPCWGRVSGSVAGG
				ł		PRQGLGLPLSLCISPGSLNKDPS
		1				YSLQVQRQVPVP/EGLCVIVSC
						NLSYPRDGWDESTAAYGYWFK
		1				GWTSPKTGAPVATNNQSREVE
		1				MSTRDRFQLTGDPGKGSCSLVI
	ŀ	1			ì	RDAQREDEAWYFFRVERGSPL
		ļ.				TQKPDVYIPETLEPGQPVTVICV
		1				FNWAFKKCPAPSFSWTGAALSP
		1				RRTRPSTSHFSVLSFTPSPQDHD
		1				TDLTCHVDFSRKGVSAQRTVR
	ļ.	į.				LRVASLELQGNVIYLEVQKGQF
		1			i	LRLLCAADSQPPATLSWVLQD
		1				RVLSSSHPWGPRTLGLELRGVR
		1				AGDSGRYTCRAENRLGSQQQA
		İ				LDLSVQYPPENLRVMVSQANR
		l	1			TVLENLGNGTSLPVLEGQSLRL
		ŀ				VCVTHSSPPARLSWTRWGQTV
		ļ			GPSQPSDPGVLELPPIQMEHEGE	
	l	į.				FTCHAQHPLGSQHVSLSLSVH/S
						PSTAAGPLLLLGG*GSALQLLL/
						SRPARPPLCAGGLGRSCWRGTA
		ŀ				VRAPSRSPPAQPGPGPTAP*AS
						MEGSAPASGSAVRPGTSTGPRV
		į.				ALSSSCYQGSWSMGEDLAWGL
1000	15105	<u> </u>	14440		1570	PWELASLPCSLSVPALSSSG
16057	46425	Α	16148	3	1578	VTQLLCTSNGRRALEFALFPGR RFRPVATNHQSREVEMSTRGRF
						OLTGDPAKGNCSLVIRDAOMO
		1				DESQYFFRVERGSYVRYNFMN
	i	1			İ	DGFFLKVTGMEWGGNPCLSH
		1	ļ			WGGTLGTAYGLSREGSQGPLQ
		1	1			HKN/HPTTVSVPALTQKPDVYIP
						ETLEPGQPVTVICVFNWAFEEC
		1			i	PPPSFSWTGAALSSQGTKPTTS
		1				HFSVLSFTPRPQDHNTDLTCHV
						DFSRKGVSVQRTVRLRVAYAP
					i	RDLVISISRDNTPALEPQPQGNV
						PYLASPK\GQFLRLLCAADSQPP
		1				ATLSWVLONRVLSSSHPWGPRP
						LGLELPGVKAGDSGRYTCRAE
	ĺ	1				NRLGSQQRALDLSVQNPPENLR
		1				VMVSQANRTVLENLGNGTSLP
			1			VLEGQSLCLVCVTHRQPPSQAE
						LDPEGTGSEPLPALRPRGSWSW
		1				LVGSSGARRRVHLPRSAPTGAP
		1	l	1		RRTLLPSPCTTPRSCWAPPAPGR
			l			LRVCTAAAPPRPARPPLCAGGL
				1		GRSCWRGTAAQGLLRGSPPAQ
				I		PGPWAQTASPEPSMEGLNSGPQ
	L		L	L	L	I OI HAVIASI EI SIMEOENSOFQ

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop eodon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
16058	46426	Α	16149	90	1029	MLLPLLLSSLLGGSQAMDGRF
						WIRVQESVMVPEGLCISVPCSFS
		l				YPRODWTGSTPAYGYWFKAVT
			ŀ			ETTKGAS\VAPNPP\SREVEMST
			ļ			RGRFQLTGDPAKGNCSLVIRDV
		1	Ì			OMODESOYFFRVERGSYVRYN
						FMNDRVL\LKVTALTQKPDVYI
		1		1		PETLEPGOPVTVICVFNWAFEE
		1		1		CPPPSFSWTGAALSSQGTKPTTS
		1		1		HFSVLSFTPRPQDHNTDLTCHV
		1				DFSRKGVSAQRTVRLRVAY\PP
	l			1		ETFGISIFTVTNTPDPPENLRVM
						VSQANRTVLENLGNGTSLPVLE
						GOSLCLVCVTHSSPPARLSWTQ
						RGQVLSP
16059	46427	Α	16150	270	1001	CCCTVYRAFIRKRLKRSSDSVY
					1	RRKNPSASYDRDAEASLAAVK
		ŀ				SGEVDLHQLASTWAKAYAETT
l		1		ŀ		LEHARPEEPSWDEDFADVYHD
				İ		LIHSPASETLLNLEHNYFVSISEL
		1				IGERDVELKKLRERQGIEMEKV
	l				i	MQELGKSLTDQDVNSLAAQHF
				İ		ESQQDLENKWSNELKQSTAIQK
	1			1		QEYQEWVIKLHQDLKNPNNSS
1			İ			LSEEIKVQPSQFRESVEAIGRIYE
	1					EQRKLEESFTIHL*AQLKTMHN
16060	46428	Α	16151	60	648	LAMSLSHLYRDGEGRIDDDDD
						ERENFEITDWDLQNEFNPNRQR
						HWQTKEEKGSLQRKEFFTDLV
				ŀ		GLCFCAYRARDYSAPVNFISAG
			1	İ		LKKGAAEEAELEDSDGFLRFFFI
	1			l		LFFH*LSFDFSFLQGGNFKPSQK
			1			GFAGGTKSFMDFGSWERHTKG
	1					I*FTYMNCCDRKTLFFFC*NSSG
						IINPIEAKQRKGKGAVGAYG
16061	46429	Α	16152	237	450	LAMSLSHLYRDGEGRIDDDDD
	1				/	E/REENFEITDWDLQNEFNPNR
	ŀ					QRH\WQ\TKEESTYGVWAERDS
						DDERPSFGG
16062	46430	Α	16153	12	85	VSFLSMGSGHCIRSTRGSKMVS
						WSVIAKIQEIWCEEDERKMARE
						FLAEFMSTYVMMNIHMIVEKN
				1	1	T*SPFCPWARATVSGPPVAPKW
		<u>L</u>				SPGP
16063	46431	Α	16154	49	481	
16064	46432	A	16155	20	248	
16065	46433	Α	16156	493	728	VSFLSMSSGHCIRSTRGSKMVS
1	1			1	1	WSVIAKIQEI*CEEDERKMAREF
1	1	1		1	1	LAEFMSTYVMMVSGRAARSG
		L_				WALPGPSMTPSPF

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
16066	46434	Α	16157	136	306	ASSSREGLTKFAKFTKFTKIHQI *ITLTSYSIKSLEKVCADLIRGTK EKNLKVKGPV
16067	46435	A	16158	563	1216	MMFWPELQPRVCWMGLSWVN HQNGRRRKNQKHH*QKVPLL IMASK*KLLEFLNRETKASANL SETVTKPPLPQKNTAQVGASSQ TRKPNKLAPHPAVPAFVKNTCP SRPRERQTHFLRPREDRMVAL KPIKVLPPVFMPFSSPQGIRSR MPTQHLYCRWVAPKALVPTCL FTHSLSRKEEKPKMDTPFLPY SRPPSGEWLLIVLWFFNRSQRS
16068	46436	Α	16159	1	143	
16069	46437	Α	16160	40	230	KQAAQPAVATLSGPLPHCGSFV LSLFAINLVAAHSLGPHCLYEL* HSPRRSTASLREGPRLHS
16070	46438	С	16161	233	319	
16071	46439	Α	16162	290	472	EFLDTFCYIPKVVDQ*D*THKQ QHNVAIIPHVSSAQMSTFC*RT MPTISDDPWHMASMRAV
16072	46440	Α	16163	3	553	
16073	46441	С	16164	270	608	
16074	46442	А	16165	2598	2943	HISPRGSAASFLKSVRPRTHQFR TQEDRLSPGIQDQPGQPSNTPSL QKL*N*LGVMGRICSPSYLS*P WREDHLSPGG*GCSEP*LHHCT PAGVTKSDRVSKNK*INKNKIN NDNQ
16075	46443	Α	16166	2	58	
16076	46444	Α	16167	218	342	
16077	46445	Α	16168	734	872	
16078	46446	A	16169	1233	1706	CLVFWLLYYGG,QLPFHLLPHS LGSGQQSSEESAATPSLAEGRR EAAFRCGPAGLARQAWRPHAR LPGPAAPLAAPSLAPLPTGRSG RWLFMLCAASC*SPSPAMSVYP QRRLGQGGAEDSEGGPVSRGC RAPGPQRPLAAPGEQTAARTQ AICLIW
16079	46447	A	16170	598	1159	CROTGVKIYDVWFFWLLYYPG LQLPHLLPHSLGSGQQSSESA ATBSLASGRREAAFRCGPAGLA: RQAWRPHARLPGPAAPLAAPS APLPTGRSGRWLPMLCAASC'S PSPAMSVYPQRRLGQGGAEDS EGGSVSRCCRAPGPGRPLAAPG EQTAARTGASVYLLLPHSPPLL SALHIHHLLPPS

SEQ ID	SEQ ID NO:		SEQ ID NO:	Nucleotide	Nucleotide location of last	
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
		l		sequence		
16080	46448	Α	16171	834	1185	RSLFRHHRPSAAFPRTPCSDCPR
						CSAGTMEDCWLVLGSPELR*KS
						LHERPFHWLPSPSRARCCLPRSE
1						TPAGPVPPRPGPRRARRPRGTS
						RPPPASSRGRGALGSLPASEPLP
					1	ARAT
16081	46449	Α	16172	78	478	VVKNSLIFLVNQVLNSRDFHVF
ľ						FKTT*NCPAQAHTAALYQGLGP
						ACSQRASHWMSSSSKRSSKSLK
İ					l .	KSA*TAFSLAAKSIKSPGAASRL
		1			l	GNGKARLCQVRFPKEQVISALQ
İ	ì	1				GHYPHKKRRWVRGNRLKLEST
		ļ				F
16082	46450	С	16173	1323	1656	
16083	46451	A	16174	77	231	RSCMTLMWPRSTP*FGLMERR
	1	1				RHMFDWLLITMLWMLPTKLGS
	1	1		l		SKLSPAA*F*SSCLIL
16084	46452	Α	16175	1	255	STSKGEKPAIRAMAHFLEPHPIN
1	1					FLGARARKADLSPT*YHFFKHL
						DNFLQGKCFHNQQDAENAFQQ
						FFKSQSTNFYAGSSFVTEV
16085	46453	Α	16176	690	1020	SPVLQRAFKNGPGTANERTVQ
						WWFKKLCKGDESLEDEEHSG*
		1				PSEIYNNQLRAIFKADPLTITRE
l						EVFPHPLYSPDLSPTSYHFFQHL
						DNFLQGKCFHYQQDAEHAFQE
16086	46454	A	16177	1	383	MHRSCGSDAYALLGERSVSLR
	İ	ľ				RCAVRHAGGIRSANADISNDKA
		į.				GEKPARRKTKGSCPTLIGAGLV
						QSLSPIQSAADAGELGSNGILPD
						VESLRIPVQYLANLLTAGDTKP
		l				VLRALKRMLAMRHYKRAETV
		1				DGKVDTRALEEVGLTEAQAQE
		1				MYRYLAIANYEDRFVVPSSHRE
						LAREAFPEKNGCGFTFGDGCH
	1	l				GSDTKFNLFNSRRIDAID*PCPD
		l			1	*RWTGTLGLPASGLFTRFIVTY
	1	1		I	1	VSIRTSDTSSMPHSTPSQA\TERS
1	1	I	1	l		PNNA*ASLQTC

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	tocation of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
16087	46455	Ā	16178	740	1977	SASASRSLEHITVTPSTGILTCFP
						STTPFGLAL/GGTLGLPASGLFT
				ŀ		RFIVTKSSIFSVTPLVQPKPSCN
				l		GYSPPPPPVPHRREFQRRVIAEK
	į			1		IFCQHHRAKLNRLEERQYLTVN
		1		1		FRAIAQRVNIGITGLQITIDANA
l				1		AINROPGASCOGREPGAVRCGG
				1		NYRIHFDIALAVORWPECONPF
				1		FPAPVTEISTADERPSPLTGCLQ
		1		l		RLVTFGSVIFGIINMIMRLAPIGR
				1		FGAMAFTIGKYGVGTLVQLGQ
				1		LIICFYITCILFVVLVLGSIAKAT
1		1		l		GFSIFKFIRYIREELLIVLGTSSSE
				1		SALRRMLDKMEKLGCRKSVVG
1				1		LVIPTGYSFNLDGTSIYLTMAA
1				1		VFIAQATNSQMDIVHPITLLIVL
				1		LLSSKGAAGVTGSGFSVLAATL
						SAGGPIAGSGSGADPRYSTALC
16088	46456	A	16179	757	1037	FLDPSPEPNVTVTPSTGILTCFPS
10000	10.00	ľ.	1	l'*'		TTPFGLALGVDSPCPD*RWTGT
				1		LGLPASGLFTRFIVTYGVTPALD
		1				TGLM*LRSCGPPRSML*HRTQQ
						KC
16089	46457	С	16180	1	313	
16090	46458	Α	16181	178	290	LLLGLASEN*HCPIASEAP*TTT
		<u> </u>				DTELWVTLTVEGKS
16091	46459	A	16182	1	251	
16092	46460	С	16183	129	1136	
16093	46461	С	16184	117	748	VII OI I I PROPERTIES I PORTE
16094	46462	Α	16185	636	748	LLLGLAAED*RCPIASEAPQTIT
	14140	١.	15101			DTELWVTLTVEGKS
16095	46463	Α	16186	37	444	DPQVGKLLQHCPARIKMTVTF
						NNHRKPQLSKFHQLYSEDTQQ
						QIIRETFHLVFKRDENVCKFLGT
				i		IWSLTTGKLNRGQAPLFGIFHT
				i		VELHLEIRSSCQGIVHF*LTCFSS CPCSGPFVNSPFYLPLESGHSK
1.000		l.	16187	179	422	
16096	46464	A	16187	1179	422	LQLGPKEKQSRVLGSFFQVPSC
				l		GKMGCGSSGSRHIGFPP\PQLSG
				I		GPLDPRQGSGISEMK*TE*GGY
15007	16165	<b>L</b>	16100	1064	1274	PKGSPQHYSRKHQGS
16097	46465	A	16188	1064	1374	KEQCLQALSSVKNREKRPSSFH
				ĺ	1	PICWSAVSFSVGREGDMWPLAP
		1	1	ŀ		FPDSENVAGAGALLLRLAALPG
		l	l	1		LSWALRPPPPAPVRSWATSGW*
		Ц.	L	l	L	GGQGREPGRGIPPRW

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NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
16098	46466	A	16189	44	515	VGGGGVQPSMTMGDKKSPTRP
10070	10400	ľ`	10107		1	KRQAKPAADEGFWDCSVCTFR
						NSAEAFKCSICD\VRKGTSTRKP
						RINSQLVAQQVAQQYATPPPPK
						KEKKEKVEKAGQKRKPEKRPR
						KFSP/SVVTKKNTNKKTKPKSDI
						LKDPPS\EANSIQSANATTKTSE
						TNHTSR
16099	46467	A	16190	382	795	DSGRSWKRLLSPPRPMCDTWA
10022	70407	n	10170	502	1,75	LGSYPRLCFAVSPPFSCSLPLPSL
		l				FPHSPLLGRPKRQAKPAADEGF
						WDCSVCTFRNSAEAFKCSICDV
					i	RKGTSTRYLKICVTWVVVVI*Q
						VFIEHTAICALGVQWYKDRPGP
		ĺ	}			CSYGA
16100	46468	١.	16191	2	343	CSTGA
16101	46469	A	16192	472	625	KTSLFOHWLWKVTIVIVMF**L
10101	40409	^	10192	472	023	RVNVGKLLNNIHRYNSENLASL
						GSOWKFP
16102	46470	١.	16193	343	693	KTSLFOHWLWKVTIVIVMF**L
16102	464/0	A	16193	343	693	
		1				RVNVGKLLNNIHRYNSENLASL
			1			GSTQIPLKAFTNPCHTSFTLCKH
		l				MVIQAHQEKQLIQQILYLGDLL
						ET*HFQAFWQALDENMTLLESI
16100	46481	_	16104	240	534	TGFEGF
16103	46471	Α	16194	340	534	TAIMNDMVTI*TRKFMTNQRLQ
		ĺ				RKQMVIDVLHPGKATVPYLILI
		<u> </u>				EQLRFARHCAWYGGDSDETSH
16104	46472	A	16195	80	552	PIPHLEKFHAPTRRTFRGNQM\V
						IDVLSPPGKADQCP*AQEIPGKT
						*PKMYQDPHPDVI\FVFWIPELH
			İ			FGSRGKTKLAFGNDFMTSLGFI
						AKEKWNPKHRTLQGHGPGME/
						ERKKTSKGKPTERERQGTGLEG
						KFQGGLAKGPFFGAWAKRRNE
		L_				VSSS
16105	46473	A	16196	248	474	YPETPESPTQLSSGQPHREQPPE
				l		MPESPTQPSSGQSCQEQPPETPE
						LPM*PCLAQPSQKHMIKG*QNN
		_				KHHENKM
16106	46474	Α	16197	223	669	PRPSLPACSPWRIVDDCGSLKS
				l		WKRVCQWLQPCPNALP\$CLGS
				i		PLRCEFSGFPRN*LGLGSTTGSF
				l		AVWGGLFSTIDCGLVRRPGPSP
						FHPVLPALTSVSLPPTPPGGPLA
		1		l		MVGSAMMGGWSGEWEILHLA
				l		SSTHPYPSLPSPAPPFLE

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NO:	of peptide	hod	in USSN	location of first	eodon for last amino acid	*=Stop eodon, /=possible nucleotide
	sequence.		09/540,217	eodon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
16107	46475	Α	16202	188	484	HFGRVEVGRSQGQEFQTRLAN
	l					KAKHHLYSFMNESQISPIGC*P
	1					M/PPKLIRKVHREKNCAGRNLT
	1			i		R\QRSGFKTGPPGPPARPSSPTLP
	Ì					PPPPLPRLPRRP
16108	46476	Α	16203	36	409	
16109	46477	Α	16204	651	893	NTSVKNNFSFMNESQISPIGC*P
						MAPKLIRKVHRERNCAGRNLT
						RAEKRLQTPGLPVPPARPSSPSS
						PPTPPLPAATPGGR
16110	46478	В	16205	13	441	
16111	46479	Α	16206	3	205	NSSNSFSIQFCSFAGEELCSFGG
					EEAFWFLEFSAFLRCFFLIFRDL	
						STFGL*CAPLEEKRHSGFWNFQ
						PFCAAFSSSSGIYLPLVFDAGDL
						QMGFLCGCPFC
16112	46480	Α	16207	23	841	EKAKEFRRAEEKKKEVPAVPET
						LKKKRRNFAELKIKRLRKKFAQ
						KMLRKARRKLIYEKAKH\YHK
	1					EYRQMYRT\EIRMA\RMARKA\
	1					GNF\YVPA\EPKLAFVIRIQRVS
	1					MGVSPKGSERCCKLLRPFVKIF
						NGNLL*KLNKGFRLTML\RIV\E
						PYIGMGGTPILKSVNELIYKR\G
	l .					YGKIH\RKRIA\LTDYALIARSLG
	l					KYGIVCMEELNHEIYTVGKRFK
		ĺ				EANNFLWPFKLSSP\QGG\MKK
						KTTHFVEGGDAGNREDQINRL
						HRRNELTRLTWIFF
16113	46481	Α	16208	1137	1200	PPSAPAPG*LRPPALSSGSP*PPS
	1					APAPG*HAPPPSAGTPPP

SEO ID	SEO ID NO:	Mar	SEO ID NO:	Nucleotido	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
16114	46482	A	16209	1	1480	MNECRGVEITTVCSEDWIQRHL
	i					PGAVVPLKGEGNVGVATEDHY
	l .					QEDSFGFGLRGTGKPLKLEKSR
						PGAVTHTSPSDGLTQYVPDSLT
						AMPAAAVVIWVIRPGCGVOOO
						IGFLRHSNIDDIRPRTIIRAVAPV
						KLHGIRIKMASFTSATRLTDEO
					l	VITAPADSGIVIPRFSDNWVAG
						GKTHLTHKDSHKLKVKGWKK
	1			i		AFHANGHQKQAGVAILTSDKT
	1					NFKATAVKKDKEGHYIMVKGL
						DQQENITILNIYAPNTGAPKFM
			ŀ			KOLLIDVRNEIDSNTIIAGDFNT
						PLTALDRSSIOKVNKETMDLNY
				l		TLEOMOLKDIYRTLHPTTAEYT
	l .			1		IYSTVHGTFSKIDYMTGHKTSL
						NKFKKSEIISSSLSDHSGIKLEID
				l		SKRNHONHANTWKLNNLFLNN
						RWVNNEIKMEIIOLFELNNNND
						TTYONLWDTAKVVLRGKFIAL
	l			l		NAYIKKTERAKKTIYSHTSGI*K
				l		QEQTKPKPSRRKEIIKIRAELNEI
				•		TTKKTIOKK
16115	46483	A	16210	32	398	ASERLGGPGSPG*/PVNPRTDGS
	ļ				1	GAAWLSQRAQCTQSDPRV*EV
	ŀ					PEHLSPSTPSQEYRGLPAL\PHTS
				1		RPSHCLPACPLPSRTOPWVPVK
	1	1	ŀ			PGPTACRGFLQHSPTPGSPSP*S
	1			1		FOGSSWWDTDL
16116	46484	A	16211	2	681	AEPWDEGGDGVPCRVPSSGSV*
				l		V*TLYLDSSVQLCGTEAPQHPV
				l		DGPPGGKLCHEGSLHLRQGQIP
				l		GPRLVLQFVQQAGVCGPGGNA
		l		l		VYSTPRDSASLVSGRTSMLFLR
		l		1		KFGKTWRKGKLHORGPPASPV
	l .					LGRECNWG*VIGRHPAOSS/SGP
	1	l				ACAKDAAELGAAMPGLVSGPL
						GAALQPRGAGVQLGAATGPGS
				l		CSK/RGSPKADAR/PRHSOEPGO
	1			l		VPPHAPQGPGLS
	1		L		L	

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NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	Į į	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
		_				
16117	46485	A	16212	102	1005	VQWSARPDATPLSTEPSLADYP
						EAQSHIPRRGPRRPEKQGRGGK
		l				PPRALGRERAGGGSRGPPASPD
		ı				PLSRPCSQAPPPGASAGA*DAP
		l				ACRREAGSDGVPCRVPSSGSV*
		l				V*TLYLDSSVQLCGTEAPQHPV
		l				DGPPGGKLCHEGSLHLRQGQIP
		1				GPRLVLQFVQQAGVCGPGGTD
		l				GSGAAWLSQRAQCTQSDPRV*
İ	l	l				EVPEHLPQVDTHKGELYQ*PGG
	i	l				RDGPGWEEPPQCGMGVSEAHG
	l	l				GAGGPGEAGKGRLQRKFGKT
	Į.	l				WRKGKLHQRGPPASPVLGRPR
		1				PE*VLLRCD*EG*PPSAGQLL
16118	46486	Α	16213	378	494	GTACLQIPQTQGV*QRGFLAEY
1		ı				IQWQLRMRSGSIPVRTG
16119	46487	Α	16214	18	894	SVGSLCCLQETPGLRAFGVPWR
		l				SAQRRWPRRSAASLLSLVLPGR
						AHSPRPTLAPGPLEAQQPPPGG
1		l				SALAQHSRTAPAGTSAACLWP
ĺ				l		VSEQGAAPMCQVTRPPGSQAP
						CSQPSAHAHKHLTTGSSSPAEA
				l		SALPRA*TGSRWETKSSERVSSF
				l		SA*GTACLOIPOTLRRRTG*RO
				l		VGRRLPGSGGFDGCSIFS*S*PV
1						TYSLRSVSATSSNEATOLGTT*S
}						NSIIFEFCSAQSTAVRCRLFST*T
İ						DAPWSRSSSTTKTCFSITASCSA
		l				VLPLLLEALMEAPCPCLACSSA
1		l				s
16120	46488	Α	16215	340	582	
16121	46489	В	16216	93	711	
16122	46490	Α	16217	1378	2081	LSRKKPNWPSSMPWYQFSLIWL
		l				MSVKTSPSWKPSSPWFSGWKS
		l				YSTLOLGWSRGGMLLLGVOM
		l		l	İ	DLLEDWKGDEAAILGTVVQGK
				l		PPLDCSGSPRSK\APRTWAYTPA
1						WGVRKLPASCA*ASLPARPGSA
1		1				WPASGRSAAPPP/AARS*LICSM
l						SVSRRLCMLVSATSLESSNFSSA
		l				WRSSSSGILPCRFSMSRESFTSA
		l				RCFMDSPASSSASLKLDSLPSSF
		l				WWRIRHSLRSPSDCG
16123	46491	A	16218	191	288	
16124	46492	A	16219	67	209	
16125	46493	A	16220	96	341	
16126	46494	В	16221	1	1185	
10120	40474	D.	10221		1105	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
16127	46495	Α	16222	1192	703	AMPSCTRAGLAFVCHVRRRGC
				Ì		LSCRGVIPASSOCLFPAPMGTTE
		l				ATLRMENVDVKEEWQD*DLPR
		1				PLPEETGVELLGSPVEDTSSTSN
		l				TLNFNGAHRKRKTLVAPEINISL
	i	l				DHSEGSLLFDDFLDTLDDLDIN
		l				VDDIETPDETDSLEFLGNGNEL
						EWEDDTPVATAKNMP
16128	46496	Α	16223	8084	8251	TAGDERHGPSRVRMFRIKGRRL
						GWMGPLGRGKR*VTRGMWPG
						KGPAYPGSSASSF
16129	46497	Α	16224	645	1317	WGASRLREPPSPRTLHSPRPGP
		1				ASAPPLRPLPQNRTPSPSAASTT
ŀ		1				APPQPSEASRLPA*KAKPKPHPP
ŀ						SAPRRGGSPPRHSAQPACGRRR
l		1				PRSVGGAAPYAAERRNSAPQGP
						PQRLRRTAEGGKRPSNPRQRSH
				1		PRQRGDSLP*LGPWSRDRRAGR
ľ				1		DGRDGSAGGTRRSPSPRYASPE
						PLGPAAPASPAGASWTGGPGRR
				[		ADDSWRASVFGAQSSACFPRA
16170	46400	В	16225	72	378	RVL
16130	46498 46499	A	16225	72 151	372	GGQHWAKAWRQTLGPEMPER
10131	40499	l <sup>A</sup>	10220	131	372	TGACGCGSL*PFTTPPPPAICVD
						GTFHKYVFTPDGNCNREAFDV
						YLDICDDDDF
16132	46500	A	16227	182	1083	HPGPCPDHEOVGSMGLVEDPV
10152	140300	ľ.	1022	102	1003	SPGLPLTLNLGPDNPPTCPAVLI
l		1				WDDAREGKD*EG*SSLGIPPPP
		1				HGHPVLCDTHRIVIVLKNROLC
		1				PF*DAASSSAAHPTPHLHTLGL
		1		İ		CELPCGLLAPSLHTTPTSDSSLL
						PODLASTKPGTSSAPFTINAHOS
						DIACVSLNQPGTVVASASQKGT
						LIRRVCMVGW*PHTT*HVGITA
						DLSSSINFSHDSSFLFPTLPCPCP
		l				PAHLPYLGLASAACRLARVGK
		l				VGPMIGQYVDSQWSLASFTEM
		1				PERTGACGCGSL*PFTTPPPPAI
	1			1		CVDGTFHKYVF
16133	46501	Α	16228	202	517	GVHCHGFSAGQAAGQEPTSVH
					1	l
i .		1			l	ETLLPHQLQDQSALRGGVQNR
						ETLLPHQLQDQSALRGGVQNR QRHQAAEGPGERAGAAVSVGL

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	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
16134	46502	A	16229	141	633	WENARPEPSQGDLRAASVVSPR
1				İ		LPPRKGQGGLGYFGRGAGHAH
						GTAGQGASESETLLPHQLQDQC
				i		ALRGGVQNRQRHQAAEGPGER
				1		AGAAVSVGLGEPQCH*VGAGR
İ						AARGPPILEVPAGGGDAAAECP
İ		l				AGPHGQNARGQQSGISQLRHE
						REFLLRPFPQAPQL
16135	46503	A	16230	65	466	VVFAEAAEASLMTSGVGGGAA
						QSPRSRRGGWWPLGEMPYANQ
	1	1				PTVRITELTDENVKFIIENTDLA*
					į.	GYRGKRLAALGRGRPKPGPRG
						RGRGCSGWGGGDVLPELPPCT
		l		1		RALALGACGAGPACRGCSAFTP
1		1				LGF
16136	46504	A	16231	42	491	SGGKEAQGQSGTDQTVVVLSN
		1				PTYYMSNDIPYTFHQDNNFLYL
	1	l	Ì		1	CGFQEPDSILVLQSLPGKQLPSH
		l				KAILFVPRRDPSRELWDGPRSG
		l		i		TDGAIALTGVDEAYTLEEFOHL
		1				LPKMKGNKWEQKSHYKPDWD
1		1				*NLSCLFRQVLNFVIVAPP
16137	46505	Α	16232	531	976	NOSIVRVNVDNSLSIPVIAAELG
		1				VRKPSEKGMQQKKKTKDLGFR
		1			i	AGKESKTEWRK*GLODMASO
						MFASPLK*PVTAAFHDSSMPSS
						LLQIEMEQLFLEARLQLDSKSE
						ARRNOCDSMLLRNOOLCSTCO
						EMKMVOPRTMKIPDDPKAS
16138	46506	A	16233	2	419	SFLLSSSYTRTKSILRWPSLKKR
10150	10000	· ·		_		ESGFPLNSSNSGVRKSC*LSSDP
1						KSGTIVCPRFSNTISPSSSSSSSSS
		l		l		CSKTFL\PSFSCLPQKAAPNLAR
1				1		SWGLPGSRTARLSQGPDRGPRG
						VCRLGSGAAEPSORRGKPSRDE
		l				iv
16139	46507	A	16234	27	792	INSIRILSTCKMGHPRFAPQAPG
10137	10507	ľ.		Γ΄	I	PLRTSEKGPAVLPAWGNSSSDH
				i		SSEPSVGFYFNEDSDGSHPVLQ
						MRACSPDPAQGARPSAEAPGQP
			1			*HSASRGSDPKVASEWRLPHAE
			İ		1	ASPOLPGFSGAASPAPKHSCSSF
			1		1	SCLPQKAAPNLARSWGLPGSRT
1			l		1	ARLSQGPDRGPRGVCRLGSGA
			1		1	AEPSORRGKPSRGTHRPEPRAG
					1	GRLSPAERSPETEHAOCGRRGS
			1			LRND*TSPVLRGAQKEVGRRD
			1		1	CRGSSAILRAGEL
	L		L		1	CKOSSAILKAGEL

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
16140	46508	IA	16235	343	969	YDKTRLFNTVPLPPPHKKIIKKII
		1.				ODIKGEILRAFPLRTGTKHRCPL
	İ	1				SPLLFNILLEVLARAIRQEKEIKS
						IQIGKEEVKLSLFADDIIIYLESP
		1				KYSSRKLQELIKEFSKVSRYEIN
						VHKSVALLYTNSNQAENQIKKS
1		1				TPFTIAAKNKIKYLGIYLTKDAK
		1				DGYKENYKTLMKEIIDDKNKQ
		1				KYIP*SWKGRINIVKTTILSTAIY
16141	46509	A	16236	15	403	ICESRRGRVCSALVRRYVGEGF
		1				GKAGSICMPOAPDKSSRWTILI
						RPPRFPPS\PSCSPGKEAPGGSEL
		Į.				/SPLPHAWPSDPVSPLGDRVTA
						NPAEIR*EPGPOSAAPGFREORR
						RGQMG*IWYLTPTPPGGQ
16142	46510	A	16237	19	454	KGKSLLCTSPKVCRGRLRKSRK
101.12	10010	ļ.,		1"		PETKVTHICMPQAPDKTSRWTI
		i .		ì		LIRPPRFPPS\PSCSPGKEAPGGS
		1				EL/SPLPHAWPSDPVSPLGDRVT
		1				ANPAEIR*EPGPQSAAPGFREQR
1		1				RRGOMG*IWYLTPTPPGGORPS
i i	1			1		SAASPRGFPLV
16143	46511	A	16238	276	898	MKGTAPWRCGSRRGRVCSALV
10145	1.0511		10250	1-1-4		PKVCRGRLRKSRKPETKVTHIC
					l .	MPQAPDKTSRWTILIRPPRFPPS
		İ				SILOSWEGGTGWLRTLPLPHA
1						WPSDPVSPLGDRVTANPAEIRIL
		i	ĺ	l		GEDPESPEETLNLILRTPIPPKPR
						GNAKSHP/GGHRSHR*EPGPQS
		1				AAPGFREORRRGOMG*IWYLT
		1				PTPPGGQRPSSAASPRGFPPTNN
						SSRLPAEPE
16144	46512	В	16239	177	284	
16145	46513	Α	16240	253	416	CCPVLPGPWAAGHPGD*PDGP
		1				G**AQPHKECRGGFAPLQVTLG
		1		l		PKQPSGKRVNK
16146	46514	Α	16241	1401	2246	NIYLLLQVFDCWGLQGILGVSN
		1			1	PSYSIRRCYTAGQSPRGLPDPGR
				1		F*G*EESTGEQADCP*GSHRRSR
		ŀ		ŀ		SAAGAADGGLDPGAHTITCGC
l		1		l		LSHRGRLVPAQKSSAAL*APSG
		1		ľ		AKPAPTVAPVHDPARQG*GGQ
		1		1	1	ARGQGARQPHSHREGLCEC*A
1	1			1	1	VTTL*EPHLRNSSAPA*ERGPQG
				1	1	IRVPEGQSGDQESSAEEHHGGD
1				1	1	PGGGKPRCGQHQEPLGAGWPS
		1		1	i	PAGVEPLLGGLQKGSDGAP**E
		1		Į.	1	PORGCVDEAQOSSPGAVPEAK
1	1			1	1	AIAVOPPAPDVFAAVARCD
	J					P.III. C.III. C.IIII.

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino aeid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
16147	46515	Α	16242	30	461	IPAETTC/EPAKHFHCFTDGSSN
						GKASYSGSKGKVFOTPYISAOK
		ļ				VELVAVIEVLTAFDMPINVISDS
		Į.				SYMVHSTOLIENAOLRFHTDEO
						LIIKTKKGGNRDYGTAQTQLNL
						ALLTFHFSSLPKGQMLPAAEQH
		1		l		LQKPAAKTQAE
16148	46516	Α	16243	I	573	
16149	46517	Α	16244	1	1689	
16150	46518	A	16245	1	1416	
16151	46519	A	16246	27	779	KNHFNWKDKFPPRLRISFLMVA
l						TVKPPEPTPLKRLTEKPIWIEKW
1						PLSK*KLEALEKLVTEQLENGHI
						APTFSPWNSPVFIIKKKSGKWR
ļ		1				MLTDLIAINSVIQPMGALQPPGL
						PSPAIIPKNWPLIVTDLKDCFFTI
						TLAKQDCEWFTFIIPAVNNLQP
						AKHFHCFTDGSSNGKASYSGSK
	ļ					VKVFQTPYTSALTAELVAVIEV
		1				LTAFNMSINMISDSSYVVHSTQ
- 0	ļ.	1				LVENAQLQFQTDDTNDFIYPVA
						NSS
16152	46520	Α	16247	2	394	
16153	46521	Α	16248	63	1123	ELDVMGLPEERVRSGSGSRGQE
				1		EAGAGGRARSWSPPPEVRLVSL
1	1	1				LRLNMSQKINDIWASISVAEFW
1	1	1				GDIAKEFYWKTPCPGPFLRYNF
	1	1				DVTKGKIFIEWMKGATL*LCLF
						LVWGRSYTPNHWFFLVCLREG
		1				NEPGGQLDGREQVAARRVHGS
		1				YSVLLPAGIQKGDRVAILSNPFL
		1				HSLNPWGFLLSLRLSSLP*GPM
		1	1			DIVPTRQHGAY*GLECLLLPKD
		1				MDMGGSCQVPFEPTRLPL*AFL
		1	1			FSRGFPVRCCIVVKHLALTLSSH
		1				SLYTWTLQGQGTGVSCPHLELF
						TVLPCPSLQISWNQGIDLWWHE
		1				LMQEAGDECEPLPSLHLVVSRG
		1				GHKTLTCSPFFPQGVVHTVGGY
16154	46522	Α	16249	35	219	ALGVHFVLGPVGDGSRAVDCG
		İ		1		QQL\PTSSACTTSGLSISRRCSGI
1 _			l			WRMNQKKQVRGPSPKE

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=linknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
16155	46523	A	16250	1934	3213	WPAPPSQVPSLDYGLALWFDA YVSVHOTOETSQCSPESSLTPRI LCGLRILOPY AERIPVVATAL INFTLRGYAWPNGALPASTVPC GFAACGEFLCSVNGRQAPAGS SGFLPPYBSLCPHTVCRATFQCK EDSTCISLGRPPWGSETHLLCPA PIPSVPGVPCGTFTFQCEDRSCV KSLSASPLPLLCPPHHLPSPD CGLOGPSSRIVGGAVSEGEWP WQASLQVRGRHILGRGSFLPPH LTPPHPTPPHPSMASTVLWTVF LGKVWQNSKWPGEVSFKVSRL LLHPYHEEDSHDYDVALLQLD HPVVRSAAVRPVCLPARGRIEN RGSRLLRSHFCP*PRTGPISNAL QKVDVQLIPQDLCSEVYRSSPG KGGALTLLQSFLLSPFQGDSGG KGGALTLLQSFLLSPFQGDSGG KGGALTLLQSFLLSPFQGDSGG
16156	46524	А	16251	511	853	CCWNMALIQTFQMSMEIPLCTT LS*TALHLASANGNSGVVKLLL DRECQLNVLDMKKETALTKAV QCQEDECALMLLEHGTDPNIPD EYGNTTLHYAIYNEDKLMAKA LLLYGADIESKNKVEEEMKH ESNNVGLLENLSNGVTAGNGD DGLIPQKKSRTPENQOPPDNESE EYHSHTETELFSRIYP
16157	46525	А	16252	1050	1350	CDPQMCCCFRPEAATPG*REAA SAGPWDSAPPSPARTSLPSAHSS DYPLPRSRSSSASAASRSPPRPL STIARRLNPRRSGRSLPSGQPAG PSDPRGFCL

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide inscrtion)
				- Carrier	1	
16158	46526	Α	16253	2	3486	SSQSGAAAGAFCGLCVDLELTA
						SCDLEADSEDRTEHLATLQLRP
		1				DFSGSRCPAPQKHLQTHRPHSK
		l				PWPIY*PT*RSYLAISPHSW*AP\
		ı				PPSRRRAPPAFHPHTQACPSTCY
		1	İ			CHTLASRRGPSNGRYHRPGYPH
		1				PTAVQRDPPAGPRGCQSPC*HQ
						PPACRRPCGRHYR*HGQHDPPP
		1				WQ*HC*SRSPCHPPSQRDAVTW
		l				PFIHIPAED/SHTQPQKSP\PAFRP
		1				HTKTCPFTCYCHTFAGRRGPSD
						GRHHHLGYHHPSAVQWDPPAC
		l				*RGCWRPCQREPQTCPCFCGR/P
						PPGTSLA*PPHPRVPLKEKLCQY
						DEFSEGLRHSAHLNRHQRVPTG
						EKSVKSLERGRGVRQNTHIRNH
						PRAPVGDMPYRCDVCGKGFRY
1		l				KSVLLIHQGVHTGRRPYKCEEC
						GKAFGRSSNLLVHQRVHTGEK
						PYKCSECGKGFSYSSVLQVHQR
						LHTGEKPYTCSECGKGFCAKSA
						LHKHQHIHPGEKPYSCGECGKG
1						FSCSSHLSSHQKTHTGERPYQC
1						DKCGKGFSHNSYLQAHQRVH
						MGQHLYKCNVCGKSFSYSSGL
1						LMHQRLHTGEKPYKCECGKSF
						GRSSDLHIHQRVHTGEKPYKCS
						ECGKGFRRNSDLHSHQRVHTG
						ERPYVCDVCGKGFIYSSDLLIH
		ŀ				QRVHTGEKPYKCAECGKGFSY
						SSGLLIHQRVHTGEKPYRCQEC GKGFRCTSSLHKHORVHTGKK
16160		١.	16254	222	695	
16159	46527	A	16254	333	695	ISVFRSPGQSTSQHDAATWPFL
						HISGEGPTPSRRKAPPAFHPHTQ
						ACPSTCYCHTLASRRGPCNGRY
		l				HRPVYPHPTAMQRDPPAGPRG CQSPCWHYTPACRHPCGRHYR
		l				*HGOHDPPPWQ*HC*FGSPGQS
		1				
		1				TSQHDAVTWPFLHIPGERPTAS
1				i		RRKAPPAFHPHTQACPSACYCH TLASRRGPSNGRYHRPGYPHPT
1		1		1		A VQRDPPAGPRGCQSPC*HEPP
1		1		1		ACRHPCGRHYR*HGOHDPPPW
	l	1				0
16160	46528	A	16255	9	437	SCNMSLCRCNVCIRAAFKEGTP
10100	100220	l^	10233	2	,,,,	ALLVYSAILSFTPVSLAKSCSISI
1		l		1		AIVSNILSWLDPFKRGVVSELSR
		1	1	1		LPSRVLL*L*LVHSLLKETSFRS
	l					SSFSSCRACFLRSSQ/STAGPCR
				1		HLCRPTSAGIGEORRCRPESHH
		1		1		EIVDRGI
	<u> </u>	l				DIVDROI

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
16161	46529	ĪΑ	16256	619	1138	SCNMSLCRCNVCIRAAFKEGTP
		1				ALLVYSAILSFTPVS*DPEAFSP
		1				HLPSNCWSLPPSLSSNVSRDRG
	1	1				AEAMQAGKSPWCVFPP*EPGPT
		1				GCEPPRTLPPAPFKLCSL
16162	46530	A	16257	408	801	SQRRGSVCRLVHGRHGQPGKG
		1				TSPHSSLWDWQPGPQPSGPPWF
		1		1		EGGASPGTPSLIPRS*SASCCFP
		1				WHPGCSC*GAPASQC*VALSPQ
		1		1		PWFPLPCLSVPSPVGAQATGPK
		1		l		HVRTPPGSDSAPPQLQPQSRI
16163	46531	Α	16258	1	199	
16164	46532	A	16259	665	1006	IGSPDGRNVIRERTVTNETQTEG
		1				EREKEEERESFHTGDVLKVGDL
		1				GPQGSSREFQLLSNLTVPNFIDI
		1		1		QFPK*VSAAC*DGPSHTHSSYIS
						SSLFIIRASQSSPGDFSISVRY
16165	46533	A	16260	247	404	
16166	46534	В	16261	258	934	
16167	46535	Α	16262	519	924	NRTIQADLLYPDDAGNPLPARN
		1		1		TRQASASADPPGARAGERRRG
		ı		Ì		AAGPSPGR*QQAPGPPPPGEGA
		1	İ	1		GARPG*EGDAAGGATRFVGED
	1	ļ				ARLLRAGCHRGGRGEAEEPLQ
		1				ALRHPGLQGLL*EGAPHGELAL
16168	46536	A	16263	121	214	VAFAHL
16169	46537	A	16264	139	272	
16170	46538	В	16265	1	1962	
16171	46539	Α	16266	2373	2554	SATPWLPTGLAAPTPGLAAPGT
				1		RSPPGQT*PERSPAASPKRPERP
				ļ		ALDFOPPROPPPPP
16172	46540	Α	16267	919	1653	WNCFVCSADTMAQIMAEQEVE
				i		NLSGLSTNPEKDIFVVRENGTT
		1				RRPLQPPPRGRAS*GGAGRLCS
1		1				QLITEQADIALTRGAEVKGRCG
l		1				WRPLGLRTQTLRGRLKRTSPAQ
		1	i			QESHNMSKGPEATCQLSGTLG*
		1		1		EQ*GF*LLLWALAVAGKHTAN
		1		ŀ		SHHLSALVTPAGKSYECQAQQ
		ŀ			1	TISLASSDPQKTVFCRTYDSGCF
		ł				DQSSLLFFFPIAEHKCPVDEREQ
		L	L			LEETLPLILGLILGLVIMVTLAIY
16173	46541	Α	16268	2	321	PAWPPWPGITGFCPQQDSPSNT
		1	1	1		FVVPAAHTV*CSHPCSYYKGIR
			l	1		QMVGLPQPLFHPDCPVTPQAHT
		1		1		DSLNTLGVLGGPPVCSDATLPQ
		L				IINALEEDPAAQKMQLAF
16174	46542	Α	16269	120	327	
16175	46543	Α	16270	540	791	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)  DRVSLLPRLRQENRLNPGGRGC
						SELRSHHCTPAWATE*GSVSKK KKKKKNQKKNQFDFISLALPPS PHCPPLSQSLLLQPSSSAN
16177	46545	A	16272	3	343	DIHHVRKSMEVNFLSYVVLTV AALPMLKQSNOSIVVVSSLAET AMKAVSGIVHMQAAPKEECAL EIIKGGALRQEEVYYDSSLWTT L/LIRNPCRKILEFLYSTSYNMD RFINK
16178	46546	В	16273	48	407	
16179	46547	А	16274	35	646	DLTGFIKFSLLIGLFMAYYYYS ANEEFRPGKYPCVSFWRNFFK KHRGAYAYHLAKMGAHVVV TARSKETLQKVRVLCSQICVPS HAQMCSYIPDMTAEQFVAQA GKLMGEA VSLTSSSELCPWGH QELLDIHHVRKSMEVNFLSYVV LTVAALPMLKQSNOSIVVVSSL AGK WDRDIGG*KKKNARDD AVQTPGSKSAI
16180	46548	A	16275	221	393	LLYPANCVYMRCPQMLHFQGI QRPILL/HVSSGGAIHLQTGVET EEMRSAIAPDPIPLT

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
16181	46549	A	16276	2025	4146	SDEWIISAGSVSGDYNSSAAVS KNDILLGIEHISVESETNIHSSEE. FIKTAKSQLVEIEPATQNPKTSIS SYERLQALQETCKENKGVPKQ GDTFLSFSAACETDVSSVYPPEK FEFETSATGSSMQSGSELLLKE REILTAGKQPSDSBFSASLLAG GKSVAKTGPSSMQSGSELLLKE AYAQTQSSLFYSPSSPMSSDDE SEIEDEDLKVELQRLYREHIQEV VILQTTQNKELQELYERLRSHIQEV VILQTTQNKELQELYERLRSHIQEV SKYAKTGELDELYERLRSHIQEV KILRSRPQSLTHVDNGIVVIDPL VESNAASCQQSPASKKGMFTD DLHKLYDDWTKEAVGNSLIK SLNQLKQSQHLAFNHVDKIV QLESVYHREDEATWLPQLRAQ VAYPACAAAIASAHRSMGVC GFQEFLEKRCFGAVVPVDLLKI ARTVSRQQQQHLHRQLPFT AALGAYSGGAGPIRHHPAHH FHHHQGAQGWAMALGYPPLPP LCGARVLVDAGSALPRLPGPPPP LCGARVLVDAGSALPRLPGPPPPP LCGARVLVDAGSALPRLPGPPPPP LCGARVLVDAGSALPRLFGGT CTDWVCGGQWAMALGYLSAI CQACAYPGGDGLELVWFPCC LIGKDRLAEWGRECQAERCTAG LIVGHIVGNKGTPPPRAWFLPP
						SEYALYNIPSYYSSHALKLSWN GKNLTTNQFLMQEVAKQLGLI
16182	46550	A	16277		542	MRAPPKSGQLQHCRPSRGALE; GDLPWEINPLSSCSLLHEKDPP MTSGPQTNQPKEHLTNFKSGV RP/LQGRLPWSFTLSGKSRFSGE GASTPTPYIS/GAPIPYFRTPTSY LCAPIPYVRTPTSYLCALTPFPL FWRHIRTSKRLN/LQQPGIPPEP, PPG/CLLQVPEI*PPGGQMPAAQ
16183	46551	A	16278	3	351	VRPRRDACLGPSPLAASPAFLG KGQVPQPLISLCPDPLFPHPNLE LRPNPLCPHPDL/GISVP*PLSRF SGGT*ELPNA*TAAA/AAF/LPE PPPG/CLLQVPEI*PPGQGMPAA QDSS
16184 16185	46552 46553	A	16279 16280	774	513   1007	ARSVTSSSELCGSWCLQASRHT HVPWCQL*KLPVVHLVQPQPC RGPAPGAALPAGSLEMPGTTEF ERGCHSPGLGIS

SEO ID	ICEO ID NO:	Mat	SEQ ID NO:	Nucleotido	Nucleatide teention of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	ļ ·			sequence	' '	,
16186	46554	A	16281	507	520	LLLGLAAED*CCLIASEAP*TQS
10180	46334	^	10201	307	320	LFGGLFTRTHMKFGAVTQIRGP
1						PLGDKSPVLLLFALERORRHVL
1			l			
i						SMDPKLRCWSRTGKAAFPWCL
						IIAEMPDYSPTFQRCQTTQGRLP
		1				WSFTLSSKSRFSGEGARACYKC
		Į				QKSDHQAKECPQPGIPPKPCPIC
Ì		ŀ				AGPHWKSDCSTHLAATPRAPG
	ļ	Ļ				TLAQGSLTDSFLA
16187	46555	Α	16282	269	607	RARSEGAGLWSVVAPSAVSVFF
	1	1				VSDPRCAPFHRSPSCCSPVDRV
ļ.	1	ł				CRCLRRVALAPAALVLVCSGSH
ŀ	1	l				SQSPWNSGLKLSDRLLLGLAAE
						D*RCPIASEAP*TTTDAELTIPGL
16188	46556	С	16283	I	1752	
16189	46557	В	16284	146	372	
16190	46558	Α	16285	336	753	ARTPLAAASRGSGGTRGGAAW
						VAGDDLRGPAPGPAEPGPARRR
						RGKGTPSSRPRTQRRPRSAAMH
						GHRCPQPARRSREHPNTYPAGR
			ļ			RPPELRRGRSGVPPPRP*RRPGE
i		l			1	APRAPRPRAAEL*ARLPRPSVRP
						APARRV
16191	46559	Α	16286	1	768	FDELREEGFRQSVITNFSELKKD
1						V*THRKEAKNLEKK\LDEWLTR
			ĺ			INSVEETLNDPMELKTMAQELR
ł		1				DACTT*FREKRVKRNEQSLQEI
		1				WDYVKRPNLRLIGVPESDGEN
						GTKLENTLLDMIQENFPKLARQ
1						ANIQIQEIQQIPQRYSSRRATPR
1		1				HIIVRFTKVEMKEKMLRAAREK
		l	ŀ	1		GWVTHKGKPIRLTADLSAETLQ
						ARREWGPIFNILKEKNFQPRISY
		1				PAKLSFISEGEIKYLTDKQMLR
		1				DFVTTRPALKEL
16192	46560	Α	16287	345	894	EQRHNIPESLGHI*STSAGDTPA
						DRVWSGPPANSSRPAAEGPDC*
		1			i	KEN*QRARTS\NQNPICTSPSSK
1						TKEAKNLEKRLDEWLTRINSIE
		1				NTLKDLMELKTRARELRDACR
1	1	1		1	1	SFSSQFDQVEERVSVIEDQMNE
1	1	1			1	MKKEEKFREKRVKRNEQSLQEI
	1	1				WDSVKRPNLHLIGVPESDGENG
1	1	1		I	1	IKLENTL
16193	46561	A	16288	1	1206	
1.0175	1.0001	1		ı <u>.                                    </u>		

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	eodon for last amino acid	*=Stop eodon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
16194	46562	A	16289		1882	MAPVSASEDFWQCPETSLISQL
1015	10302	ľ.	10207	ľ	002	ESAPGIOLMEARDADKSLIMHE
		1				IAPTSNRELPVHKISIAKPCSML
		1				MISWFFVNTGOSFORKDOAAIF
	l					AVLOPLLVIHROTGSGVDLOOT
						PTDLOLRDLTVRRKNNKOKGI
	l					ASTSRKRTSTPKPHLODHSSSPA
						MEOSWMOKDFDKLAEVGFRR
	ł					SVITNFSELKEDVOTHHKEAKN
						LEKRLDEWLTRINSVENTLNDL
1						MELKTMAQELHDACTSFSRQF
						DOVEERVSVIEDKISEIKQEEKF
		1		İ		REKRVK\RNEOSLOTIWDYVKR
		l				PNLHLIGVS
16195	46563	A	16290	l	1008	MVRFGDELGGRYGGPGGERA
10193	40303	A	10290	l'	1000	RGGGAGGAGGPGPGGLQPGQR
		l			1	VLYKQSIAQRARTMALYNPIPV
		l				KONCFTVNRSLFVFSEDNVVRK
	į.	l				YAKRITEWPPFEYMILATIIANC
	1					IVLALEOHLPDGDKTPMSERLD
		1				DTEPYFIGIFCFEAGIKIIALGFV
1	1	1		1		FHKGSYLRNGWNVMDFVVVL
	1				İ	TGRKAGLGCCGSGVESGGWGD
	1					RSSSPAMEOSRMENDFDELTEV
		i				GFRKSVITNFSELKEDVRTHRK
		1				EAKNLEKRLDEWLTRMNSVEK
		1			į .	TLNDLMELKTMARELRDACTS
		1		ł		FSSOFDQVQEMVSVIQDQISEM
İ				l	l	KREEKFREKRVKRNE/OSLO*I
		1				WDYVERPNLRL
16196	46564	В	16291	1	1257	WBT VEIG NEIGE
16197	46565	A	16292	3	467	KTPFVGYOHORPKVDKTTKMG
1017/	70303	1	1.02,2	ľ	1	RNOSRKAENSKNOSTSSPPKDP
	1		1		I	GSLPATEQSWTENDFDELTEVG
	1				1	FRRSAITNFSELKEHVLTRRKEA
		1			I	KNLEKRLDEWLTRINSVEKTLN
					1	DLMELKTMAOELRDARTSFNS
						*FNOVEKRISVIEDOIDEIK*EDK
16198	46566	c	16293	115	498	THE TERRISTIED GIDEIN EDR
10128	40300	<u>_</u> _ا	10293	1113	1770	

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				ocquene.		
16199	46567	Α	16294	2	1455	TERDSININKKDIYTKTQSVGRQ
	İ					HQRPKVDKTTKMGRNQNRKA
	į.					ENSKNQSASSPPKDCSSSPAME
	ì					OSWMENNFDELTEIGFRRSVIT
						NFSELKEDVQTHCKEAKNLEK
1						K\LDEWLTRINSIEKNLNDLMEL
		1			ļ.	KTMAQELRDACTSFSSQFDQVE
						ERVSVIEDOMNEMKQEEKFRE
						K\RVKRNEQSLQEIWDCVKRPN
						LHLIGIPESDGENGTKLDNTLQ
			i			DII*ENFPHLAR*ANIQIQEIQEIQ
			ĺ			RTPORYSPRRATPRHIIVRFTKV
		l				DMKEKMLRAVREKGFKPTKIR
ł		1				RDKEGHYIMVKGSIOOEELTIL
						NIYAPNTGGPRFIKQVLSDLQR
						DLDSHTIIMGDFNTPLSTLDRS
						MRQKINKDIQELNSALHQVDLI
					i .	DIYRTLOPKSTEYTFFSAPHRTY
		ı				SKIDHVVGSKTLLSKCKRPETT
l		1				TNCLSNRSAIKLELRIKKLTONR
1						SAAWKLNNLLLNDYWVHNEM
		1				KAEIKMFFETRTKIOHARISGIL
16200	46568	A	16295	395	656	FOLORPASCSSPIOHRKHIPRKP
						A\SQSSLPHTGKSARQPQEPQNR
						ENCLLRILIRVASEATRRWTRPS
						EFSSRSENPRAHHPRRALR
16201	46569	Α	16296	671	1126	RRKVSELEHRRPVWKCPRRPPE
						VRKPESARVSFSPRGGARRSRP
						GATRSPQPRVPAAASASFGFGG
						LGRGGRGERARRGRGPKLEGP
		1				ESSAVLA*RNFPSRPRRRRPGRA
		1	l			GVEIARLGGTGSSPRPCPKPDPT
		1	ļ			ASLSELFMIPSDIPRRRN
16202	46570	A	16297	2571	2716	THGMLEKRCCLQENMPIIPGKD
			1		i	FMTKTLKAIATKVKIGK*DLIKS
						FCT
16203	46571	В	16298	54	576	
16204	46572	A	16299	475	719	VTWIRNNNACFTLNWFYHERS
l l		1				HIWILKSTLQCGQIIIGNDVESR
l		1				HK\CPKPS*LVGSVELEIADNVL
						PQKFPAAKTIFALYF
16205	46573	Α	16300	395	830	LSPCHNSFFFFFQAFDDIAKYFS
						KKEWEKMK*ATVPGPSLPLKK
1						*TFCSFLGFKVTLPPFMRSVSLE
		1		1		FGNLYQQRKILM*L*STVEMSLI
1			1		1	LFICDLHIVKIMPKKPAEEENGL
		1		1		KEVPEASGPONDGKQLCPPGNP
						STLEKINKTS
16206	46574	В	16301	54	576	
		_				<del></del>

SEQ ID	SEQ ID NO:	Met				Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
16207	46575	A	16302	475	719	VTWIRNNNACFTLNWFYHERS
						HIWILKSTLOCGOIIIGNDVESR
	ŀ					HK\CPKPS*LVGSVELEIADNVL
		1			ŀ	PQKFPAAKTIFALYF
16208	46576	A	16303	393	822	LSPCHNSFFFFFQAFDDIAKYFS
					1	KKEWEKMKSATVPGPSLPLKK
	i	1		ļ		*TFCSFLGFKVTLPPFMRSNSLE
	l					FGNLYQQRKILMYF*STVEMSL
						ILFICDLHIVKIMPKKPAEEENG
						LKEVPEASGPONDGKOLCPPGN
						PSTLEKINK
16209	46577	A	16304	1	447	
16210	46578	Α	16305	75	565	LLFSGFSLLHGYLPHWYLCHLP
						RSRSLGLRDKRWKVKGDTDFL
						SPSHPEYLLKEENDGHLCSLSFR
	ŧ	1				MGNQFSSPLPAYTPLECILNHW
			Ì			DGFYP*NLEEKHLIALRTKGWP
	i .	1				NYDLQEGLSWPQEGTIHFNTT
l		1				WQLELFCRHEDRWSEATYMQ
l						AFYILQGNRDLG
16211	46579	Α	16306	1	1620	
16212	46580	Α	16307	128	223	
16213	46581	Α	16308	1	1578	
16214	46582	В	16309	592	883	
16215	46583	Α	16310	1	344	MHQTTAKTPHTSYPNNYEEHN
		1				RRANRSKNYDRIRHTTIILKRTN
		1			i	PAQTITNLLKSRFNRYNYVQPR
		1	l			SCRSIFIHIPGERDLNLCIAPNPP
	1	1				AIFPTSIGYLGPDLNNLPTYAPFI
	1	ł				TTNLTGPAPTTTHPVGNLGTTG
		1				NPEPGGCGILIVWCCVNWACL
		ŀ	l			WDSVVAAPREPYMPAGLLRHR
ŀ						RHYRHRREDLIAVPAARQTDE
		1				NRRPALCHEYAVGHRKIKTNV
1		1				EHTEPYILPLITHSQPLNRGAFF
		1			1	CPGVRFLVVSVLDFEKRLAFAS
		1				*SCGVQLRIRGKVQGVGFRPFV
		1				WQLAQQLNLHGDVCNDGDGV
	<u> </u>	_				EVRLAYRVLVGQPQHYPRGRP
16216	46584	A	16311	84	237	DGIVLSTYYHFYWHHF*ILEGP
					1	LPANTGDLCLPLQVQPDREQVR
	1	1				WALFKK

SEQ ID	SEQ ID NO:					Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
16217	46585	A	16312	2887	3537	HLDRSGLFNIQVIPVCRKLGKE
10217	10303	^	10312	2007	5557	GNDEKQCVTTSRSNAAFFLLHF
						FLLATFTWMGLEAIHMYIALVK
						VENTYIRRYILKECIIGWGKPLK
						IFLVLFFPHENCQVYGKESYGK
						EKGDEL*VIKTFCDE*ISFVS*SG
					1	VMFFLNIAMFIVVMVQICGRNG
					1	KRSNRTLREEVLRNLRSVVSLT
	l				1	FLLGMTWGFAFFAWGPLNIPF
						MYLFSIFNSLQGKINCT
16218	46586	Α	16313	302	547	QIGLWTPNFRARTFCVWTGGL
						VLCF*GFCFQEAAGARDTSSFA
1						MGVSPWEFRHG*LWPEMRSME
						QILELLVLEEFLTITGQ
16219	46587	Α	16314	1	1174	WEEKENKEYLKSLFEILILMGK
İ						QNIPLDGHEADEIPEGLFTPDNF
				ŀ		QALLECRINSGEEVLRKRFETT
						AVNTLFCSKTQQRQMLEICESC
						IREETLREVRDSHFFSIITDDVV
						DIAGEEHLPVLVRFVDESHNLR
						EEFIGFLPYEADAEILAVKFHTM
					i	ITEKWGLNMEYCRGQAYIVSS
						GFSSKMKVVASRLLEKYPQAIY
						TLCSSCALNMWLAKSVPVMGV
						SVALGTIEEVCSFFHRSPQLLLE
	ł					LDNVISVLFONSKERGKELKEIC
	1					HSQWTGRHDAFEILVELLQALV
	ŀ				1	LCLDGINSDTNIRWNNYIAGRA
		1		1		FVL\CSAVSDFDFIVTIVVLKNV
				1		LSFTRAFGKNLQGQTSDVFFAA
				İ	i	GSLTAVLHSLNEVMENIEVYHE
	1	l				FWFEEATNLAHOT
16220	46588	A	16315	717	902	GALOSWPCYLPROCGATVONF
						CGVPTCMRKSTWSNLVVFRFP
1	l	l	l	I		ODPSRCAN**LDCCTACTO
16221	46589	A	16316	-	374	EHSEPPIGVOIVDYLLROEKVT
1.0221	1.0007	ļ.,	1.05.0	ľ	ľ.,	DRMDHSKVETETVLSFVDDIIS
	1		ł	I		GAKSPCAMPSQVPDK/QAQEIA
	l			ŀ		DKIYNLFNGYTSGKEQQTAYN
				1		TLLDLGSPTLHRVLYHYNOHY
		l	l	1		
1.6000	46500	١.	16217	2	1293	ESFGEFTWRCEDELGPR
16222	46590	A	16317	2	1493	

ſ	SEQ ID	SEQ ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown.
	NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
-		sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1			ĺ		sequence		
١							
-	16223	46591	Α	16318	219	1912	PHPTRTRSAQSVQYIEKDWGPG
1							EGLEEGGVLGQLVAFDSFTVSF
			l				HFVSAGNSPSDESEERERDPKV
١			l				LTFPEYITSLSDSGTKHMAAGV
١							RMECHSKGRCPSSCPLCHVTSS
١							PDTPAEPVLLEVTKAALLNTQS
1			[				FPCSLMQLLQEATMSSLWCSGT
١							GDVIEDWCRCDSTAFGGCVPVS
1							CSFLSAHRLRLSTVHEPSSTLVV
			l				LEWEHSEPPIGVQIVDYLLRQE
1							KVTDRMDHSKVETGEHLLLHG
1							LVLIQGDKTKTKKNALPHGFAP
-			ı				GPQYPRAMQEEQGEEEAVLLL
-							QEAAVLLPLRVRDIRSCCFRHR
-							ELLFLMLFPFLLLWAETVLSFV
-			1				DDIISGAKSPCAMPSQVPDKQL
-							TTIYFOPLIARFSFSSRKGLLRIM
-			ĺ				SSHCHGDCDVSTLDSYTVSAN
-							HALPLPARFTLWGVDNTGRRS
-							RPSDVIVYM*ITYFPFPPSSEIAD
-							KIYNLFNGYTSGKEOOTAYNTL
-							LDLGSPTLHRVLYHYNOHYESF
-							ASF*LKYPLCLIHRKAGLILSQL
-							GDLSSWCNGLLQEPKISLRRSS
-							LKYLGCRYSEIKPYGLDWAELS
1	16224	46592	A	16319	T.	2031	
ı	16225	46593	A	16320	1	739	MKRAGSSGGRGECDISGAGRL
-			1				GLEEAARLSCAVHTSPGGGRRP
-							GQAAGMSAKERPKGKVIKDSV
1							TLLPCFYFVELPILASSVVSLYF
-							LELTDVFKPVHSGFSCYDRSLS
-							MPYIEPTOEAIPFLMLLSLAFAG
-							PAITIMVGEGILYCCLSKRRNG
-			l		l		VGLEPNINAGGCNFNSFLRRAV
-			l		l		RFVGVHVFGLCSTALITDIIOLY
-			l		l		TGHOAPYFLTVRTPNYTSLNVS
			ı		l		CT*NSYLAEDIRSRSDLTLTHSG
- 1		1	1	1	I.	l	OT 149 I PAEDIKSKSDFIFTH20

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
16226	46594	A	16321	48	1359	GDK NQNPRN WPLGEGKGNSLG
				i		RKETGRSNSRSHSSRSKSR*QSS
l				l		SRSRSRSHSRKKRHSSRSRSRTY
						SRSWSRDRMYSRDDRH*YEVIV
		l				DCSRHGREYKGREPRHGSGSLE
		l	l			RPTEQETSQPKIRKEIVETKGTA
						RGNCGTTGLLRPKTMMVERSY
l		l				GPQDRVAVGTWPHPGTERWAS
						SWDVSSSVRHQSEGVVQGWEH
			i			RCTHKSQQEVGACVNFRTPKVI
		l				LIYNLYLPVSHQFSKTFMSIVIV
						QKNLYLHNDFRALNVTHIYRLT
		l	ŀ			IPNTTTCFTATQDEDKQIFHTAA
		1				QHRSHTSSYQYLSLTRSHRYEI
		1		i		VFYTRGLGAPFPAGDGHGKFQ
		1	1			RLGKPYSHSVHFVIPQDKTQHIS
ł						INTPHKNSETTKQHTCSFAYGL
						YYYQQKEDNPYAWPQVPAAA
		l		i		EMVSRLAQSRHSQQSILIHFSHQ
						SYHTDHISTV
16227	46595	Α	16322	227	3020	SCIKPRRKEMGRSNSRSHSSRSK
						SRSQS\SSRSRSRSHSRKKRYSS\
		1				RSR\SRTYSRSRSRDRMYSRDY
						RRDYRNNRGMRRPYGYRGRG
						RGV/YYQGGGGRYHRGGYRPV
			l	i		WNRRHSRSPRR\GRSRSRSPKR
						RSVSSQRSRSRSRRSYRSSRSPR
		l				SSSSRSSSPYSKSPVSKRRGSQE
					i	KQTKKAEGEPQEESPLKSKSQE
						EPKDTFEHDPSESIDEFNKSSAT
						SGDIWPGLSAYDNSPRSPHSPSP
L						IATPPSQSS
16228	46596	В	16323	258	3728	
16229	46597	В	16324	1	435	
16230	46598	A	16325	1120	1209	ASSDNPP*SEPRVSLTIEGQEIDF
						FLDTGTAFSVLSSCPGWLSSRS
		L		l		VTIRGILGQPVTRYFSHLL
16231	46599	Α	16326	1291	1582	IHQSALCI*LKVCKHTNQQPVSS
						SGFVNAPIDTLYLATLVGPWRT
		ŀ		l		LCVHTLYLVNLVGMWRTFVSS
						SGIVNAPISALSKQTTWLYQSA
						GCGWGQIRE

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
		<u>L</u>				
16232	46600	Α	16327	2	840	APAVATEVLPGAGLTAGVLLW
		1				SDPKEPSNPGSSHRVGASDLDN
						PAHPTLLSYTMQKLEEELDVVL
		1		i		FDRSGHRTKFTNVGRMLLERG
		1	ĺ			RVLLQAADKLTTDAEALARGW
						ETHLTIVTEALVPTPAFFPLIDK
ľ						LAAKANTQLAIIT*VLAGAWER
						LEOGRADIVIAPDMHFRSSSEIN
		ŀ		1		SRKLYTLMNVYVAAPDHPIHO
						EPEPLSEVTRVKYRGIAVADTA
	ł	l				RERPVLTVQLLDKQPRLTVSTIE
	İ	l				DKROALLAGLGVATMPYPMVE
		1		1		KDIAEGRLRVVSPESTS
16233	46601	A	16328	3	923	RFLSDGTIISVDSAGKVOFWDS
10233	40001	l^	10320	ľ	1223	ATGTLVKSHLIANADVQSIAVA
		1		i		DFFPGHESRATEALCWAEGOR
						LFSAGLNGEIMEYDLOALNIKY
		1				
		l				AMDAFGGPIWSMAASPSGSQL
1		1				LVGCEDGSVKLFQITPDKIQFER
1		1				NFDRQKSRILSLSWHPSGTHIA
1		1				AGSIDYISVFDVKSGSAVHKMI
1		1				VDRQYMGVSKRKCIVWGVAFL
1		l				SDGTIISVDSAGKVQFWDSATG
1		1			1	TLVKSHLIANADVQSIAVADQR
1		l				RQFRGGHSRGNSLPFSAGPC\AS
İ						NSS*EAVGADKTVPASHS*RAH
						CGPTAQQR*YLGGTDTHLVFRP
16234	46602	Α	16329	2	1059	
16235	46603	A	16330	582	1540	
16236	46604	Α	16331	1	720	
16237	46605	Α	16332	1	477	
16238	46606	À	16333	1	540	
16239	46607	Α	16334	1	261	
16240	46608	A	16335	964	1574	LRWCCGSQLFRGYWGGVTGR
		1				YLTVLPPHLAVGCMAPWGPFS
1		1				VRIAAVVFIQIFAGEVFWCPVM
		1				CVRGLCTPVLTGVPGHGNSHIP
1		ı	l			AIVFTCSLQTLVGGTRRWWRC
	1	1	l			CAAGDVTKFPALVGVGGETPR
1	1	l	l			PQLPIGVTTVILLQVLVWKFGR
		1		1		NVSMSVWALRVPGLAFQSRH/
1		1	1			ASWKFCRHSFLHCNAYIPLHTQ
				_		ECRSSHISFLDQ
16241	46609	A	16336	3	87	
16242	46610	A	16337	ī	1398	
. 02 .2						

SEQ ID SEQ NO: of per			Nucleotide		Amino acid sequence ( X=Unknown,
	ptide hod	in USSN	location of first	codon for last amino acid	*=Stop eodon, /=possible nucleotide
seque	ence	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			sequence		
		<u> </u>			
16243 4661	11 A	16338	1596	2205	LRWCCGSQLFRGYWGGVTGR
	i		1		YLTVLPPHLAVGCMAPWGPFS
	- 1				VRIAAVVFIQIFAGEVFWCPVM
	- 1				CVRGLCTPVLTGVPGNGNSHIP
1	ı			İ	AIVFTCSLQTLVGGTRRWWRC
	- 1			İ	CAAGDVAKFPALVGVGGETPR
1 1					PQLPIGVTTVILLQVLVWKFGR
l i	l l				NVSMSVWALRVPGLAFQSRH/
		1			ASWKFCRHSFLHCNAYIPLHTQ
		1			ECRSSHISFLDQ
16244 4661		16339	276	442	
16245 4661		16340	1	300	
16246 4661		16341	1	903	
16247 4661	15 A	16342	119	889	RQHILESHSRPILCTTWLPLLIIQ
	l l				DPRTLQSAAMLLTQSLFGGIFT
1 1					RTRMKFGAVTWIGGPPLGDQS
1 1		1			P\SSCSLLREKDPPTTSGPQTHQ
1 1	i				PKEHLTNFKSGVRPRRDACLGP
	- 1	1			SPLAASPAFLGKGQVPQPLISLC
i l	- 1				PDPLFPHPNLISLRPNPLCPHPD
					LVSLCPDPFPAFLEAHKNFQTPE
					PQQPGIPPEPPPPGACYKCQKSD
	i				HQAKECLQPRIPPKPCPICAGPH
	- 1				WKSDCSTHLAATPRAPGTLAE
					GSLTDSFSA
16248 4661	16 B	16343	1	498	
16249 4661	17 A	16344	3	903	
16250 4661		16345	1	684	
16251 4661		16346	2	1028	
16252 4662		16347	1	338	
16253 4662		16348	2	392	
16254 4662		16349	790	2184	
16255 4662		16350	773	890	
16256 4662		16351	467	606	
16257 4662		16352	1569	1841	
16258 4662	26 A	16353	430	980	LLTEDALDDLIPSFLLTGQQTPA
	1				FGRRVSGVIEIADGSRRRKAAA
1 1					LTESNYRVLVGELDDEQMAAL
					SRLGNDYRPTSAYERGQRYASR
			l		LQNEFAGNISALADAENISRKII
			l		TRCINTAKLPKSVVALFSHPGE
1 1			l		LSARSGDALQKAFTDKEELLKQ
					QASNLHEQKKAGVIFEAEEVIT
					LLTSVLKTSSASRTSLSSRHQFA
1					PGATVLYKGDKMVLNLDRSR*
1					RGIT*AAGI*PS*AEKSWGDI*S*
1 1	i	1			RSYHSFNFCA

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
16259	46627	A	16354	1	343	MKRAPVIPKHTLNTQPVEDTSL STPAAPMVDSLIARVGVMARG NAITLPVCGYDVKFTLEVSGVI VLRRPLGYGQVMNVTRSCLLR THWMISSLLFY*LVNRHRRSVE EYLVS
16260	46628	A	16355		584	MLRDLLKNVDLKGFEPDVRILL TKYSNSNGSQSPWMEEQIRDA WGSMVLKNVVRETDEVGKQI RMRTVFEQAIDQRSSTDNFGAP VIPKHTLNTQPVEDTSLSTPAAF MVDSLIARVGVMARGNAITLP VCGRDVKFTLEVNSQVIVLRRPL GYGQVMNVTRSCLLRTHWMIS SLLFY*LVNRHRRSVEEYLVS
16261	46629	A	16356	62	350	SLPNLDNAAICSSSSSPTRTR*SL SVSAAALRRRLPSAISDHTREVF STLSPRSTSRVNFTSRPHTGKV MALPRAITPTRAINESTIGAAGV DNEV
16262	46630	A	16357	291	502	RLFEVHHHVHKHLLGDNRYPI WIMQPSAHHP/RSPTRTR*SLSV SAAALRRRLPSAISMTPDTLRP NAGVC
16263	46631 46632	A	16358 16359	159	378 433	SYVKYFPHQPAQKYFQQIHSAI GLHNADHVHKHLLGDNRYPIW IMQPSAHHP/RSPTRTR*SLSVS
						AAALRRRLPSAISMTPDTLRPN AGVC
16265	46633	В	16360	1	624	
16266	46634	Α	16361	3	299	
16267	46635	Α	16362	163	699	
16268	46636	A_	16363	795	980	
16269	46637	Α	16364	663	734	
16270	46638	A	16365	391	1248	
16271	46639	Α	16366	1	1143	
16272	46640	A	16367	1	271	
16273	46641	А	16368		493	MSKRR WLTGNGSDRENIRLDL GFL VSDEEKRYKCEDCGKAFN RSSNLTTHKKIHTGEKPYKCEE CGKAFKRSSILTTHKRIHTGEKP YKCEECGKVFKYLSSLSTHKIH TGEKPYKCEECGKAFNWSSHL TTHKRIHMERNPTNVKNVAKA LSTPLPLLNIK
16274	46642	Α	16369	728	1428	
16275	46643	A	16370	3689	3864	NYKSFFKWS/SQMQSMTKIYRG PLDHPDSPCSNVNDIEGTPPEEI STAQPLLHPRPAGSS

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
16276	46644	A	16371	2	126	I WPLLLLGCLSLTKEWGFQA*LE KHVKRVKFPSHNLVPGRSI
16277	46645	Α	16372	728	2207	
16278	46646	C	16373	1	873	
16279	46647	Α	16374	1220	2097	
16280	46648	A	16375	73	1438	ODLRLYYLKDTMFSKLAHLOR FAVLSRGWISVASATSVATKK TVQGPPTSDDIFEREYKYGAHN YHPLEVALERGKGIYLWDVEG KKYPPELSSYSAVNQGHCHPKI NALIKSQVQQON*PLTSRAFYN NVLGEYEEYIKLFNYHKVLP MNTGVEAGETACKLANKWG LYTTVKGJQKYKJKKIFNAGNIP WGRTLSAISSSTDPTSYDGFGPF MPGFDIIPYNDLPALERALQDP NVAAFMYEPIQGEAGVVYPDP GYLMGVREUTEHQVLFIADEI QTGLARTGRWLAVDYENVRPE IVLLGKALSGGLYPVSAVLCDD UMLTIKRGEHGSTYGGRPLGC RVAIAALEVLEEENLAENADK KGLINANYIKETKDWDAWKVC LGILRNGLIKKPSDVTAVRG KGLLNANYIKETKDWDAWKVC LRILRNGLLAKPTHGDIIRFAP
16281	46649	A	16376	600	806	L TIKEDDERGSIBIINK TIESI

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
16282	46650	A	16377	li	2255	EPDVCAKMAGRSMQAARCPTT
				-		ELSLTNCSVVNEKDFOSGOHVI
						VRTSPNHRYTFTLKTHPSVVPG
	ŀ	l				SIAFSLPQRKWAGLSIGQEIEVS
						LYTFDKAKQCIGTMTIEIDFLQK
		l		i		KSNDSNPYDTDKMAAEFIQQF
1	1					NNOAYSVGOOLVFSFNEKLFG
				ľ		LLVKDIESMDPSILKGEPATGK
		1				ROKIEVGLVVGNSOVAFEKAE
		1				NSSLNLIGKAKTKENRQSIINPD
		1				WNFEKMGIGGLDKG\FSDIFRR
		l			i	AFASRVFPPQIVEQMGCKHVK
		i				GILLYGPPGCGKTLLARQIGKM
		l				LNAREPKVVNGPEILNKYVGES
		1			1	EANIRKLFADAEEEQRRLGANS
		1		l		GLHIJIFDEIDAICKORGSMAGS
						TGVHDTVVNQLLSKIDGVEQL
		1				NNILVIGMTNRPDLIDEALLRPG
						RLEVKMEIGLPDEKGRLQILHIH
		1				TARMRGHQLLSADVDIKELAV
		ĺ				ETKNFSGAELEGLVRAAQSTA
i		l				MNRHIKASTKVEVDMEKAESL
						OVTRGDFLASLENDIKPAFGTN
1						QEDYASYIMNGIIKWGDPVTRV
1		1			·	LDDGELLVQQTKNSDRTPLVSV
l		1				LLEGPPHSGKTALAAKIAEESN
		1				FPFIKICSPDKMIGFSETAKCQA
1		1				MKKIFDDAYKSQLSCVVVDDIE
						RLLDYVPIGPRFSNLVLQALLV
						LLKKAPPQGRKLLIIGTTSRKDV
			l			LQEMEMLNAFSTTIHVPNIATG
						EQLLEALELLGNLKDKERTTIA
16283	46651	В	16378	1	2181	
16284	46652	Α	16379	1	441	
16285	46653	В	16380	47	482	
16286	46654	Α	16381	1	636	MRDPNTKRSRGFGFVTCATVE
						EVDAAMNARPCKVVGRTVEPK
		1				RAVSREDSQRPEDTEELHLRDY
İ						FEQYGKIEVIEIMTDQGSGKKR
						GFAFVTFDNHDSMDKTVIQKY
1		1				HTVNGHNCEARKALSKQEMAR
1						ASSSQRGRSGSGNFGGGRGGGF
						GGNDNFGRGGNFSGHGGFGGS
						HGGGGYGG/SGDGYNGFGNDG
		_				GGGSYNDFVNYNNQSSHFGPM
16287	46655	A	16382	1	762	
16288	46656	В	16383	59	1042	
16289	46657	В	16384	179	848	
16290	46658	В	16385	11/9	1400	l

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
16291	46659	A	16386	27	372	VGSLRRPGPPREETRRLRERRRS LEPWAFLLKEAKVG*QPSSLFQ WEGPMGLCSTPLVMNMGDSLI TK\HLFQVPPLTITSPGPRTRRPH S*YPSPSLATGVWAAVWCKQP HFPAK
16292	46660	В	16387	134	284	
16293	46661	Α	16388	1	2013	
16294	46662	A	16389	313	770	IFGFVVAMHGAPGQAVLELLQ LTGDQSLGLSQRHMAALDALV HLLHGGLAVLTTAGAPEHET RGIAGLREEQCRNPRCVKRGW AQEKQA*PGQRGGRKSSPFWSF TL/DSASAGPRAALHLLPDVLS LQTLHHGLHRLLHPELLQLSHG
16295	46663	Α	16390	1	2753	
16296	46664	Α	16391	1	1363	
16297	46665	Α	16392	26	181	
16298	46666	Α	16393	1	867	
16299	46667	Α	16394	1	1447	
16300	46668	A	16395	31	659	APALPGCEHMMAIRELKVCLL GOTTGVKSKSIVCRFVODHFDII NISPTIGIASFMTKTVPGGNELH KFLIWDTAGQERFHSLLPLYLIR GSAAAVIVYDFTEAGFHFHPLK KWVKRLKELGPENIVMAIAG KCOLSDIREVPPEGMLKEYVA ESIGAIVVETSAKNAINISELFQ GISRQIPPLDHENGNNGTIKVE KPTMQASRRCC
16301	46669	A	16396	1	1182	
16302	46670	Α	16397	1	513	TFYTCFSPSVIPFSFSIHTKPYPG
16303	46671	A	16398	146		THY TOPSPSUIPFSFSHTIKPYPG HHQSFYMTNVSSNNPTISPLTT RPPFSLISPALGSHAAPNPA*SSP EKHRPFSLHTTPQKFHRPNTSTL F
16304	46672	A	16399	1	435	
16305	46673	А	16400	56	477	ARAAKGESCEGPGVGRCFSFSS YRQTPPCCQRLVNVPKTRIRTF CKKVCGKHRPHKVTGYKKGKD SFYA\QGRRRYDRKQSGYGGQT KPIFRKKAKTTKKMGLRLECV EPNCRSKRWILAIKRCKHFELG GDKKRKGQVIQF
16306	46674	Α	16402	183	373	IHGSSENPTPERETLFWHAENG SALASC*KSGGQAPKRKVRTTL ILKAEILILGMLVLRSHGM

	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
ŀ				sequence		
16307	46675	Α	16403	1	881	MPFKCKKQHTFNKTSPKEGAII
						FTHGCLCTSPFNSELSEHLGNL
						KLSSWEHLHHRSQQTLSVRLH
						VPTPQPVEHEFIQLIYIHTGAKL
1						QASKVIIATKDGKRRKSPLWQL
						KYPKLILREASSVSEELHKEVO
		1			1	EAFLTLHKHGCLFRDLVRIQGK
					1	DLLTPVSRILIGNPGCTYKYLNT
						RLFTVPWPVKGSNIKHTEAEIA
i	İ	l				AACETFLKLNDYLOIETIOALEE
		ŀ			l	LAAKEKANEDAVPLCMSADFP
	İ	ļ.	l			RVGMGSSYNGQDEVDIKSRAA
						YNVTLLNFMDPQKMPYLKEEP
1						YFGMGKMAVSWHHDENLVDR
l			ŀ			IOLOLWDPVDGTTASSAVPKO
i						GRDKRREVPNTLSQPNSQEGLI
						SAFHSRCVHAVFYKLTSAPKTT
	İ	l				SLPDVPSDLLAEGLAASRAGOA
		l	ŀ			LWRCDKKSLLTLVRKINLOGK
	ŀ					RDGGRSATNQQSQPHLDNTGL
						ERQLEQKVGRCRSPWRGLGHL
l						EGNAOKGHLLHGVNKNGOHL
l		l				L*MPPSPLPGGQKGRLVGMLS
		1				WVLT*VYKIQH/GT/PAAVEG*D
	İ					EAFLAVWLGEGVGDFSPLVPSL
1						LWHS*RGCCSIHGIPELELNPVH
	1					QIFIM/SASSLPFSPCQNKVPLSG
16308	46676	A	16404	1	459	QII THE SALES ET SI CONTROL TESO
16309	46677	A	16405	1	2025	
16310	46678	Α	16406	I	816	
16311	46679	Α	16407	1	217	
16312	46680	Α	16408	3	135	
16313	46681	Α	16409	21	218	
16314	46682	Α	16410	392	3744	LNYKMLLKNLSPMSMLKAFSF
						AIPMQPPAQTNLPTAKPNGFQP
						LLLSQYNACPPPQ*EAG/QVDL
						CSTIPLNLLPDSLPLTVPTGPLPQ
						GSVGLVLGRASSSAKGITIHTGL
						INSDSVDEIKLITSAKVPVSILAG
						ESIAQLLLLPNIILNKGDKTRGP
						GMGSRGEKAAYWINVISKQRP
						TCTIHIQGRKFEGLVDTGADVS
						VISSSLWPSSWLKHPTNMGLVG
						VGKAEEVYGSTFILPCTGLDGO
						KGTIQPYIM
16315	46683	Α	16411	1	783	

NO:	SEQ ID NO: of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
16317	46685	A	16413	3	1381	KIPFVGYOHORPKVDKTTKMG RNOSRKAENSKNOSTSSPPKDR SSLPATEQSWIENDFDELTEVG FRRSAITNISSELKEHVLTRKEKE KNILEKRLDEWLTRINSVEKTLN DLMELKTMAQELRDARTSFNS *FNQVEKRISVIEDQIDEIKQDD FNQVEKRISVIEDQIDEIKQDD ALMSKLNCAGPMARDSIGEVP PVPWRTVVGSGIAGEAKLDHL RLVSLIGREVNKGELHQLA FSPQAGALAOGONYAKPA SHOWATANLLNSRLNCAGPMARDSPAATRWL KQRPRLVAAAVQAFYLRDPID LRACRVFKTELPETRINTSYYAI EWSLWTLVDVLHAENSSSAHM SINSYOPPSOVAHLTHLPMSP IPDYIIARFRYRHRSRVRLTARK LLSPAMCGSCEIQRYSTMLERG FNGGYCKSTYRVVTEATRML
16318	46686	A	16414	1	1191	
16319	46687	-	16415	1	1909	
16320	46688	В	16416	1	1791	
16321	46689		16417	1	1818	
16322	46690	Α	16418	1	1044	
16323	46691	_	16419	1	1140	
16324	46692	Α	16420	1	1062	
16325	46693	В	16421	j i	972	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
16326	46694	Α	16422	I	1758	MDTFLQAERKDYMEAYELIEQ EEQGVKELNRPLTAPSALHPRD
		1				EAHLIMVDKLFDVLLDSVCOYF
		l				IEDFCIDVHHINSRWI/AVCQYFI
		l		l		EDFCIDVHHINSRWIKDLNVRP
		l				KTIKTLEENLGNTIODIGMGKD
		l				FLSKTPKAMATKAKIDKWDLIK
		l				LNNFCTAKETTIRLPVPNPCGPV
		1				AETPLSRVFVLREARKTLKPHO
		1				STCLSKGRDNSIDSWKTAARVL
		1				KTAISSTPTIPILKDQTQEWSVS
		l				ATFTSDGKIRLFYTDYSGKHYG
						KQSLTTAQVNVSKSDDTLKING
		١.				VEDHKTIFDGDGKTYQNVQQFI
	i		1			DEGNYTSGDNHTLRDPHYVED
						KGHKYLVFEANTGTENGYQGE
	l	ł				ESLFNKAYYGGGTNFFRKESQK
	ľ	1				LQQSAKKRDAELANGALGIIEL
						NNDYTLKKVMKPLITSNTVTDE
						IERANVFKMNGKWYLGELGW
						RREWSSGDRKSLARLSKTGTLG
						LAALTYKCTRDQWTVYCRVIR
	1					EKNLCQDMRWYQRCCQTCRD
						FYANKMSPATAELVTRSPKGRS
						KLRLRYQLVFISLKGKPARKGK
						ASSGSKLSLLSSSKTVALAGMG
						RGDEFQMELESEDLTSERDGIL
1.6205	16605		16400		1110	TPTSSNQKKSKAYGSLIRT
16327	46695 46696	A	16423	3	4449 3859	OFLPNLDSTVLGENYFDGTYO
10328	40090	A	10424	l <sup>3</sup>	3839	MLYLLVKGTIPVEIHTATVIFVS
						FOLSVATEDDFYTSHNLVKNLA
						LFLKIPSDKIRISKIRGKSLRRKR
						SMGFIIEIEIGDPPIOFISNGTTGO
						MQLSELQEIAGSLGQAVILGNIS
						SILGFNISSMSITNPLPSPSDSGW
						IKVTAOPVERSAFPVHHVAFVS
						SLLVITOPVAAOPGOPFPOOPSV
			1			KATDSDGNCVSVGITALTLRAI
		ı	1			LKDSNNNOVNGLSGNTTIPFSS
	l	i l	l			CWAN

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
16329	46697	Α	16425	65	1905	RTSSRKTTNHCSEIKEDTNNWK
		1				NIPCSWIGRINIVKMAKLPKPPL
						VIPRQTGSGVDLQQTPTDLHLR
-		1		ŀ		VLTVRRKTNKQKGHPHQNPIC
		l				SPSSKTKVLEVLARAFRQEKEI
						KGIQVGKEEVKLSLFADDMIVY
						LENPIVSAQNLLKLISNFSKVSG
		1				YKINVQKSQAFLYTNNRQTESQ
		l			i	IMTELPFTTASKRIKYLGIQLTR
						DVKDLFKENYKPLLNEIKEDTN
			ì			KWKNIPCSWVGRINIVKMAILP
						KVIYRFNAIPIKLPMTFFIELEKT
	İ				i	TLKFIWNQKRARIAKSILSQKN
						KAGGITLPDFKLYYKATVTKTA
		1				WYWYQNRDIDQWNRTEPSEIM
		l				LHIYNYLIFDKPEKNKQWGKDS
						LFNIWCWENWLAICRKLKLDPI
		l				LTPYTKINSRWIKDLNVRSKTIK
						TLEENLGNTIQDIGMGKDFMSK
		l			ŀ	TPKAMATKAKIDKWDLIKLKSI
		l		l		CTAKETTISVNRQPTEWEKIFAI
		l				YSSDKGLISRIYNELKQIYKKKT
		l				NNPIKKWVKDTNRHFSKEDIYA
	l					AKRHMTKCSSSLAVREMQIKT
	1	1	i		ľ	TMRYHLTPVEEVRAGEMAKTR
	1			l		RCQNVKGASEEGIRA/HCFVSH
	l	1	İ	1	i	*PHCP/LWRATTLMETLKFKPIE
		_				VPCKPLEKSVSLLLL
16330	46698	В	16426	I	2348	
16331	46699	A	16427	1	660	MPNFFIDRPIFAWVIAIIIMLAGO
					l	LAILKLPVAQYPTIAPPAVTISA
	1	l				SYPGADAKTVQDTVTQVIEQN
	1					MNGIDNLMYMSSNSDSTGTVQ
	1				l	ITLTFESG\QVQNKLQLAMP/LL
	1				1	PQEVQQQGVSVEKSSSSFLMVV
	1		İ		l	GVINTDGTMTQEDISDYVAAN
			1			MKDAISRTSGVGDVQLFGSQY
	1		1	i	l	AMRIWMNPNELNKVERNSRRQ
		1				DVGERDISSGSRKVNKESREDE
		<u>L</u>				EVT
16332	46700	Α	16428	1	975	

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon,/=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
16333	46701	Α	16429	1171	2007	AVDIVQGLVRGWGRQGWLLS
		l				GRGIPEGPLLLWGATVGSWRR
						LLPLTGVCGLPLGAVPVLIS*LL
						GGAQVQLLREEEAGHELVQQL
ļ	1					VDGALVLLLDGRLPLHVVADE
						RCCVLQDLPVLVHKDEVRLAR
				İ		GGTAALRVLLLVLVVDALDLV
		l		l		EQALGAQGLGVVLLEVHSLVV
		l				KGLEVRLLILLPPDLVEALLGLP
1		l	1			PLLFLGLQSFQDNGDSGDRVLL
						EALDDLRGLVAIDAINGTALDH
						LRRASQGVVQPELLLVFRRHPR
						QLLLHTFQHTDCGQVRLQDIV
16334	46702	В	16430	1	768	
16335	46703	A	16431	1	2553	
16336	46704	Α	16432	3	573	CEMHSVQKNEHDKTPEHSRKR
ļ		1	}	l		SRPSLLRPVSAPAKKKMKLRGT
				i		KDLSIAAVGKYGTL/PGIFFL*Q
		1				GPPGAEEPGGV*KLPPLHRTLQ
		l				PGAGVWL*APAARQPISGVSS*
		l				LPRAP*GGSVPVNSIYLVFSYCF
		l	l			*AMIVLF*NPVY*LT*LI*LLIPM
		l	ł			HL*GAIHHLGTLQLVPLPVTSV
						VSILTRIQWVLE
16337	46705	A	16433	110	1347	LTTATGMELSMGSTTWTSLCK
		l	İ			AENAACQQEKPHIWLCSISSFL
l		l				RLKRRRTTTKNTGTKKIASTVA
						VTIPPITPLPTAFCAPEPAPVLLT
l		l				SGIPPRLNASENPQLLSGS/SSSD
		ı	ł			STGTVQITLTFESGTDADIAQVQ
l		1				VQNKLQLAMPLLPQEVQQQGV
1		l				SVEKSSSSFLMVVGVINTDGTM
		l				TQEDISDYVAANMKDAISRTSG
		l	İ		ł .	VGDVQLFGSQYAMRIWMNPNE
		l			l	LNKFQLTPVDVITAIKAQNAQV
		l			i	AAGQLGGTPPVKGQQLNASIIA
		l				QTRLTSTEEFGKILLKVNQDGS
		l				RVLLRDVAKIELGGENYDIIAEF
		1			l	NGQPASGLGIKLATGANALDT
		1	1	1		AAAIRAELAKMEPFFPSGLKIG
						YPYDTTPVVNISIHEVGKTLVE
			1	l		ANNLVFLAMNLVLQEFPADVIS
L		_	1000	ļ		TIAGPPSLRSSRVPGL
16338	46706	В	16434	1	2550	
16339	46707	В	16435	1	630	
16340	46708	A	16436	270	455	a L approximate private a series
16341	46709	Α	16437	174	492	GALQPPPCTVGAPFWAGQGWS
l			1			PLPQLAGRCGGRGT\RGTGAAC
						GACGPAGVPGGLGLGGPRTRSS
		1				RPALLAPGNGGLSTRASGCGGC
	<u></u>					TESPSSGWPTSAALDFLPGP

SEQ ID NO:	of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Aminn acid sequence ( X=Unknown,
16342	46710	Α	16438	3	413	
16343	46711	Α	16439	31	507	
16344	46712	Α	16440	I	537	
16345	46713	A	16441	152	247	
16346	46714	A	16442	44	208	EEMTSKMYKVIIRKTMKASVC TQVKHPAIASICKAVL*VGPWS GHFKYAGLPTL
16347	46715	A	16443	1	549	
16348	46716	В	16444	376	862	
16349	46717	A	16445	2	1603	TNVSTTIATVUNALARATKIL PPOHRRSPNPATA AASSPTIL HCSLRSHHQPLRGEQQPQAIRT TAGGRCKALSSCPSFFEGSRSSG APPGACGGIFVSNAKLEPQAR PSSPVTGGPLDLMACRVVAST REMAMLIAQAUQTINYGRODE NGHTHSACEVHHGGRVPELSV PSFSWRNRNPSFIMGSITPTDY LISKCYLPREDVVLIIYCGVSTN EQPDEEVPRTRFPTVAVSIGFAK ROELFFGVIVHCLEVSLYTGR GRGAFCNGQRLRVSGETASGM LPGIQQHHQQEONLYGGSTESL LPGIQQHHQQEONLYGGASTEL LFGIQHHQGEONLYGGASTEL KICWGKKSGREIKIEDYFPEYA NYTVPEDGHLSAVHLKPPTGHTSTY HSMCLLNOPGWLRTISIILFLNN KICWGKKSGREIKIEDYFPEYA NYTVPEDGHLSAVHLYBGGLCM WLQHSQDSILYTDYRRGGEN FSVMVNSVALNGDGCGGEST EALIEVSHRLNCSREVGEHLNA
		乚				TGELGEERAHGRQQAACGFTIA
16350	46718	Α	16446	1	648	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
16351	46719	A	16447	329	2497	GEGOAVLOGKMGGEEKPI\GA
						GEEKOKEG\GKKKNKE\GSGDG
l						SRAELNPWPEYIYTRLEMYNIL
1						KAEHDSILAEKAEKDSKPIKVT
		ŀ				LPDGKOVDAESWKTTPYOIAC
				ļ		GISOGLADNTVIAKVNNVVWD
						LDRPLEEDCTLELLKFEDEEAO
					ľ	AVYWHSSAHIMGEGMERVYG
				l		GCLCYGPPIENGFYYDMYLEEG
1						GVSSNDFSSLEALCKKIIKEKOA
1		l				FERLEVKKETLLAMFKYNKFK
	l	1				CRILNEKVNTPTTTVYRCGPLID
						LCRGPHVRHTGKIKALKIHKNS
						STYWEGKADMETLQRIYGISFP
1				1		DPKMLKEWEKFQEEAKNRDHR
	ĺ					KIGRDQELYFFHELSPGSCFFLP
						KGVYIYNALIEFIRSEYRKRGFQ
						EVVTPNIFNSRLWMTSGHWQH
						YSENMFSFEVEKELFALKPMNC
		1				PGHSLMFDHRPRSWRELPLRLA
		ŀ	ļ			DFGGLHRNELSGALTGLTRVRR
						FQQDDAHIFCAMEQIEDEIKGC
		ŀ	ŀ			LDFLRTVYSVFGFSFKLNLSTRP
		l				EKFLGDIEVWDQAEKQLENSL
						NEFGEKWELNSGDGAFYGPKI
						DIQIKDAIGRYHQCATIQLDFQL
						PIRFNLTYVSHDGEDKKRPVIV
		l				HRAILGSVERMIAILTENYGGK
		l				LAPFWLSPRQVMVVPVGPTCD
		1			1	EYAQNVRQQFHDAKFMADIDL
		1		ĺ	1	DPGCTLNKKIRNAQLAQYNFIL
		L				VVGEKEKITGTVNIRTRDNKVH
16352	46720	С	16449	189	456	
16353	46721	Α	16450	3	1414	
16354	46722	Α_	16451	95	293	L

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
16355	46723	Α	16452	li .	1136	MKKRPGHSLFQFQFLMFRLFSE
			l			ARQPLSEEDVASLSWRPLHLPS
						ADWQRAALSLWTHRTFREVLK
						EEDVHLTYODWLHLELEIOPEA
						MLFQILNGRTSTSGRSMSTFSL
	İ	l				SPRLQGAVTETCRLRVPFLSTH*
		1			ļ	WISTKAQGVMTTQKILIWSLVA
ł		1				AQEMRILFPDCRRW*LTWSCSK
Į.					1	TS*CLSATPLPRSTSSLRFSADG
		l				SRL*QAGGAWLPAFRDRGSC*C
l						TNGSSSACLRLSSAAAASRQNS
ĺ		l				PSLPDASSSSTWSTLR*ETSAPT
		1				EVP*HRTSLPTS\QGPPERLSAE
		l				QRPLPDGR/RSYWPSARRNA/RL
		l				ILT/FCSGVVAEPGACAALPVEE
		l		1		TLPEPAAPGTAEATRRPAVCQR
l		1				VRVGAIGFPFLLLLDGPAVVTS
		1				DLK
16356	46724	Α	16453	3003	3482	HRPRTRPCPWRRNHHLGHRAP
		1				L*PQRARR*SPNPPEDGSEDEHL
						*QLC
16357	46725	Α	16454	598	759	KVILGLWTEEAQVGGQGLRAP
	i					TPRLLHHVLK*DIKR*AHRPDA
		<u> </u>				VAHACNPNTLG
16358	46726	A	16455	1	1767	
16359	46727 46728	A A	16456	2	572 726	
16360	46729	A	16457	155	1334	HALGRRGGSOELSAAAGAASP
10301	40729	A	10438	133	1334	SGSERRAPGALPCAWAAALLV
				l		LGAPPASRPGGFAAGKTMLLK
		l		l		E\YRI\CMPLTV\DEYKI\GQLYM
		ı		l	į.	ISKHSH\EOSDRGEGVEVVOKE
	l			l		PFEDPHHGNGQFTEKRVYLNSK
					l	LPSWARAVVPKIFYVTEKAWN
					l	YYPYTITEYTCSFLPKF\SIHIET
		1	ļ.		ŀ	KYEDNKGSNDTIFDNEAKDVE
		ı				REVCFIDIACDEIPERYYKESED
1		1			1	PKHFKSEKTGRGQLREGWRDS
1				l	i	HOPIMCSYKLVTVKSEVWGLO
			ĺ			TRVEQFVHKVVRDILLIGHRQA
				1	1	FAWVDEWYDMTMDEVREFER
1	1	1	İ	I	1	ATQEATNKKIGIFPPAISISSIPLL
1	1		1	I	1	PSSVRSAPSSAPSTPLSTDAPEFL
1				1		SVPKDRPRKKSAPETLTLPDPE
	l	1	l	1		KKATLNLPGMHSSDKPCRPKSE
16362	46730	A	16459	26	355	
16363	46731	A	16460	86	489	
16364	46732	В	16461	1	201	
16365	46733	Α	16462	3	367	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
	1	<u> </u>				
16366	46734	Α	16463	58	553	VARSAPPDGAVCAGPGSRRTE
						MAEQSDEAVKYYTLEEIQKHN
l	1	l .				HSKSTWLILHHKG\YDLTKFLE
						EHPGGEEVLREQA\GGD\ATENF
		i i			1	EDVGHSTDAREMSKTFIIG\ELH
	1	1				PDDRPKLNKPPEP*RRCFKETLI
	1	1				TTIDSSSSWWTNWVIPAISAVA
l						VALMYRLYMAED
16367	46735	A	16464	185	489	7710,77110
16368	46736	A	16465	134	345	
16369	46737	A	16466	572	1017	
16370	46738	A	16467	911	1013	
16371	46739	A	16468	1	157	FGGNOKGERTGOKGKGERGAK
103/1	40/39	^	10400	l'	137	RKDFPGAVCISALGLLAKGCG*
						SWRPSSSAN
	46740	ļ.	16469		369	SCGLSLIKMTTSQKHRDFVAEP
16372	46740	Α	16469	71	369	
	1		1			MGEKPVGSLAGIGEVLG\KKLE
	1					ERGFDKAYVVLGQFLVLKKDE
1	i				1	DLF\REWLKDTCG/APNAKQSR
						DCF*CLREWCDAFL
16373	46741	Α	16470	1	831	
16374	46742	A	16471	368	679	SSQLNKAPSLFNPVSEEFCLWL
	l	1				LLLQKELLTRITSLEKNTNDLV
	ı	1				DLKNTA*ELHEAHTSINS*IDQV
1	ı	1		ŀ		EERISECEDHLTEIRHSEKMKTA
						LLK*DMQTRREKKK
16375	46743	Α	16472	536	717	
16376	46744	Α	16473	1	1632	
16377	46745	Α	16474	1	651	
16378	46746	A	16475	1	903	GGGGRMKLIDYGLSGYQEESA
	1	1	l			E\VKAMDFITSTAILPLLFGCLG
	1					VFGLFRLLQWVRGKAYLRNAV
						VVITGATSGLGKECAKVFYAA
	1					GAKLVLCGRNGGALEELIRELT
						ASHATKVOTHKPYLVTFDLTDS
	1					GAIVAAAAEILOCFGYVDILVN
1						NAGISYRGTIMDTTVDVDKRV
			ì			METNYFGPVALTKALLPSMIKR
						RQGHIVAISSIQGKM\SIPFRSGI
					\	CQPSKHATQAF\FDCLAVPEM\E
						OFEIEVTVISPGYIHTNLSVNAIT
1		1		1		ADGSRCGVMDTTTAO\AEALW
1		1		1	1	RWPRMFLLLWGRRRKM
16379	46747	A	16476	359	1094	KWI KWI EEEW GIGGGE
16380	46748	A	16477	1	906	
16381	46749	A	16478	i –	371	
16382	46750	A	16479	h	257	
16383	46751	A	16480	2	419	
16384	46752	A	16481	1	2514	
10304	170732	Ι^	110401	1.	1	L

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nuclentide insertion)
			İ	sequence		
16385	46753	Α	16482	262	822	AGCTRKTRIIDVVYNASNNELV
	ŀ	1				RTKTLVKNCIVLIDSTPYRQWY
		1			1	ESHYALALGRKKGAKLVRVTS
		1			l	L*GLWGGQPDSSLLVMKTLSSS
	ŀ	1		1		ATEGREMRAF*AEEGQHWGVQ
	1	1		1		GSRKLPGPAFLP*AHIFVSPFQT
	l	1		i		PEEEEILNKKRSKKIQKKYDER
İ		l				KKNAKISSLLEEQFQQGKLLGE
i		1				KADELEVGSRRD
16386	46754	A	16483	2	799	SQWLKLPSPLPHAGISRY\NWD
	ŀ	l				QAP*KTGGPRESPYHKKREVM
		l				KLGRPSCPN/NPKIGPPAGIQHSP
	İ	1			i	VCRGG*QVNTRAPEVWTVGNF
	Ì	l				\SWGLICRCTP*NKDPSIVVLQC
		i				HLNNGA WFRTQGPWVEEFCIV
	ŀ	l				ASSDQQQPYR\QWVRSPNLCAC
		1				PLGPAKKGEPKLDSLRKEEIFK
						QKNDLKKLRKEI*LKRKKNCQI
	ŀ					PAVLPGREQFPARGKLSCRA/SR
	1					FQGPGQLWAEQDGFCA*EGQK
	ł					SLEFLSFRKNPRPRKGQIKFLVF
						VFHPC
16387	46755	Α	16484	1	681	
16388	46756	A	16485	287	694	IISSRPAPASAPRRWGLSWSWQ
	1	1				RCWC**TPSPSPRPRPAEG\CLR
	i		1			GRGRGAGGGLPFRPHGSLVHS
	i	1				GAQPPHFPHLPGGARQTCGAPP
		ı				GSWSCVL/CRPAETGAAAAGSP
						AAAGSTRKRLGRAQGRGCRVA
	l					ALRLSPTH
16389	46757	Α	16486	189	381	QGAGSVGRTGQQLLKPGPFFLE
		l				KLLSLGCT/LSG*ALRARACCSP
	1			i		CCRPGAGCQPQAPVAQAGHP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
16390	46758	A	16487	1	2388	QGRLVAKPPRPARSTAADSSTP RDMLGLRPPLLALVGLLSLGCV
						LSQECTKFKVSSCRECIESGPGC
						TWCQKLNFTGPGDPDSIRCDTR
						PQLLMRGCAADDIMDPTSLAET
						QEDHNGGQKQLSPQKVTLYLR
						PGQAAAFNVTFRRAKGYPIDLY
						YLMDLSYSMLDDLRNVKKLGO
						DLLRALNEITESGRIGFGSFVDK
						TVLPFVNTHPDKLRNPCPNKEK
					Ì	ECQPPFAFRHVLKLTNNSNQFQ
						TEVGKOLISGNLDAPEGGLDA
						MMQVAACPEEIGWRNVTRLLV
						FATDDGFHFAGDGKLGAILTPN
						DGRCHLEDNLYKRSNEFDYPS
						VGQLA\HKLAENNIQPIFAVTSR
						MVKTYEKLTEIIPKSAVGELSE
						DSSNVVHLIKNAYNK/LSSRVFI
						DHNALP\DTLKVTYDSFCSNGV
İ			ŀ			THRNO\PRGDC\DGVOINVPITF
		1			ì	OVKVTATECIOEOSFVIRALGFT
		ŀ				DIVTVQVLPQCECRCRDQSRDR
						SLCHGKGFLECGICRCDTGYIG
					ŀ	KNCECOTOGRSSQELEGSCRKE
						NNSIICSGLGDCVCGQCLCHTS
						DVPGKLIYGQYCECDTINCERY
						NGOVCGGPGRGLCFCGKCRCH
						PGFEGSACOCERTTEGCLNPRR
						VECSGRGRCRCNVCECHSGYO
						LPLCQECPGCPSPCGKYISCAEC
						LKFEKGPFGKNCSAACPGLOLS
						NNPVKGRTCKERDSEGCWVAY
16391	46759	A	16488	353	1205	THE PROPERTY OF THE PROPERTY O
16392	46760	A	16489	11	440	FRALTEGDTQLNWNIVSFPVAE
10392	70,00	l^`	10707	l'''	""	ELSHHENLVSFLETVNOPHHON
		l				VSVPSNNVHAPYSSDKEHMCT
		l		l		VVYFDDCMSIHQCKISC\ESMG
		1	ĺ			SHPNIR WVSLMACCECIGPECIE
		l	l	1		
		ĺ		I		YGSKTVKCMNCMF*RRQMQT
	L	<u> </u>	L	L	L	KAT**NNRYKKLKK

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
16393	46761	A	16490	515	1808	KRKQTGEFGFNSFE\WCDSDLC
10370	10701	1	10150			EMNAGMPKGNLNEODPKHCPE
						SEKCLLSIEDEESQQSILSSLENH
		l			i .	SQOSTQPEMHKYGQLVKVELE
		1				ENAEDDKTENOIPORMTRNKA
	l	1				NTMANOSKOILASCTLLSEKDS
						ESSSPRGRIRLTEDDDPQIHHPR
	1		i			KRKVSRVPQPVQVSPSLLQAKE
	1					KTQQSLAAIVDSLKLDEIQPYSS
					i	ERANPYFEYLHIRKKIEEKRKLL
i		1		ł		CSVIPOAPOYYDEYVTFNGSYL
	,					LDGNPLSKICIPTITPPPSLSDPL
	ł	1				KELFROOEVVRMKLRLOHSIER
						EKLIVSNEOEVLRVHYRAARTL
		1				ANOTLPFSACTVLLDAEVYNVP
		1				LDSQSDDSKTSVRDRFNARQF
	Ì	1				MSWLQDVDDKFDKLKTCLLM
		l				RQQHEAAALNAVQRLEWQLK
		1				LOELDPATYKSISIYEIOEFYVPL
		1				VDVNDDFELTPI
16394	46762	Α	16491	1	699	
16395	46763	В	16492	6	5954	
16396	46764	Α	16493	22	585	
16397	46765	A	16494	1	837	
16398	46766	Α	16495	1	1422	
16399	46767	Α	16496	13	189	
16400	46768	Α	16497	193	366	GRPGIFKSFCRWW*C*FHMEFI
		1				WKSSA*/WSGVWHAGNICLSIS
						NPEDLRASQFCSSG
16401	46769	Α	16498	1	888	
16402	46770	A	16499	3	531	DAWADAWADAWALQS
ŀ						RRRRRRTQLTLSSPHDCYRGLQ
ŀ				1		SLLLILCKMATLKEKLIAPVAEE
1						\EA\TVPNN\RITVLGDGQVGMA
İ						CAISILGKSL\ADELALVDVLED
						KLKGGNDGSFQHG\SLFL\QTPK
			1			\IVGRIKDYSG\TAQF*RIVVGN
l				l		WQGVRSARRGKVRSNLVQRN
	L	_				VNVFK
16403	46771	Α	16500	2	406	
16404	46772	A	16501	2	394	
16405	46773	A	16502	1	399	C. P. A. P. P. L. V. C. P. P. P. V. C. C. V. C. V. V. C. V. V. C. V. V. C. V. V. C. V. V. C. V. V. V. V. C. V. V. V. V. V. V. V. V. V. V. V. V. V.
16406	46774	A	16503	74	464	FAFNMPEPAKSAPAPKKGSKK
			1			AVTKAQKKDGKKRKRSRKESY
		1				SVYVYKVLKQVHPDTGISSKA
1		1				MGIMNSFVNDIFERIAGEASRL
		1				AHYNKRSTITSREIQTAVRLLLP
	ļ	_				G\EL\AKHAVSEGTK\AVTKYHQ
16407	46775	В	16504	84	832	
16408	46776	В	16505	201	829	
16409	46777	A	16506	1	804	

SEQ ID	SEQ ID NO:		SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
io:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
6410	46778	Α	16507	3	615	PECIIGIDILSSGQNPHIGSLTGF
						VRAIMVGKAKRKPLELPLPRK
	l					LNQKQYRIAGGIEEISATIKDL
	ŀ					DAGVVIPTTSLFDSPIWPVQKT
	ŀ					DGSWRMTVDYRQINQVATPIA
	1					AAIPDVASLLKQINTSPDTW/P
	ŀ				1	RPPISNGD*GVSGR*ACCLEPL
	l l					GPHR*ITSEASRILEQGPAIFCR
		1				LLSF*ETALGLLLGFGGN*TFD
6411	46779	С	16508	25	153	
16412	46780	A	16509	I	1317	
16413	46781	A	16510	1	1557	QVPGCIIGIDILSSWQNPHIGSL
	l					GRVRAIMVGKAKWKPLELPLI
		l				RKIVNQKQYHILGGTVEISATI
		l				DLKDTEAVTPTTSPFNSPIWPV
		İ				QKTDGSWRMTVDYCKLNQV
						TPIAAAVPDV/VSLLEQINTSPO
						TWFEWSPK\KALQQVQAAVQ
						ALPFGPYDPADPMVLEVSVAL
						RDAIWSLWNAAIGESQRRPLO
	ŀ					WSKALLSSADNYSPFERQLLA
			ŀ			YWALVETERLTVGHQVTLRP
						LPIMNWVLSDPSSHKVSGAQO
					1	HWKCAVHT/IIKWKWYIRDW/
						QAGLEGTS*LYWPRASRYQQC
					į.	HQDLFILRSDLPSQVFIRDKLM
						RRNRRTGRTEKARIWEVTDR1
						VRTWIGEAVAAAAADGVTFS'
						PVTPHTFRHSYAMHMLYAGIF
				1		KVLQSLMGHKSISSTEVYTKV
				1		ALDVAARHRVQFAMPESDAV
						MLKQLS
6414	46782	Α	16511	41	428	
16415	46783	A	16512	1	1026	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
		<u> </u>				
16416	46784	Α	16513	648	1886	LDPEVAWAKWQHSTVKGPQK
	1	1		1		QFAFSWQGQQYTFTGLPQGYIN
		1				SLSLCYNLIPRDLDRFSLPQDIT
1				l		LVHYIDDIMLTGSSEQELAYTL
1		1				DLLVRRLCAKGWEINLTEIQEA
		1		l		STSVKFLRVQWCGACQDIPSK
	1	1		1		MKDKLLHLFPPTTKKKASLFGF
		1				RRQCIPHLECGPEQEKALQQAQ
		1				AAVQAAVPLERYDPADPMVL/
		1		ŀ		V/ELTWLWPLLSAQFASSGDQH
		1				*ALHMAPFLGVVSQLPGGKLIII
		İ				DIFHHGKGRVLFSLE*TLTPDM
		Ì			i	GLPILHIMLLPRLPSVNSONALS
1		İ				TVMPGFTGPGIKGWKWHHSPS
1		1	l		I	PLVIH*QNFCFLFP*HYVLLA*R
1	1	1				S*FQRKEPCHQET*Q*FH*TGS*
l		1				GCQLDTLGSCYF*VNKLRRELQ
		ļ				CWLG*LTQTIKMKSVYYSITEN
		i				CWMKRSPVKRRKILELEEA
16417	46785	A	16514	1	402	
16418	46786	A	16515	i	396	PTRPGERSVHVEIPRRVGSGAG
10.110	1.0700	1		ľ		HAQWAGPVRVARPQLNAQLE
		1				GWLSOVOSTKRPARAIIAPHAG
				1		YTYCGSCAAHAYKOVDPSIT\O
		1				RFRYSYYDESOGEIYRSIEHLDK
						MGMSIIEQLDPVSFSNYLKKYH
16419	46787	A	16516	2	358	MONSHEQEDFVSFSIVTERRTH
16420	46788	A	16517	2	769	
16421	46789	A	16518	Ĩ	1017	
16422	46790	c	16519	54	294	
16423	46791	A	16520	159	245	GISVSCSMYL*PDRSAGYYGLF
1.0.123	10///	ľ.	10020	1.57		KDRKEK
16424	46792	A	16521	1	1227	
16425	46793	A	16522	1	2697	
16426	46794	A	16523	200	696	YGIVTGPSLCAGDKQPKKQEK
		1				NPVLVSPEFVDEALCACEEYLS
		1				NLAHMDID/IGPGGPAVPOPPRA
		ı				GPSSSSVT\PSGPVSPLQLGLWA
1		1				VGRCLGIDPFCLVOPLPLPOASR
1		1	l			SFTPLFCSGTLEDSHCLRDRVW
		1				ATFLGSWHSIVTKSMDCATKW
		1				TAHYPKCVLCGC
16427	46795	В	16524	1	960	TATITACVECUC
16427	46796	В	16525	1	2183	
16429	46797	A	16526	306	1844	
16430	46798	A	16527	59	189	YNSGCLYGSQCSVCRCL*GVRN
10430	40/20	l^	10327	"	107	QVRSQQQAMMAMAILVNKKG
		1				G G G G G G G G G G G G G G G G G G G
16431	46799	A	16528	i -	2034	9
16431	46800	B	16529	1	855	
16433	46801	A	16530	1	834	
10433	140001	١^.	10000	P	1057	

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				sequence	,	
16434	46802	A	16531	65	172	
16435	46803	Α	16532	321	429	
16436	46804	Α	16533	460	647	
16437	46805	С	16534	529	804	
16438	46806	Α	16535	3	433	
16439	46807	A	16536	1	484	
16440	46808	Α	16537	511	681	QQGYTPFQGSGRESFLASSSFW
		1		l		WL/PGLPWLAAA*LQALTPSSH
		l				SLLSYLCSLLFCHP
16441	46809	Α	16538	51	634	PVPTFGLPARHTGAEKRRKNSO
		1				GEQLSKNNLYIRGLPPGGTDQI
		l				LIKLCQPYGKIVS\TRAFLDKTT
		1				RCKGYGFVDFDSPAAAQKAVA
		1				SLKANGVQAQMAKLQERDPA
		1				GLSVSSLLL\SMYEOELENMLK
		l			ł	PFGHVISTRILRDANGVSRGVG
		l				FARMESTEKCEVVIOHFNGKY
		l				KTPPGIPAPSEPLLCKIADG
16442	46810	A	16539	1	759	KITTGITATGETEECKIAEG
16443	46811	A	16540	74	352	
16444	46812	A	16541	1	747	GSAVYLCYKKSVAKTNTVSYK
10-1-1-1	70012	<u>۱</u>	10541	ľ .	/ - /	AGLICRYPOEDYESFSLPESVPL
		1	ľ			FCLPMGATIECWPSNSKYPLPV
		l	ł			FSTFVLTGASAEKVYGAAIOFY
		1				
		l				EPYSEENLTEKQRLLLGLTSAD
		1				GKSDSSKTIHTNKCICLLSHWP
						FD\AFRKFLTFLYR\YSISGAHVI
						PIEKHISHFMHKVPFPSPQRPRII
				ŀ		VQLSPHDNLILSQPVSSPLPLSG
		l				GKFSTLLQNLGPENAVTLLVF#
		_				VTEHKILIHSLRPSVLTSVTEAL
16445	46813	A	16542	319	969	
16446	46814	A	16543	131	342	NSDMGLNLGSALTG*PWVAIE
		1			}	CCFGFFQIIIVFSCLLGWL*VAP
						HPNLPSSPAEYMDFREAQEGTI
		_				VIY
16447	46815	Α	16544	1	1086	
16448	46816	Α	16545	469	759	
16449	46817	Α	16546	3	598	
16450	46818	Α	16547	227	604	
16451	46819	A	16548	416	1814	
16452	46820	Α	16549	763	867	
16453	46821	Α	16550	1	1419	

SEQ ID	SEQ ID NO:	Met	SEO ID NO-	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			İ	sequence		
		<u> </u>		915	3125	I SLAGMRLTGTVSGGEVRV/TAK
16454	46822	Α	16551	913	3123	
					ì	AGARVGPPELVGRPLEGECWY
		ĺ				FSGVSRTQAQQLLLSPPNEPGA
ļ						FLIRPSESSLGGYSLSVRAQAKV
		1				CHYRVSMAADGSLYLQKGRLF
1						PGLEELLTYYKANWKLIQNPLL
						QPCMPQKAPRQDVWERPHSEF
		l				ALGRKLGEGYFGEVWEGLWL
l				1		GSLPVAIKVIKSANMKLTDLAK
		l				EIQTLKGLRHERLIRLHAVCSG
		1				GEPVYIVTELMRKGNLQAFLGT
1	1	l				PEGRALRLPPLLGFACQVAEGM
1						SYLEEQRVVHRDLAARNVLVD
				i .	l .	DGLACKVADFGLARLLKDDIY
						SPSSSSKIPVKWTAPEAANYRV
1				1		FSQKSDVWSFGVLLHEVFTYG
1				1	1	QCPYEGMTNHETLQQIMRGWF
1		l		1		FGCISRSEA VRRLQAEGNATGA
						FLIRVSEKPSADYVLSVRDTQA
						VRHYKIWRRAGGRLHLNEAVS
						FLSLPELVNYHRAQSLSHGLRL
						AAPCRKHEPEPLPHWDDWERP
						REEFTLCRKLGSGYFGEVFEGL
	l			1		WKDRVQVAIKVISRDNLLHQQ
					1	MLQSEIQAMKKLRHKHILALY
	1					AVVSVGDPVYIITELMAKGSLL
1						ELLRDSDEKVLPVSELLDIAWQ
ı						VAEGMCYLESQNYIHRDLAAR
i i						NILVGENTLCKVGDFGLARLIK
1	ł					EDVYLSHDHNIPYKWTAPEALS
1	İ	l				RGHYSTKSDVWSFGILLHEMFS
						RGQVPYPGMSNHEAFLRVDAG
16455	46823	Α	16552	1	990	
16456	46824	A	16553	1	2847	MTAREHSPRHGARARAMQRAS
1		1				TIDVAADMLGLSLAGEPHRACT
1						GLQTTGYPGL\DPSG*TRK*GRG
		1				MSALFL*TASAGA*LH*FSSLVA
		1				GAPPG*CGNVQVF/WLAHAQA
1		i				MGTNNPIFLSSIAFFQDSLINQM
						TQVKL\$VYDVKDRSQGTVKSA
1	1	1			I	ESDRVGNITVIGWQMEEKSDQ
1		1			1	RPPVTRSVDTVNGRLHPPAPTV
					l	MHSLSHRHSKKNSNFRALALM
		1				VLPVDESLTEALGIRSKYASLR
16457	16025	L	1654	1	327	KDTLLKSVFGGAICR
16457	46825 46826	A	16554	259	3109	
16459	46827	A	16556	262	3159	
16460	46828	A	16557	1	1398	
16461	46829	A	16558	123	393	
16462	46830	A	16559	245	424	
.0402	1.5050	1	1.000			L

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
16463	46831	Α	16560	1	531	
16464	46832	Α	16561	2348	2775	
16465	46833	А	16562	373	555	LRIQVTFDDVAVEFTPEEWALL DTTQKYLYRDVML\ENYMNLA SVGKSNITLLGMVACTCS
16466	46834	Α	16563	165	457	
16467	46835	A	16564	310	349	K*TMK*EMGKFK*FY/IYLEQED YANANALLSPAPALPKEKRTDS NGRVYFVNHNTRITQWEDPRS QGQLNEKPLPEGWEMRFTVDG IPYFVDHNRRTTTYIDPWSTRP
16468	46836	Α	16565	1	2217	
16469	46837	Α	16566	1402	1860	
16470	46838	A	16567	461	696	KRMCFCTSLSSARSSGSMYMSC RICCSMMPPFSSVFRSISSRYSR AAFWAWTETRLCWQAAMPRQ QPPGLLHQWTTSP
16471	46839	Α	16568	1	601	
16472	46840	Α	16569	468	1213	
16473	46841	A	16570	2	365	EGCFQKIKLDHILSPPPMPFWK CSNPDVAFGPGKSLKYKRQLS* DGRQLRRGSLGGALTGRYLLP NPVAGQA WPASAETSNLVGMR SQALGQSAPSLTASLPCVSKCW ENIPPWMNCPPIK
16474	46842	С	16571	220	408	
16475	46843	A	16572	840	1091	QSLQHDVTL*VPVLLSYPEPAPS GHGLLRGSAQIAL*TIPADPAGT YLKTREPTLGCQTVPLPAPHLS VDTVCRCLSSSVWPQ
16476	46844	Α	16573	I	1356	
16477	46845	В	16574	1	1084	
16478	46846	A	16575	2	526	OPRGKKESKNKPRKQNFPTPKH MRVVLPPF/PPLKFFIFPKGLKFL EGGCPNISPPQKKGSLPKIPR*V LIRPPIRKKLFPCTARVKLGPPQ GSFKTAAPSSSSP*SADPVYLAG K/PRQSSSPGGTGGLNPPPRRLQ PQPHPGPSWHSSSSRGPGGHPR RESAERSRCASGNPGQ
16479	46847	Α	16576	36	167	RQLFENTQSDETKQEQNKQNK K*STATESRKVPQTGKSKSYWP
16480	46848	Α	16577	171	527	
16481	46849	В	16578	1	471	
16482	46850	Α	16579	1	294	
16483	46851	Α	16580	185	299	GLQYLKGKSGLKVKRGKVW*S ACCKKKGAALGTVASPL
16484	46852	Α	16581	3	414	

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
16485	46853	A	16582	462	928	WGVPGLPGRHLLPLPSQPPPSW
						LSILYVSWAALTCFLNSGESTA
						AKFFCPNLSAISYHTEAIPTTWO
	1					GVHLSWAFGNGAPDIFSGPGGL
	ļ	1	l			L*PA/POP/DLALGALFGAGVLV
		l				TTVVAGGITTLLLFIQHHTTQEI
						H*OIVOWIKTTL*ILATVSYVIG
16486	46854	A	16583	1	654	, , , , , , , , , , , , , , , , , , ,
16487	46855	A	16584	66	323	RVSLEIHVIOKRRPHHLSLLSFW
10.01						TRMKTFRRRK/WGEAEESATDT
	1	ŀ			į .	TSETNKVGTGVFVLSLWVPVL
1					i	VRNLAGPGVVLGNICKHFPVC
16488	46856	A	16585	1	1530	
16489	46857	A	16586	615	873	FVFLWSLMMVMYRWGFGVAV
10.00	10007				1	LSVC*FSF*OSGPSAAGLLEFAG
						GPFOTPFA WVSVVEAAEQRIML
						NSKRCCVIVPLVVSSORGTRP
16490	46858	A	16587	286	626	PCKLFPCCNTCYS\RV*DFFRVA
10490	70030	1	10307	1200	020	GKRSL\LNNYTSWVNTSMLVPR
		1				VAFACGFPLQQAAVLCVHLLG
						SPILGAADSSVTPPFCWMANAH
		ł				ICGLOLONTLSFAEPIYLGOEHA
				l		ols
16491	46859	A	16588	226	489	PYLSVIFFFDYGINEEOCORPIO
10491	40039	^	10500	120	107	GDGQNFHRHNGWIKINPSCISF
1		1				AIFFPFGAEKNMWSTPVTEAFN
		l				LLST*AF*LFGYKCTLVISSS
16492	46860	A	16589	1	1344	DECT ALL EL CITACIDADES
16493	46861	A	16590	li .	257	
16494	46862	A	16591	73	374	ESETEHKRPGKHSPKRSCNMCG
10474	70002	ľ`	1000	,,,	J	QWAFHASLTVSYCLLTWCNET
				ľ		CSGDGCEGGMRIDIDPPVSQTR
1						FFITLL*LC\FPGAGPOPAYFCTO
1		l				TOCHVETPRVSQ
16495	46863	Α	16592	h	666	
16496	46864	A	16593	95	1840	
16497	46865	A	16594	1740	2026	
16498	46866	A	16595	39	487	SRLDPRVRLLFRQFCETRPGLEC
1	1.000	Γ.	1	1	1	YIQFLDSVAEYEVTPDEKLGEK
1		1			1	GKEIMTKYLTPKSPVFIAQVGQ
1	1	1		1	1	DLVSOTEEKLLOKPCKELFSAC
	1	1		1	1	AQSVHEYLRGEPFHEYLDSMFF
		1		l	1	DRFLOWKWLE/RVCACQVRAT
		1		1	1	GK\MYACSRLEKKRIQKRK
16499	46867	A	16596	1	591	GRWITACSKLEKKKIQKKK
10499	140807	I <sub>M</sub>	ספנטון	11	1221	L

SEQ ID						Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence	l	
16500	46868	Α	16597	71	1994	EQEQRGRQGGLLAPPAPAAAA
		l				AARAAAAAAAAPOALTAPPAG
						SVADRRLSMELENIVANTVLLI
		l	1			AREGGGGKRKGKSKKWKEILI
	i				l	FPHISQCE\SLRRTIDRDYCRVC
		l				DKQPIG\RLLFRQFCETR\PGLE
		1				YIQFLDSVAEYEVTPDEKLGER
						GKEIMTKYLTPKSPVFIAQVGQ
					l	DLVSQTEEKLLQKPCKELFSAC
						AQSVHEYLRGEPFHEYLDSMF
					l .	DRFLQWKWLERQPVTKNTFRO
					1	YRVLGKGGFGEVCACOVRATO
	1					KMYACKRLEKKRIKKRKGESN
	1	1		I	I	ALNEKQILEKVNSQFVVNLAY
	1	1		I		AYETKDALCLVLTIMNGGDLK
	l .	1				FHIYNMGNPGFEEERALFYAA
	1					ILCGLEDLHRENTVYRDLKPEN
		1				ILLDDYGHIRISDLGLAVKIPEG
	i	1				DLIRGRYGTYGYMAPEVLNNO
						RYGLSPDYWGLGCLIYEMIEG
		1				SPFRGRKEKVKREEVDRRVLE
						EEVYSHKFSEEAKSICKMLLTK
	1	1				DAKQRLGCQEEGAAEVKRHPI
						FRNMNFKRLEAGMLDPPFVPD
						PRAVYCKDVLDIEQFSTVKGVI
						LDHTDDDFYSKFSTGSVSIPWC
		l				NEMIETECFKELNVFGPNGTLP
		1			ŀ	PDLNRNHPPEPPKKGLLORLFK
		1			l	ROHONNSKSSPSSKTSFNHHIN
16501	46869	A	16598	1	963	KUNUNSKSSFSSK ISFNIHIN
16502	46870	A	16599	192	609	RPKGARELRLHPGPRYGRTSPC
	1.00.0		,			NCPWARPGCLHEAL*G\WKICL
	1	ł			1	HCKCPQEEHMVTVMPLEMEK*
						ISKLMFDFQRNSTSDDDSGCAL
		1				EEYAWVPPGLKPEOVHOYYSO
		ı				LPEEKVPYVNSPGEKLRIKQLL
						HQLPPHDNEV
16503	46871	A	16600	1	915	
16504	46872	В	16601	30	820	
16505	46873	Α	16602	99	248	RLEKHINCSRVI*SWAASPGLTA
	1	l			1	AAYRVTLNPPGTFLEGVAKVG
		1				QYTFT
16506	46874	Α	16603	1	717	
16507	46875	Α	16604	271	556	TAACLQSHHFKSSGQLSFERKV
				İ		PKVGTITRSIASLLSGPVFGLHH
	1	1		l		LAFSAHVPREGPTTPWNYFPRV
	1	l		l		AAP/RRWTPGEHARTTTGLGA/
				1		PCVLLWA
16508	46876	С	16605	135	341	
16509	46877	Α	16606	125	226	
16510	46878	A	16607	194	547	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /-possible nucleotide deletion, \=possible nucleotide insertion)
				sequence		,
16511	46879	A	16608	2073	2338	
16512	46880	Α	16609	1127	1282	
16513	46881	С	16610	1	2094	
16514	46882	Α	16611	523	706	QHPLPNPCCHQPFHLCLRR*TL
		1		1		HCLRQQ*WPPLRQLPGKIMLIL
		i				LRSHPQHPCLLLDLQLD
16515	46883	В	16612	190	805	
16516	46884	В	16613	90	2812	
16517	46885	Α	16614	44	216	RCRRRLIPHPRRLSPVVIRRIQVP
ŀ				1		Q/VQPGAGPSRPGHTRDPIGAA
		l		l		AAHCPCPGDSGAH
16518	46886	Α	16615	1	1107	MTEEPLQALVLSAVLLYQEAY
		i i			\	VRRSLTALGLDTFANFAHFSEM
ŀ		1				QPLSDAPCGLVTGVTRPLVAYS
	1	1				VEVGGFTIICGLSLASGNISGWC
		1				QLYLLLTQCRRGAATLWDSGM
		1				GGGRQSSRQTSVPRWTLDSKCI
ĺ		1				PGPKLTTRPQMDTKALGGQQA
		1		1		HVEHQTHEDIRPQVDTQAPGG
		1		1		HKALGEQQDPVGHQASVGYSP
		1				QVPQDSLGQALAGQATPEIPLG
		1				LQLHTVLVQEIQELIEAQTRAP
l		1				GPCAEVRALPAPAAEPEPAWEE
		1				APPERALELEGAPAKDQTNEFL
		1				PEITA/PYC/EPLALTLELKAWLE
ŀ		1				RKVGGRG\DQHSPSQQLPCCP*S
						WARWQTCRQRAGHLAWPPVP
	1					RCREASLIH*NHSPAAAGPFILL
16519	46887	Α	16616	1	792	
16520	46888	Α	16617	1	963	
16521	46889	Α	16618	1	378	
16522	46890	A	16619	1	494	MKPRTLAVSVTVLKGGVSRVC
		İ				SFWCSDVFRVSSFWWVRGLAD
1		1			1	SGVKLRTFAVSVTPLKAARLEL
l		1			I	FVPPGGFVVSLASGVKLQPFEV
			1	į.		SVTAHKGSVDPKSEKQQDLLQ
		1	1			RGKEQSYHTGEGHPSRLP/PAG
l		1	1	İ		SGSLLLFSYLAPPTSC*LVQPSG
						LF*QGADWCIYNP
16523	46891	A	16620	137	262	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
16524	46892	A	16621	1	2786	EVSLREATQRKLRRFSELRGKL
1052	100,2	ļ.,	10081	ľ		VARGEFWDIVAITAADEKQELA
						YNQQLSEKLKRKELPLGVQYH
i						VFVDPAGAKIGNGGSTLCALOC
						LEKLYGDKWNSFTILLIHSDEW
						KKKVSESYVITIERLEDDLPIKE
						KELTELRNIFGSDEAFSKVNLN
						YRTENGLSLLHLCCICGGKKSH
1						IRTLMLKG\LRPSRLTRNGFTAL
		1				HLAVYKDNAELITSLLHSGADI
						QQVGYGGLTALHIATIAGHLEA
						ADVLLOHGANVN
16525	46893	A	16622	174	722	
16526	46894	Α	16623	1	1554	
16527	46895	Α	16624	1	843	
16528	46896	Α	16625	2	745	ECWDGEHDIETPYGLLHVVIRG
		i				SPKGNRPAILTYHDVGLNHKLC
						FNTFFNFEDMQEITKHFVVCHV
		1				DAPGQQVGASQFPQGYQFPSM
						EQLAAMLPSVVQHFGFK\YVIGI
						GVGAGAYVLAKFALIFPDLVEG
1		1				LVLVNIDPNGKGWIDWAATKL
		1				SGLTSTLPDTVLSHLFSQEELVN
						NTELVQSYRQQIGNVVNQANL
1						QLFWNMYNSRRDLDINRPGTV
l		1				PNAKTLRCPVMLVVGDNAPAE
						DGVVECNSK
16529	46897	A	16626	3	949	
16530	46898	Α	16627	1	633 1324	
16531	46899	A	16628	1	591	
16532	46900 46901	A	16632	138	832	
16533 16534	46901	A	16633	55	586	IFVHPTPAASTMPSKFDPNEIKV
10034	46902	l <sup>A</sup>	10033	33	380	VYLRCTGGEVGATSALAPKIGP
l				l		LGLSPKKVGDDIAKATGDWKG
						LRITVKLTIQNRQAQIEVVPSAS
1						ALIIKALK\EPPRDRKKQKNIKH
1						SGNITFDEIVNIARQMRHRSLAR
1		1				E\LSGTIKEILGTAQSVGCNVDG
						RHPHDIIDDINSGAVECPAS
16535	46903	A	16634		735	KHFHDIIDDINSGA VECFAS
16536	46904	A	16636	3	346	
16537	46905	A	16637	57	649	GPRRAYGGRMAGGGGDLSTRR
1.0057	1.0200	ľ	1.505,	I .		LNECISPVANEMNHLPAHSHDL
			1			ORMFTEDOGVDDRLLYDIVFK
1		1	l			HFQR\NKVEISNAIKKTFPFLEG
1			l	1		LRDRDLITNKMFEDSQDSCRNL
1			l	l		VPVORVVYNVLSELEKTFNLPV
		1	l			LEALFSDVNMQEYPDLIHIYKG
1			1	1		FENVIHDKLPLOESEEKEREERS
1		1	1	I		GLQLSLEQGTGENSFRSLTWPP
		1	L			SEQUEDEQUIORISE NOT WIT

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				Sequence	İ	
16538	46906	Α	16638	1	1665	
16539	46907	A	16639	348	1534	
16540	46908	Α	16640	1	627	
16541	46909	Α	16641	1	1343	
16542	46910	Α_	16642	76	479	IRAVSRSRERPGSRSRYLQAC*C
	ŀ					GGAFPGP*SAEISRLVRSHNLGC
		1				YSCT/EGGGGCRKGSCLLQHSC
						LLWHSCLLPASKNTVCSKDLG
				1		GCSCTQESRAPACSWSPRTQGC
				1		SASSHDLGSCRNAWETPSRQLC
	16011	<u> </u>		100	-	RSW
16543 16544	46911	A C	16643	130	675 420	
16545	46913	A	16645	1	987	
16546	46914	A	16646	li	494	
16547	46915	A	16647	360	1510	
16548	46916	A	16648	375	2187	VTAAAAATAMAESGESGGPPG
						SQDSAAGAEGAGAPAAAASAE
						PKIMKVTVKTPKEKEEFAVPEN
			i	l		SSVOOFKEEISKRFKSHTDOLV
						LIFA\GKILKDQDTLSQHGIHDG
						LTVHLVIKTONRPODHSAOOTN
						TAGSNVTTSSTPNSNSTSGSATS
		1				NPFGLGGLGGLAGLSSLGLNTT
						NFSELQSQMQRQLLSNPEMMV
		Į.		ł		QIMENPFVQSMLSNPDLMRQLI
		1			1	MANPQMQQLIQRNPEISHMLN
						NPDIMRQTLELARNPAMMQEM
						MRNQDRALSNLESIPGGYNALR
						RMYTDIQEPMLSAAQEQFGGN
						PFASLVSNTSSGEGSQPSRTENR
						DPLPNPWAPQTSQSSSASSGTA
						STVGGTTGSTASGTSGQSTTAP
		1				NLVPGVGASMFNTPGMQSLLQ
						QITENPQLMQNMLSAPYMRSM
		1		ł		MQSLSQNPDLAAQMMLNNPLF
		l		l		AGNPQLQEQMRQQLPTFLQQM
	į.	1	l			QNPDTLSAMSNPRAMQALLQI
		1				QQGLQTLATEAPGLIPGFTPGL
l		1		1		GALGSTGGSSGTNGSNATPSEN TSPTAGTTEPGHOOFIQQMLQA
	1		1	1		LAGVNPQLQNPEVRFQQQLEQ
l	1	1	1	1		LSAMGFLNREANLQALIATGG
		ŀ				DINAAIERLLGSOHHSSISVS
16549	46917	Α	16649	269	440	DITE TO THE CONTROL OF THE CONTROL O
16550	46918	A	16650	469	746	RLNLPGPLCAGTSILFAVLMEAI
						GVSCIROAGGGHVASHIY*GLM
		1	1			/PALAL*DTEPRNPSALPETCLC
						GSGPQSQMGHQTSHLLSSPGTG
	1					LSF
16551	46919	Α	16651	1	1026	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
16552	46920	Α	16652	719	906	
16553	46921	В	16653	1	1971	
16554	46922	A	16654	200	239	
16555	46923	A	16655	109	177	
16556	46924	Α	16656	1	1542	
16557	46925	Α	16657	1	453	
16558	46926	Α	16658	2	487	
16559	46927	Α	16659	1	1260	MEDAEGTVTLLAVTLVARDLN CIQPQTGPSGGIPEESIVIIGDVS
						MHVIAPEDLPVGQDVEVEDSD DDPDPVRALPLQIHACGRVGFF
						AHDDWSEGGDPAADTLIDPSQ DARYLKCEGMQAPHNSNPVAG
						KTEISYHIWIARIPREKSGKVTO TLCDLLKDLTVIHSLIPKQGCSI
						GLGVLVQGTFQPQGNTDTCTC QVSAVEGKGEGLMQLASLSRR
						VTIWAYGDSQERDLKTQLEKI AIKDMKEMQEKEYRIMEKAHS
	:					RQRKQHHKGPERKEQAAIFAV LQPPLVITRQTGSGVDPQKTPA
						DLQKRCRTVRRKTSQQKAVAS TLTKRITTQKLNAKDHNSSPTR
						EQNCTENEFDELTEVGFRRWV TNSSELKEHVLTQCKEAKNFD
						RLEELLIQITSLEKNISDLMEL*: FALSFCVVILFVNVDATAFCWI
						VFLLTVRHLFCRSAGVFWGST DPVCLVITSGGCRTAKIAACSF
						SGPLWCCFLCLEWAFSIILYSFS CISFMSLIAVIFSNWVLRSLS
16560	46928	A	16660	1	799	CIST MODITY II SI W YEROES
16561	46929	Ā	16661	1	969	MHVIAPEDLPVGQDVEVEDND DDPGQAKKTMEEQWTLVSLLS
						TSQQQGPVPPGSTASSATDKLS RWELTLLYSTTLFLAREAFRRA
						CLSGGTQRDWSQTLNLLWLTV
						PLGVFWSLFLGWIWLQLLEVPI PNVVPHYATGVVLFGLSAVVE
						LLGEPFWVLAQAHMFVKLKVI AESLSVILKSVLTAFLVLWLPH
						WGLYIFSLAQLFYTTVLGLCY\ IYFTKLLGSPESTKLQTLPVSRI'
						DLLPNITRNGAFINWEEAKLAV GFFKQFFLKQI\LTEGGRYVGG
						HFLNVLNFGDQGVYDIMNNLC SLVARLIFQPIEESFIYS
16562	46930	A	16662	1	1665	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
16563	46931	A	16663	1	1521	MDVSSPPCVDGVS1LPPLLIPRQ
		l				TGSGVDLQQNPTDLQLRVLTV
l		l				KRKTNKQKGHPHQNSICTSPSS
		1				KTKEYTFFSVQHHTYSKIDHIV
		1		ł		GSKAVLSKRKTIEIITNCLPDHS
1						AIKLELRIKKLTQNHKTTWKQN
i		l				NLLLNDYWVHNKMKAEIKMFF
				İ		ETNKNKDTTYKNLWDTVKAV
ļ		1	l			CRGKFIALNAHKRKQERSKIDT
1		1			-	LTSQLKELEKQEQTHSKASRRQ
			İ			EITKIRAELKEIETQKTVQKIHES
1						RSWFFEKINKIDRPLAGLIKKKR
					1	EKSQKDAIKNDKLDITTDPTET
					ŀ	QTTIRDYHKHLYAIKLENLEEM
İ		1				DKFLDTYTLPRLNQESLNRPITG
						SEIEAIINSLPTKKKYRTRRIHSR
						ILSEVQGGAVLEVLARAIRQEK
l		l				EIKCIQLGKEEVKLSLFADDMIV
1						YLENPTVSAQNLLKLISNFSKVS
1						RYKINVQKSQAFLYTNNRQTES
			1			QIMSELPFTIASKRIKYLGIQLTR
	İ					DVKDLFKENYKPLLNEIKED/N
						KWKSIPCPRIGRINIM
16564	46932	Α	16664	2	2315	
16565	46933	Α	16665	1	912	
16566	46934	A	16666	1	912	
16567	46935	В	16667	199	619	
16568	46936	В	16668	64	1815	
16569	46937	Α	16669	1	239	
16570	46938	Α	16670	1	242	FREDGKTACGHEPSPVLLGLRL
						GLQPWG*GWGCSHGAGSAPDL
						VAGSAHSCGLWLPGSLHHHPA
ŀ				ł		QCLPALLCGHLCLSVQDQQNG
ŀ		i				LLGR
16571	46939	A	16671	58	505	ASSRTRPSCTLARGRRWFPQPL
ł		1	l	1		SGRQRQRGGRRGSRVG/YGTA
1		1		ŀ	1	QNSTTLTSPAASASEATVSGHW
		1	1			PSTAPCCV\PAGAG\SATMWRSP
ļ						A*AACGSAAWTSTWSRRSPGP
l			İ		l	GAAAGYGGVRTFCOPAGLTR/L
		1				ANRSTAGLCGWGLTLSCRETEL
1			1			
16572	46940	A	16672	242	2952	
16573	46941	В	16673	474	2690	
16574	46942	A	16674	97	451	
16575	46943	A	16675	667	893	
10313	70243	1^	10075	1001	975	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
16576	46944	A	16676	3	639	RIRVHPTPAAFTMPPKFDPNEIK
				ł	\	VGYLRCTGGEVGATSALAPKIG
	l	1		1		PLGLSPKKVGDDIAKATGDWK
l		l	ļ			GLRITVKLTIHNROAQIEVAPSA
				1		SALIIKALKEPPRORKKLKILKL
	l	1				SGNITFDENGNICSTDMR/HRSL
		l				SRELSGTTKEILGTAOSVGCNV
	i	1				DGRHPHDIIDDINSENDKOPRKS
						KMRTSFSPOIPGHEHFHYLLLL
İ	ľ					OHVHCOLALTL
16577	46945	A	16677	350	984	VYLEVAPGGESRLPLSALGPOR
10377	10242	^	10077	1550	J**	IGPPGSCLPKKSWVNDICOROP
				l		G\DWKGP*GLOVKLTHSRTGO
		l				APDCTRVP/VLPSCP*FIQSPSRE
ŀ		1				PPKRPEKKPEKTFKHOLGIFTFL
ļ		1				NEICSTLLRQMR\HRSLSPEKLS\
						GTPLKEIPGGLPQSSWAGNV*W
						AAIPHDI\IDDIQQWVLWKCPAV
						SDIFIVTVGVKGGPPSVFTEISW
						EVLEMVTGGVG
16578	46946	A	16678	252	964	EVEENVIGOVG
16579	46947	A	16679	1	182	
16580	46948	A	16680	275	639	
16581	46949	A	16681	376	418	
16582	46950	A	16682	1135	1591	
16583	46951	A	16683	3	420	AAKEIEVGGGRKAI\KSFOKIQV
10303	40931	<u> </u>	10003	ľ	120	RLVRELEKKFSGKHVVFIAORR
						ILPKPTRKSRTKNKOKRPRSRTL
	İ		1			TAVHDAILEDLVFPSEIVGKRIR
		1				VKLDGSRLIKVHLDKAOONNV
		Į.		1		EHKVETFSGVYKKLTGKDVNF
						EFPEFOL
16584	46952	A	16684	1	879	ELLELÓE
16585	46953	A	16685	2	691	HEEKAMFSSSAKIVKPNGEKP\
10383	40933	1	10005	1	051	DEFESGHLPGLFLELE\MNSD\L
						KASAOGT*IITAS*RKLKVGGCS
		1				ESLFH*SFVPRSLKLKTFPOKNP
		1	1			KVRA*LRRIGKKKVPVGKAMS
1			1			VLYPPSEGEFLPLSPTSEKARTK
1		1				K*AKSRPPGARTLDKLVH\DAH
1		I				
1		1	1			PLRDFGPFPSGNFWAKRIPRSNL
1		1	1			DGQPGSIKVPFWTKAQQNQCW
1		1	1			NTRVETFFLVSYK\KLTGQGC*F
l _	l	L_			l	LEFPRVFNC

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	eodon for last amino acid	*-Stop eodon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nueleotide insertion)
16586	46954	Α	16686	1	452	TLLVIPRKMRSAVELQQTSTDL
		l	-			OLRDLTVRKKTNKRKATASTS
		l				QKGHLHQNPICRSPTSKTKEVG
	ĺ	l				FRRSVITNFSELKEDVRTYHKE
	l	1				AKNLENRLDEWLTRINSVEKTL
						NDLKELKTMARDLHDACTSFN
	i					RRFDQVEERVTVTEDQIN*QTE
						SNSINFTKRSSTPKPHL\RSPTSK
		l				TKEVGFRRSVITNFSELKEDVR
		l				TYHKEAKNLENRLDEWLTRINS
		l				VEKTLNDLKELKTMARDLHDA
				i		CTSFNRRFDQVEERVTVTEDQI
16587	46955	A	16687	1	618	
16588	46956	A	16688	280	353	SCNSIFARSVRACCS*VASSSFC
		l				lc .
16589	46957	A	16689	1	459	IKYSSPMKSTFVDPVDPVAVAV
	İ					IYCLAAGLVIIRIPFFQLVPLKEE
						KMVLLNMDYYEMASLSLVTH
		1				RNEAPFSGRVRSSLPATEQSWM
						ENDFDKLTEVGFRRSVITNFSEL
						KEHVLTHHKEAKNLEKRLDKW
		1				QTRINSVEKTLNDLMELKTMA*
		l				EEKMVLLNMDYYEMASLSLVT
		l				HRNEAPFSGRVRSSLPATEQSW
		l				MENDFDKLTEVGFRRSVITNFS
l						ELKEHVLTHHKEAKNLEKRLD
	1	1		l		KWQTRINSVEKTLNDLMELKT
16590	46958	Α	16690	2	403	LALSGEMTLVLFMLLAGGWVT
l		1	1			HDKPEPMPRAATSGGTRKGKT
	1	1				KAALKDLIATWKEVCVSSPATE
	1					QSWMENDFDELTEVGFRRSVIT
ŀ		İ				NFFKLKEYVLTHHKEAKNLEK
1						MLDEWLTRINSVEKTLNDLME
						LKNMA*ELTEVGFRRSVITNFF
						KLKEYVLTHHKEAKNLEKMLD
		1		1		EWLTRINSVEKTLNDLMELKN
16591	46959	Α	16691	1	676	
16592	46960	Α	16692	1	1965	
16593	46961	С	16693	1	3075	
16594	46962	Α	16694	78	152	CAAGFGLPVFY*GFLHRCSLGIL V
16595	46963	В	16695	1	904	

SEQ ID			SEQ ID NO:			Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/340,217	sequence	or pepude sequence	detection, v-possible nucleotide insertion)
16596	46964	Α	16696	1	2026	EQEASYGRDAFAKAIYERLFC
						WIVTRINDIIEVKNYDTTIHGKN
						TVIGVLDIYGFEIFDNNSFEQFC
		l				NYCNEKLQQLFIQLVLKQEQEE
		l				YQREGIPWKHIDYFNNQIIVDL
		ŀ				VEQQHKGIIAILDDACMNVGK
						VTDEMFLEALNSKLGKHAHFS:
						RKLCASDKILEFDRDFRIRHYA
						GDVVYSVIGFIDKNKDTLFQDF
		1				KRLMYNSSNPVLKNMWPEGKI
		1				SITEVTKRPLTAATLFKNSMIAL
		Į.		1		VDNLASKEPYYVRCIKPNDKKS
		ı		i		PQIFDDERCRHQVEYLGLLENV
		ŀ				RVRRAGFAFRQTYEKFLHRYK
		i i	l			MISEFTWPNHDLPSDKEAVKKL
						IERCGFQDDVAYGKTKIFIRTPR
						TLFTLEELRAQMLIRIVLFLQKV
						WRGTLARMRYKRTKAALTIIR
		1				YYRRYKVKSYIHEVARRFHGV
		l				KTMRDYGKHVKWPSPPKVLRF
		1				FEEALQTIFNRWRASQLIKSIPA
		1				SDLPQVRAKVAAVEMLKGQRA
		1				DLGLQRAWEGNYLASKPDTPQ
		1				TSGTFVPVANELKRKDKYMNV
		1				LFSCHVRKVNRFSKVEDRAIFV
						TDRHLYKMDPTKQYKVMKTIP
						LLQLTCLN\V\$NGKDQLVVFHT
						KDNKDLIVCLFSKQPTHESRIGE
		ļ				LVG\VLVNHFKSEKRHLQV\NV
						TNPVQCSLHG\KKCTVSVETRL
	<u> </u>	_				NQPQPDFTKNRSGFILSVPGN
16597	46965	Α	16697	1	1665	DI STRUCTURE CONTROL
16598	46966	Α	16698	1727	1908	FLFFYIC*RELYFQLCGQFWNK
						CNVLLRRMYILLIWGGEFCRYC
16500	16067	ļ.	16600		204	LGLLGAELNSVPGYHC
16599 16600	46967 46968	A	16699 16700	1	384 636	
16601	46969	A	16701	1744	2283	
16602	46969	A	16702	194	368	
16603	46970	c	16703	62	205	
16604	46972	В	16704	1	1257	
16605	46973	A	16705	1	1077	
10003	70773	1	10703	l'	11077	

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hed	in USSN	location of first	codon for last amino acid	*=Stop codon,/=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
	ļ	<u> </u>				Lasitama
16606	46974	Α	16706	1213	1228	AQN*QTQRTSTPKPHL\SSPSTK
						TKENDFDELREEGFRRSVITNFS
	1					KLKEDVRTHRKEAKNLEKRLD
						EWLTRINSVEKTLNDLMELKT
ŀ	1					MAQELRDTYTSFSSRFDQVEER
				]		VSVIEDQMNDMKREEKFREL/K
						RVQRNEQSLQEIWDYVKRTNL
		1				RLIGVPEKIQTTIREYYKHLYAN
				i		KLENLEEMDKFLDTYTCPRLN
		1		i		QEEVESLNRPVTGSEIEAIINSLP
		1				TKKVQDQADSQPNSTRVFKTV
l		1				CISSLGHTTASADTQDVCQLPV
ŀ	1			1		TSLLEQGLSSKSAGFLDYAVQR
		_				LWLLGTEPL
16607	46975	A	16707	33	263	
16608	46976	Α	16708	204	1756	
16609	46977	Α	16709	760	821	TMRTHGHRKGNI*QR/R**PEST
				1		KNSNKFTRKNQTTPSKREWMK
						LETIILSKLSQGQKSKHRMFSLI
						SGN*TMRTHGHRKGNITHWGL
		<u> </u>				LWG
16610	46978	Α	16710	1	879	WALLEST ON POLICE CARRIES OF DESIGNATION OF THE PROPERTY OF TH
16611	46979	Α	16711	311	514	KNAHHQWPSKKCKSKLQ*DTIS
l		1				HQLEWQSLKSQETTGTRMKME
		ł				TITLSKLSQGQKSKHCMFSLIGG N
16612	46980	Α	16712	24	1268	AGLCAARARMRLFRWLLKOPV
l						PKQIERYSRFSPSPLSIKQFLDFG
l						RDNACEKTSYMFLRKELPVRL
						ANTMREVNLLPDNLLNRPSVG
1		ı				LVQSWDMQSFLELL*YENKSPE
1		1			j	DPQVLDNFLQVLIKVRDRHND
1			l			VVPTMAQGVIEYKEKFGFDPFI
		1	ŀ			STNIQYFLDRFYTNRISFRMLIN
						QHTLLFGGDTNPVHPKHIGSIDP
				1		TCNVADVVKDAYETAKMLCE
1		1		İ		QYYLVAPELEVEEFNAKAPDKP
		ı		1		IQVVYVPSHLFHMLFELFKNSM
		l				RATVELYEDRKEGYPAVKTLV
		1		l		TLGKEDLSIKISDLGGGVPLRKI
1		1	1			DRLFNYMYSTAPRPSLEPTRAA
				l		PLAGFGYGLPISRLYARYFQGD
1		1		l		LKLYSMEGVGTDAVIYLKALSS
		1				ESFERLPVFNKSAWRHYKTTPE
						ADDWSNPSSEPRDASKYKAKQ
16613	46981	Α	16713	175	465	
16614	46982	A	16714	240	381	FFLSFPPLCQSS*NQNLLPW/ICA
		1		l		KVCSFTPEVSKTTNPLEGRNSG
		L				HI
16615	46983	Α	16715	268	1524	
16616	46984	Α	16716	1	378	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
16617	46985	A	16717	708	987	IQLPGHRSQGQAGASHTDARQ QDPGNSHSDFVRHSHSLPCLER QDRRSAGHNGSATVPGTEACG RAYKAPAGHYHSGAGQSLPAA SHRSFSSP
16618	46986	Α	16718	1	2052	
16619	46987	В	16719	1	606	
16620	46988	A	16720		541	OHORKOKROLRAQONI.SWEEL AKEYONEEDSLGGSRVVVCDI NKEMLKVGKQKALAQGYRAG LAWVLGDAEEL.PFDDOKFDIVT IAFGIRNVTHIDOALQEAHRVL KPGGRFLCLEFSQVNNPLISRLY DLYSFRVIPVLGEVIAGDWKSY QYLVESIRRFPSQEK/FKDMIE DAGFHKVTVESLTSGIVAIHSG FKL-FLCLEFSQVNNPLISRLYD LYSFQGHPCPGRGHRWRLEVLS VPCREVSEGFRLRKEFKDHDRR CRLSTR
16621	46989	A	16721	526	933	
16622	46990	Α	16722	191	468	
16623	46991	A		2	677	GKVHVLERRGFHRTEMHLOKI LLIPVLSSSSSDP/STLSVSALV RMFSSADE*SVSEASSEPSSFS RRSSCSPGSEPSASSFSSSFPDL ASLSSVFLLFRAFSISSHVM*WL PSSS*VGS/STSARAQLPSYVPS- SVKTKSGLKSALRFFPKAFCRL PSTMGPSSSSSPESDSALHRHLV LLOVWLQIKPRVRKPCCRRSHF RKRAQPAVRPLTFRSLLVVLR
16624	46992	A	16724	31	187	
16625	46993	Α	16725	215	947	
16626	46994	A	16726	1	378	
16627	46995	A	16727	2	7567	GGGARRQRRODAGGAETAP SEILSPAAEERSGRSETLRRGT AAGRMATVVVEATEIPEPSGSI ANPAASTSPSLSHRRIDSKEYLL VVVGGEIVTEEHLIRRAIGSIELGI RSWDTNLIECNL\DQELKLFVSR HSARRSPEVPGQKIL\HRSEBEF *ETVVL\LQPPHEMGGSGTEVKL MITDAARIKLLVLTQCFENT GELLQSGSFSFQNFIEIFTDQEI GELLSTTIPANKASLTLFCPFE
16628	46996	A	16728	101	365	VITGQPNPTNPNLQATPDIQGTL ARLGPA/LHPRGIIPFIGHQSA/R PHAPAPANPNKRTLFRPPPLSPP SPEPPGSGQGAGLGARPALP

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
16629	46997	Α	16729	1170	2847	VASC*ENACKONOROKPCDYL
	1					NRCRKGLWONSTTLHAKNSO*
						TVLYKTIKFOLEKTTLKFIWNO
		l				KRAHIAKSILSOKNKAVGITLPD
						FKLYYKATVTKTAWYWYONR
						DIDOWNRTEPSEIMPHIYNHLIF
	İ					DKPDKNKKWGKDSLFNKWCW
						ONWLAICRKLKLDPFLTPYTKI
		i				NSRWIKDLHVRPKTIKTLEENL
		1				GNTIQDIGTGKDFMSKTPKAM
						ATKDKIDKWDLIKLKSFCTAKE
	1					TTIRVNRQPTKWEKIFTT
16630	46998	A	16730	79	536	
16631	46999	Α	16731	232	771	
16632	47000	Α	16732	3	339	
16633	47001	Α	16733	279	416	
16634	47002	Α	16734	1	1760	
16635	47003	Α	16735	309	1718	
16636	47004	A	16736	10	417	IAIMNDTVAIRTRKFMTNRLLE
ļ	1					RKQMVIDVLHPGKATVPKTEIL
						EKLAQMYKTTPDVIFVFGFRTH
						CGGGKTTGFGMIYDSLDYAEK
				1		NEPKHRLARHGLYEKKKTS*K
		1				QRQERTNRMKKVRGTAKANV
ĺ	1	1				VAG*KPNE
16637	47005	Α	16737	96	609	EKFMT\NRLTSGETKWVI*CPFT
						PGRRTVP*AQKIR\EKLAQNVQ
					Į.	RPHPDVIFVFGFRTHFGGGKTT
1						GFGMIYDSL\DYAKEKMNPKH
				1	İ	RLA\RHGPGMEEGKRPSKKGN
		1				GKER\KNQN*RKVQGGLAKGP
	1	1				LLGAGQKEEMKCLGSELEIGSQ
						PKELKVLPMMLAVATVDFSQE
16638	47006	В	16738	1	1041	
16639	47007	A	16739	3	447	VSVPFIFIWLTCKSFLKFDLKSN
				1		TNVLQSL/GKFQSEVSKRQKLA
						TVFSSFTSTGLCQGSVAFISRCP
				ł		PLASGSDSVWRGGSVFFSFRP*
		1		ı		RLMISLLGSCVSHQFPEKLEF**
		1		1	1	KKMPYKIPTAHHQQQDDQQRG
		1				HEHKQSQPDAVPHLG
16640	47008	Α	16740	I	2385	
16641	47009	Λ	16741	1	639	
16642	47010	Α	16742	1	993	
16643	47011	A	16743	127	426	CTDKITLVFGV*MLTPKPDK/CD
	1	1	l	1		DSAV*ELLWLTNQLSACVVHP
	1	1		1	1	GLYHLHVRSIWIPYRCLFSTMC
l	1	1	l			GVCQTCTVAMQLDCLADSFNA
l	1	<u></u>		L		VFKLTEAAGHMAR

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hed	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	coden for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
16644	47012	IA	16744	3	374	SLRLQFYYKISFOTODOANKLS
10044	177012	<u> </u> ^	10744	ľ	274	DSDASHLHPLAPCSEPTRTNVH
						TKLPRERPQSQIASPYPLPPCPE
						RLKKQTNKKKNW*EPSPHILPP
1						RNAAAHTGOSRASKSLPAPPPT
						VSPRPRPGAPGT
16645	47013	A	16745	16	253	VSPRFRFGAFGI
16646	47013	A	16746	163	588	TFHAVLHIENAGYFNSIPFFRIL
10040	4/014	^	10740	163	200	NHNPLTTVEDPYLFKLPALKYL
	1	1				
	1	1				*VL*YSHESRDDLYSF*IFHQRL
	1	1				SILHLG*NVII\KF*LSY*KKVIGE
	1	1	İ			EKN*EDV*WSRQPAGEREQC*R
	1	1				THIDLE/PCRHMEEYYLTKKAK
						GKRCSLF
16647	47015	Α	16747	2	363	GTSQTLLRSLASACIFQPKVRLL
	1	1				SREEIPLNLNY*SVSPNSNPNHL
	1	1				YSRHTILTAMLTLQLGTCVLLPI
	1					GLLVPYPNCPSPTGLQVTPFLPS
ł	1	1				PCGSGWPASFTYSSNRFTTNLL
	1	1				FCVFIL
16648	47016	Α	16748	1028	1621	
16649	47017	Α	16750	1	112	LGNTWG*OPCKRLKIWLSLEFT
						KINVIRHMWKKFKRL
16650	47018	Α	16751	91	597	LKNRRRSRPSIROSIGSTSVSRW
		1				LTSLFTYLDHTADVO*V*REFIP
	1					LKPRQ*ED*MFQSWLHAWGDT
		1				LEEAFEOCAMAMFGYMTDTGT
i		1				VEPLOTVEVETOGODLOSLLFH
	1	1				FLDEWLYKFSADEFFIP\GWGEE
						FSLSKHPQGTEVKAITYSAMQV
	1	ļ				YNEENPEVFVIIDI
16651	47019	A	16752	226	668	IYFFRLHAWGDTLEEAFEQCA
10031	47019	<u>۱</u> ^	10/32	1220	000	MA\MFGYMTDTGTVEPLQTSRS
	1				i	KTQGDDLQSLLFHFLDEWLYK
			ľ			FSADEFFIPREVKVLSIDQRNFK
						LRFN\GWGEEFSLSKHPQGTEV
						KAITYSAMQVYNEENPGSFCD
		_				HWTFKTTQKIKRLPTGKK
16652	47020	A	16753	3	942	
16653	47021	A	16754	3	419	SLYHNSSQKRHWTFSSEEQLAR
						LRADANRKFRCKAVANGKVLP
		1	1			NDPVFLEPHEEMTLCKYYEKRL
l	1	1				LEFCSVFKPAMPRSVV\LTCAFL
l		1	l			ACKVDEFNVSNPQFVGNLRESP
		1				LGQEKALEQILEYELLLIQQLNF
1		1				HLIVHN
16654	47022	A	16755	312	537	
16655	47023	В	16756	209	1381	
16656	47024	A	16757	1	927	
16657	47025	A	16758	1	3987	
16658	47026	A	16759	2	175	
		<u> </u>				

SEQ ID			SEQ ID NO:	Nuclcotide		Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
16659	47027	Α	16760	2395	2700	
16660	47028	Α	16761	2	1118	
16661	47029	Α	16762	26	1205	
16662	47030	Α	16763	1	1594	
16663	47031	Α	16764	1	595	
16664	47032	Α	16765	1 .	1029	
16665	47033	Α	16766	1172	1364	
16666	47034	Α	16767	253	389	
16667	47035	A	16768	489	855	
16668	47036	Α	16769	2	401	
16669	47037	A	16770	415	694	EAKLHLNLCDMSWLCCPTKGK RKQALEVLNILGPFLAPFWLAK SYFFTSPKTQVSSL*FLRYKRIK LQCRPKTCTNPSRTRSCALPGR FIPPF
16670	47038	Α	16771	1	765	
16671	47039	В	16772	1	1095	
16672	47040	A	16773	82	311	KANSDVPFGFGVNLEHLMEAC NS/GTNLLNSKRLNNDCICLASH TDVSIIARKCCLVVSCLLLLRGL SILRSKESHC
16673	47041	Α	16774	2	683	
16674	47042	Α	16775	1	2703	
16675	47043	A	16776		555	DHNSSPAREQ/SSMENKFHELT EVGFRKITSLEKNINDLMELKN TARELREA/YTSIKSRIDQAKESI SEIEDQLNEIKCEDKYREKEMK SKKQHFGEIWDYVKRPHLRLT GVPESDRENGTKLENTLQEIIQE NFPNLARQANIQIQEIQRTAQR QSSSRATPIHIIVRFAKFEIKEKM LRAAREK
16676	47044	Α	16777	1	839	
16677	47045	A	16778	1	504	
16678	47046	Α	16779	1	2367	
16679	47047	A	16780	1	1566	
16680	47048	A	16781	146	464	VTGWTNYEGNGRWRERSRQLC GCCSRKSSSSWGISLMKGSGAP LRPGRMMWSGFRKCSDTQVM YS*R*LLETMTLASIMR*THTK* NALRKCSALKDCFLGKALTL
16681	47049	Α	16782	1	1782	
16682	47050	В	16783	221	1075	
16683	47051	Α	16784	1	627	
16684	47052	A	16785	1	1539	

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
		l		sequence		
16685	47053	A	16786	lı -	1318	LSPVLSLSPDSMSFTTRSTFSTN
						YRSLGSVQAPSYGARPVSSAAS
		l				VYAGAGGLATGIAGGLAGMG
		l				GIONEKETMOSLNDRLASYLDI
	ŀ	l	l			VRSLETENRRLESKIREHLEKK
				1		GPQVRDWSHYFKIIEDLRAOIF
		l	ĺ			ANTVDNARIVLQIDNA\RLAAD
						DF\RVKYETELAMROS\VENDI
	]			l		GLRKVIDDTNITRLQLETEIEA
						KEEL\LFMKKNHEE\EVKGLOA
	1	l				QIASS\GLTVEV\DAPKF\QDLRQ
						DSWADIR\AQY\DELARKEPRG
	1	1				A*TKYWFSADLRESTTV\VTTO
		1				F\AEV\GAA*DDASQSWRTYSPS
		1				SLGDPTWGFPWRKS*RAS\LEN
		1				SLREG*RPAYALT/QMEQASTG
	1	ŀ				LACTFESELGTDPGAEGQRQAG
				l		EY\EALLNIKVKLEAEI\ATYRRI
	İ	1				LEDGEDFNLGDALDSSNSMQT
	i	{				IOKTTTRRIVDGKVVSETNDTK
16686	47054	Α	16787	ī	253	RVRTLKTSTSTCLYWFENKDS/
		1			1	DHPERSSP*YMSPSHRYGSLVK
		1				ASITKPAFLKTSGRLFTCSSQFC
				l		PLISKISDGFSHLPPFST
16687	47055	A	16788	1	276	AAAAGPPGPLVMFTYRERVSG
		1				LRSVHILRASHTDARLRQEEPT
		1				ERLQFHSSGLLIRFSRETEPIGV
		1			}	YIKED*EEWAYKMMVFAKSHD
		1	l	1		LPFAN
16688	47056	A	16789	1	203	LLHTSTKNELWQ*GKRDPLIVF
		1				YTQYLF*EKTTRK*NQRQAGSL
		<u></u>				ALGPKPGLRLPGLNPVVENQFI
16689	47057	A	16790	8	361	RGLDGQGGRDGSSSGGGGGG
		l				RRRCLLLLAPAPAVIRASGRGP
	1					R*DCWRAGCA*AWRPC/RLAR
						RMWTLRSPLTRSLYVNMTSGP
						GGPAAAAGGRKENHQVARKR
						LNVCVFTRSVSETA
16690	47058	A	16791	674	1076	VQLFRSAGSRDHHRFLGRGRN
				l		KQTKTLYPTPIPCSLKYQRKQN
						GSLLWTSRMPSSVFPCTLTPSFS
						LPLRISQTTHPNLRGPSCPKGLG
						IALISLVRHWLKI*ATSQVQAL
	<u></u>					WSFSMWMIYFWLPVQKPHASR
16691	47059	В	16792	296	1470	
16692	47060	A	16793	1	334	
16693	47061	A	16794	718	2541	
16694	47062	A	16795	2	406	
16695	47063	A	16796	74	464	
16696	47064	Α	16797	159	610	
16697	47065	A	16798	1	273	

SEQ ID NO:	SEQ ID NO:	Met	SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
16698	47066	Α	16799	1	543	
16699	47067	В	16800	1	873	
16700	47068	Α	16801	ī	558	
16701	47069	Α	16802	27	136	
16702	47070	Α	16803	89	363	
16703	47071	Α	16804	579	994	
16704	47072	A	16805	129	362	PKIIQPRRATTRFTSIHGWRICPS IPCFPEATINRRRCVKVDSVTCH LLTQR*YKSSKVQERC*SCRIQG QKISDCY
16705	47073	A	16806	878	1811	
16706	47074	Α	16807	1	843	
16707	47075	С	16808	19	231	
16708	47076	Α	16809	I	1650	
16709	47077	Α	16810	3	404	
16710	47078	Α	16811	279	428	
16711	47079	Α	16812	3	507	
16712	47080	Α	16813	1	1128	
16713	4708I	В	16814	1	567	
16714	47082	A	16815	3	1206	GSEGQGAGPGGAATAAAME DEMPKTLYVGNLSRDVTEALIL QLFSQIGPCKNCKMIMDTAGN DPYCFVEFHEHRHAAAALAAM NGRKIMGKEVKYNWATTESSQ KKDTSNHFHVFVGDLSPQITTE DIKAAFAPFGRISDARVVKDMA TIGSKGYGFVSFFNKWDAENA IQQMGGQWLGGRQIRTIWATR KPPAPKSTYESNTKQLSYDEVV NGSSPSNCTVYCGGVTSGLTEQ LMRQTTSPFGQIMEIRVFPDKG NSFVRFNSFMHESGRIHMAIVSV NGTTIEGHVVKCYWGKETLID MINPYQQQNGIGYPPFOGWG QWYGNAQQIGQYMPNGWQV PAYGMYGGAWESSGFNSDT VFLAPWDGDPNFGSCNRLQGQ MGSLLPNRFSGYRVAGVETQ
16715	47083	Α	16816	1425	1564	
16716	47084	С	16817	151	339	
16717	47085	A	16818	67	373	FCDCHHFILMFKSPHIWPVGIFS SWLLCFFWACLHHSLSIALLSC TKRYSGLILYFLCSSFEITVSSKS SVSF*RRMVFRNQVLGSRCACC C*GVAAPRPFP

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:			Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \≔possible nucleotide insertion)
16718	147086	A	16819	1	799	MGPHWLWLHLALVLLPPSALL
						LPSCEKGVLRVRFYHEKWIYV
	1	l			i	HKESTKERHGYCTLGEAFNRL
	1	1		l		DFSSAIQDIRRFNYVVKPLLPRY
				l		KFORLNAITKDRORSSSGVOLP
i	l .	1				HAGQPQGADPTQDERRQVAGD
	1					TPGDPRALAGGGVVDRTYPGS
	1					YEASGRPGLQLALAIEDLLRDS
ļ	1	l				AIGCTFCDRCRPVGAQRLLAHS
	1	l				LALAAPGAEKREVVKLLLVAY
İ		}				VRRRPGKNLTTQNCQ\PAAGYI
				i		PPGHO*AASAHARSWKNOOPP
				1		PRVLIGSA
16719	47087	В	16820	28	438	
16720	47088	Α	16821	366	793	AWVEQSKVLIKEGGIQLLLTIV
	1					DTPGFGDAVDNSNCWQPGINYI
				İ		DSKFEDYLNAESQVNRCQMPG
	1	1				NRVHCCLYFIAPSGHGPLHN*R
	1	1				LPPSGRIG*YMFVTTWHCLLLR
	1	1				LKPLDIEFTKHLHEKVNIIPLIAK
1		1				ADTLMPEEC
16721	47089	С	16822	228	374	-
16722	47090	Α	16823	291	604	AWELEKSHLRRGLDPSHNINIR
						VEPKF*SKYGGVQLLLTIVDTP
	1					RFGDAVDNSNCWQPVINYIDIK
	1	1				FEDYLNAESRVNRCQMPGNRV
		ļ _				Q**LYFIAPSGHGPLHN
16723	47091	Α	16824	148	498	
16724	47092	A	16825	1	595	DRPRITGGGKSGTEYPENLPTL
		1				KATIENKNSVLNTATKMKDVQ
	1	1		1		TSTPAEQDLEMA\SEGEQKRLE
1	1	1	l	1		EYENNQPQVKN\QIHSRDDLDD
l	1	1				IIQSSQTVSEDGD\SLCCNCKNVI
		1		ļ		LLIDQHEMKCKDCVHLLKIKNT
l	i					FCLWKRLIKLKDNHCEQLRVKI
						RKLKNKASVLQKRISEKEEIKS
				L		QLKHEILELEKELCSLRFAIQQE
16725	47093	A_	16826	1	828	
16726	47094	A	16827	1	540	
16727	47095	Α	16828	295	460	
16728	47096	A	16829	2	1355	
16729	47097	A	16830	650	1184	

SEQ ID NO:	SEQ ID NO:	Met	SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
NO:	of peptide sequence	hod	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion
	sequence		03/340,217	sequence	or pepade sequence	and the state of t
		<u> </u>				
16730	47098	Α	16831	725	2368	AVDIIKEIKHPQKHKKLPAFQI
						PFPLREETIPCNGVSFPRCEPPO
		1		ŀ		AEVYMCLNEMLKDEKKGCM
	i					KSGAGENPQERTAQKRKFPSF
						HSSNGHSPQDTSTSPIKKKKK
						GLLNSNNKEQVKQPLECIETQ
	1			1		KAMTMLTIEQLSYLLKFAIQK
						KQPGVRRKLKPVPLEQHPDY.
		1				EYIFHPMDLCTLEKVGLRQM <sup>*</sup>
		1		•		GCTEAFLADAKWILHNCIIYN
	l					GEWLRTQIAKVVIKICEHEVC
						SQVCPECYLAACQKRDNWFC
		į.				PCVSWIYD\SACQPV*WKLVI
			ļ			MFLPM/WKADIL/RGEEG*YT:
		1		ł		LIGWL*SLSCDCSAGTSISHPS
		1				SD*RWLTEHEGRRVSWP\VN1
						YLMSKEIPFSVKKTKSIFNSAN
		1				QEMEVYVENIRRKFGVFNYSI
				1		RTPYTPNSQYQMLLDPTNPSA
		İ			1	TAKIDKQEKVKLNFDMTASPI
				]		LMSKPVLSGGTGRRISLSDMP
				1		SPMSTNSSVHTGSDVEQDAE
	1					KATSSHFSASEESMDFLDKST
				l		QLRAGERGGGPLDTGVSHGC
				1		I.GGPKQVSIKQQASVLQDTM
16731	47099	Α	16832	2	164	PSTLRAEAWPP*NGSPVPLAS
		1				QASSSRSGPTSCIPRYPVASPS
		1				RLPLPTAAA
16732	47100	Α	16833	51	498	
16733	47101	Α	16834	1	531	
16734	47102	С	16835	257	358	
16735	47103	Α	16836	63	193	SGRLAPHTSRRTSANCSDDAR
						SDSCSPSRKT*WSGRNTNRIH
16736	47104	Α	16837	1	834	
16737	47105	Α	16838	258	545	CQNPQILASPSTKDLMGLGRN
		1		1		NKDTLKACLARVVKRRSECS
						KPAS*MCTERNPTSMREVHD
		1		I		RKYAVLYQPLFD*AVLKLLM
		1				FMNLRKEGM
16738	47106	Α	16839	66	476	
16739	47107	Α	16840	1	1362	
16740	47108	Α	16841	11	747	
16741	47109	Α	16842	522	687	
16742	47110	Α	16843	112	861	
16743	47111	Α	16844	87	472	TVTFSQCRFGKMLPLEKAFAS
	1	ĺ			1	QELPSPAGSAHAGVSSRSSSR
		1		1	1	NPRPSLRGPLLTLEFSRLRFRE
		1		1	1	VYP\EAAGPHHTLARLDELCR
		1			1	WLMPEARSKEQMLELLVLEQ
		<u> </u>		L		L/SILPDKVRPWVVAQYPES
16744	47112	Α	16845	1	393	

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop eodon, /=possible nucleotide deletion, \=possible nucleotide insertion)
16745	47113	Α	16846	621	1099	
16746	47114	Α	16847	1	453	
16747	47115	Α	16848	209	1175	
16748	47116	Α	16849	1	546	
16749	47117	A	16850	187	421	LGESSQ*GSP\PPPTGGCGPATG Q*PLGQSFQRKELAAIFAVSQY SLVVPPGMGETEATGIWSRPPA NGNSPTVEWHIK
16750	47118	Α	16851	3	1654	
16751	47119	Α	16852	166	465	
16752	47120	Α	16853	1	558	
16753	47121	A	16854	51	380	RNNLLLLTHHFVLIIQFLIPRKET KYYLVITPYSLSINVLSNFFYYS PESLNDTNCYHHEEADTPWR*F LAIFEGLFNIAHQMQNMPFFLL WKQVPETLVIQQQLPRIN
16754	47122	Α	16855	3	550	
16755	47123	Α	16856	1	462	
16756	47124	В	16857	1	2811	
16757	47125	Α	16858	3	514	ASGTAPEIQARPTRPRKRRRK LLPL/TKAEAKAKALKAKKAVL KGVHSHKKKKIRTSPITRRPKT LRLRRQPKYPRKSAPRRNKLDH YAIIKFPL/TTESAMKKIEDNNTL VFIVDVKANKHQIKQAVKKL DIDVAKVNTLIRPDGEKKAYVR LAPDYDALDVANKIGII
16758	47126	А	16859	73	396	FFQFSPKKNCSVWWNCVAEVLL KYKTGETNDFELLKNQLLDPDI KRLPWLNRSQTVVEEYLAFLG NLVSAQTVFLRPCLSMIASHFV PPRVIIKEGDVDVSDSDDEDD
16759	47127	A	16860	132	357	YVSKFAGRLSSSSSESETSTSPS LMITRGGTKWGSNHAETRSEE NSLC*YKITKKSQILFHYCFDFY STKAISI
16760	47128	Α	16861	380	597	
16761	47129	A	16862	179	280	QRDIKSCVQILQWEGSTRPFTN E**YMANVRNS
16762	47130	Α	16863	2	175	
16763	47131	Α	16864	178	374	
16764	47132	A	16865	386	2120	
16765	47133	A	16866	887	1104	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1				sequence		
16766	47134	IA	16867	,	708	MEVAALEHLDHRLREKVKQQN
10/00	4/134	I <sup>A</sup>	10807	1	/08	ALRHQVVLRQRRLEELQLQHS
						LRLLEMAEAQNRHTEVAKTMR
						NLENRLEKAQMKAQEAEHITS
1						VYLOLKAYLMDESLNLENRLD
		1				
						SMEAEVVRTKHELEALHVVNQ
		1				EALNARDIAKNQLQYLEETLVR
		1			1	ERKKRERYISECKKRAEEKKLE
		1		ł		NE/LHGAQADPGSDLNPRADPP
		1				RAPAATVRRHHPGQPACQGGG
		1		ŀ	ł	AAAALEHVPDGGDLWQGQGR
16767	17125	<del> </del>	16868		1327	HWH
16767	47135 47136	A	16869	1	1776	
16769	47137	A	16870	1	397	-
16770	47138	A	16871	1	1974	
16771	47139	A	16872	1	336	
16772	47140	A	16873	3	661	GRGGHNFAPNLTARSAVTSGL
10//2	4/140	I <sup>A</sup>	108/3	3	001	GGPPAAVMVGSLNCIVAVSQN
		ı				MGIGKNGDLPWPPLRNEFRYF
		i i				ORMTTTSSVEGKONLVIMG\KK
		ı				TW\FSIPE/RRNRPFKG*EFNLVL
		1				SRELQGNLPQGAHFLSRSLDDA
		1				
		1				LKLTEQPELANKVGMVW\IVG GSSI\YKESMNHSSSLKLFVTRII
1						QDFESDTFFPEIDLEKYKFLPEY
1.0000	47141	ļ.	16874		755	PGVFFDVQEEKGIKYKFEVHEK
16773	4/141	Α	16874	38	/55	ALKTCSVNQPDAKDNIAGSSGH
İ						LRTLSPVVSRSCLKEEERRRRR
1	1					RMKRRQRSRRRRSRRRRMRRR
		1				RRSRSRRRRMKRRKRRRMKR
		1			1	RSSFILMYFFMLLLSGIPLLYME
		1				VIMGQWLHVDNIRVWKQLVP
		1				WLCSMSY/SSQSVCASVSLYNS
1		1				TIISWNFFYSFAHPLPWDHCPLV
1		1				KNISVTDWAHQYFLYHTTLHA
		1				SDHSEEAAEALVPNRSLGCLLG
	101.10	1	1.6025	ļ. ——	1000	RDHRDLDFKPEIRRGAHTGGAR
16774	47142	A	16875	1	1830	
16775	47143	A	16876	2	1142	
16776	47144	A	16877	1	435	
16777	47145	A B	16878	247	963 1092	
16778	47146	_		1	1653	
16779	47147	A	16880	1	2268	
16780	47148	A	16881		555	
16781	47149	A		301		
16782	47150	A	16883		630	
16783	47151	A	16884	731	834	
16784	47152	A	16885		2277	
16785	47153	A	16886	45	2446	
16786	47154	В	16887	625	696	I

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
16787	47155	A	16888	193	315	WPGGGYSLLCFWCPLSFAGAA G/W*PPPGHH*PYSPKQEHYRT NSDTLIFLSSRTLVLQGS*GIKV AGSEGPKYNE*PRNPVLPSLCL HLFGC
16788	47156	Α	16889	1	588	
16789	47157	Α	16890	2	229	
16790	47158	Α	16891	1	502	
16791	47159	Α	16892	516	576	
16792	47160	Α	16893	144	435	
16793	47161	С	16894	1	996	
16794	47162	Α	16895	424	632	
16795	47163	В	16896	446	1944	
16796	47164	С	16897	207	470	
16797	47165	Α	16898	1	396	
16798	47166	Α	16902	1	585	
16799	47167	Α	16903	141	906	
16800	47168	В	16904	99	276	
16801	47169	Α	16905	1	756	
16802	47170	Α	16906	1	383	
16803 16804	47171 47172	A	16907 16908	3	582 615	PECIIGIDILSSGQNPHIGSLTGR
						VRAIMVGKAKRKPLELPLPRKI LNOKQYRIAGGIEEISATIKDLK DAGVVIPTTSLFDSPIWPVQKT DGSWRMTVDYRQINQVATPIA AAIPDVASLLKQINTSPDTW/PI RPPISNGD*GVSGR*ACCLEPLA GPHR*ITSEASRILEQGPAIFCR* LLSF*ETALGLLLGFGGN*TFDY
16805	47173	A	16909	3	415	PVK/VGA*GGQVINGVLAQV*L TVGPVGPRTHPVVIFPVPECRIG RDILSSWQNPHTGSLTGRVRAF MVGKAKWKP*ELPLPRKTVNQ KQYRIPGGIAEIS/A/TIKNLRRG VVIPTTSRRNSPIWPVQKTDGS W*TAADY
16806	47174	Α	16910	232	633	
16807	47175	A	16911	1	1677	
16808	47176	A_	16912	328	381	LLKLQH*MQSPYLVGPSQ
16809	47177	A	16913	3	811	
16810	47178	Α	16914	1	1125	
16811	47179	A	16915	1	1191	
16812	47180	Α	16916	113	485	
16813	47181	A	16917	1	357	
16814	47182	A	16918	12	398	
16815	47183	A	16919	498	595	TEMASTTTCT/RFHDEYQLFEEL *KGAFSVNGT
16816	47184	Α	16920	5	367	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hed	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
16817	47185	A	16921	190	2005	VLYPLHLGTGTGKGAGGASSG
10817	47103	<u> </u> ^	10921	1190	2003	EEGSEARRRRRIGGLWGRRPHA
1						TLSGHLPSRPAPAHTPSRASYFR
						TRKVRAALGDSAAGPVPGLAA
						RLLASGPSRSQPGHSPGPEMAS
1				1		TTTCTRFTDEYQLFEE\LGRGAF
1	l			1		SVVRRCMKIPTGQGYAAKIINT
					Į.	KKLSARDHQKLEREARICRLLK
	1	l		l		HPNIVRLHDSISEEGFHYLVFDL
1						VTGGELFEDIVAREYYSEADAS
1						HCIQQILESVNHCHLNGIVHRD
1					1	LKPENLLLASKSKGAAVKLADF
1						GLAIEVQGDQQAWFGFAGTPG
1		1				YLSPEVLRKDPYGKPVDMWAC
						GVILYILLVGYPPFWDEDQHRL
		1				YQQIKAGAYDFPSPEWDTVTPE
				1		AKDLINKMLTINPAKRITASEAL
1	l					KHPWICQRSTVASMMHRQETV
	1	1		1		DCLKKFNARRKLKGAILTTML
						ATRNFSAAKSLLKKPDGVKEST
i		l			i	ESSNTTIEDEDVKARKQEIIKVT
		1				EQLIEAINNGDFEAYTKICDPGL
						TAFEPEALGNLVEGMDFHRFYF
1		1				ENALSKSNKPIHTIILNPHVHLV
		i				GDDAACIAYIRLTQYMDGSGM
					ŀ	PKTMOSEETRVWHRRDGKWO
						NVHFHRSGSPTVPIKPPCIPNGK
		İ				ENFSGGTSLWQNI
16818	47186	Α	16922	1	288	
16819	47187	A	16923	318	458	
16820	47188	A	16924	11	578	
16821	47189	Α	16925	803	1068	
16822	47190	A	16926	1	660	
16823	47191	A	16927	2	325	TSSENNNGPKR*IHSTESLYLLO
					1	GSVVADHDYIGLPEIPIGAYQA
						NILVEDATIGIVDNELLTSSKDR
			1			ELLEYRNTKISPLIDDHSSLEKQ
				1		TFSLLDSSNQVLEYLS
16824	47192	A	16928	156	573	
16825	47193	A	16929	405	599	GLEPPOKPGLVTSILOANPVPLP
1		1		1	İ	CGNSQSR*TSTRCWYEHLQCTQ
			1		i	SHLQMQQYHEAYQSACALA
16826	47194	В	16930	1	1676	
16827	47195	A	16931	1	1125	
16828	47196	Α	16932	27	818	
16829	47197	Α	16933	1	4986	
16830	47198	Α	16934	1	4401	
16831	47199	Α	16935	153	370	SVLETCMSTAFPVSCHSSFKTA
		1	l			VLRISLS*ISAQGGPIDLFSQCHP
1			1			SSSTGVSS\NHRGSWDTPGQSL
1		1	1			VVICL
				1		

SEQ ID NO:	SEQ ID NO: of peptide		SEQ ID NO: in USSN		Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
NO:	of peptide sequence	hod	09/540,217	location of first codon for peptide	of peptide sequence	deletion, \=possible nucleotide deletion, \=possible nucleotide insertion)
	ocquence.			sequence	J. p. p.	, · <b>p</b>
16832	47200	В	16936	47	501	
16833	47201	A	16937	49	1714	
16834	47202	A	16938	1	999	
16835	47203	Α	16939	140	2029	FAARAGPGGSRRARRGNKWA
		l			i	MPYEIKKVFASLPQVERGVSKI
	1	l			i	GGDPKGNNFLYTNGKCVILRN
		1				DNPALADIYTEHAHQVVVAKY
		ı				APSGFYIASGDVSGKLRIWDTT
		1				QKEHLLKYEYQPFAGKIKDIA
		l				TEDSKRIAVVGEGREKFGAVFI
						WDSGSSVGEITGHNKVINSVDI
		l				KQSRPYRLATGSDDNCAAFFE
		1				PPFKFKFTIGDHSRFVNCVRFSI
		l				DGNRFATASADGQIYIYDGKT
		l				EKVCALGGSKAHDGGIYAISW
		l				PDSTHLLSASGDKTSKIWDVSV
	1	l				NSVVSTFPMGSTVLDQQLGCL
		l				WQKDHLLSVSLSGYINYLDRN
		1				NPSKPLHVIKGHSKSIQCLTVH
		1				KNGGKSYIYSGSHDGHINYWD
	1	ı				SETGENDSFAGKGHTNQVSRM
	1	ı				TVDESGQLISCSMDDTVRYTSL
		l				MLRDYSGQGVVK\LD\VQPKC\
		l				VAVGPGGYAVVVCIGQIVLLK
	1	1			l	DQRKCFSI\DNPGYEPEVVAVH
	1	ı			l	PGG\DTVAIGGVDGNVALYSIL
		l				GTTL\KDEGKLLEAKGPVTDV
		l				YSH\DGAFLAVCDASKVVTVFS
		1				VADGYSENNVFYGHHAKIVCL
	1					AWSPDNEHFASGGMDMMVYV
	1	1				WTLSDPETRVKIQDAHRLHHV
1 400 4	10001	ł. –	16040	21	440	SLAWLDEHTLVTTSHDASVKE
16836	47204	A	16940	31	449	
16837	47205	A	16941	1	53	ON APPEAR LANCE OF COLUMN TO THE COLUMN TO T
16838	47206	Α	16942	1	389	GMPTSTIASCSQDGRVFIWTCD
			l			DASSNTWSPKLLHKFNDVVWF
		l	l	l		VSWSITANILAVSGGDNKVTEC
		l		I		QQNEQ*QDRWGLAPHPPAPGL
						PLPGPTNQTTGKSPQLQQDYFP
16026	47207		16042	ļ. —	420	RRSYRCSHRLIICLNVIGNAL
16839	47207	A	16943	1	438	
16840	47208	В	16944	1	1267	
16841	47209	A	16945	635	808	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
16842	47210	A	16946	37	1319	QGEGHGRGLHGFLGRPESQIPS
						WSRSAPLHRLEIWGALAPSLAD
				İ		HSEGSPEVSVINTVDTSHEYMI
						Y\DAQMDYYGHPPGQPASSDRS
			•			VKIF*CAQWEGRSLFADLQGS
						WRGPVWQVGWGFTPLLRATS
						WAFVASLLTGKFIYSWERGKT
						GTLGRRATSNAGTRLLKLNFGC
						CWAPHGLTVLHSWACWVVSD
				ŀ		RGPSSL\LDFTPGEGQWEVKKIN
		l		ŀ		NAHTIGCNAV\TWAPACCTWK
		l				PHRRPHRGQKPNYIKRFASGGC
		l				\DNLI\KLWKEEEDGQWKEEQK
						LE\GHSDWV\RDVAWAPSIGPA
		1				HQHHRPAAPRMGRVSIWTCDD
						ASSNTWSP*IV\DKFNDVVWHV
		l		ł		S\WSITANILAVL\CGDNK\VPL
		l				WKESS*WAKWVVPSSDVKQRC
						PGLPYQPSSDQEGPARNEQVNK
						DQGGALAPPPAQLPGPAPSPGP
16843	47211	Α	16947	1	1021	MSGEFIDHSHIARIIYPGIFGTDA
		l				GSCIDQRGITGKLQQPPEDRRL
						GEGKLTNTKDIHTKTPSVRHHH
						QRPKVDKTTKIGKKQSRKTGNS
				İ		KNQSAPPPPKECSSSPAMEQSW
				ŀ	\	TENDFDELREEGFRRSNYSELK
						EEFRTHGKEVKNLEKRLDEWL
		l				TRITNAEKSLKDLMELKTKARG
				ŀ		LQRVSVMEDEMNEMKQEEKFR
		l				EKRIKRNKQSLQEIWDYVKRPN
				ł	1	LRLIGVPESDGENGTKLENTLQ
				l		DIIQESFPNLARQANIQIQEIQR
		ŀ				MPQRDSLRRATPRHIIVRFTKV
						EMKEKMLRAAREKA\HIALIPK
		ĺ			1	LTT*LEVKLSSANVKEQKL*QT
16844	47212	A	16948	i	393	VFQTTVQSN
16845	47213	A	16949	1	2631	
16846	47214		16950		1155	
16847	47215	A	16951	1	1185	
	47216	Ā	16952	1	942	
16849	47217	Ā	16953	1	615	
16847 16848	47215 47216	Á	16951 16952	1	1185 942	

SEQ ID NO:	SEQ ID NO: of peptide	Met	SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
10:	sequence	иоц	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
16850	47218	A	16954	474	2678	IKPQRWGKKQSRKTGNSKNQS
	ł	1				ASPPPKERSSSPAMEQSWTEND
				1		FDELREDSFRRLVITNYSELKEE
	ŀ			1	1	VRTNGKEVKNLEKKLDEWLTR
		1		1		ITNAEKSLKDLMELKTMAQELF
		1		į.		DQCTSLSSRCDQLEERVSVMED
		1				EMNEMKCEEKFREKRIKRNEQ
		İ				SLQEIWHYVKRPNLRLIGVPES
		1				DGENGTKLENTLQDIIQENFPN
		1				LARQANIQIQEIQRMPQRYSSR
		1				RATPRHIIVRFTKVEMKEKMLR
		1				VAREKGQVTHKGKPI\RLTADL
					ł	LAETLQARREWG\PIFNILKEKN
					l	FQPRISYPAKLSFIDRSTRQKVN
		ŀ		1		KDTQELNSALHQADLIDIYRTL
	İ	1		1		HPKSTEYTFFSAPHHTYSKIDHI
		1		1		VGSKALLSKCKRTEIITNCLSDH
		1		1		SAIKLELRIKKLTRNHSTTWKL
	i i	1		l		NNLLLNDYWVHNEMKAEIKM
		1				FFETNENKDKTYQNLWDTFKT
		1				VCRGKFIALNAHKRKQERSKID
		1				TLTSQLKGLEKQEQTHSKASRR
						QEITKIRAELKERVGRWRIGEA
			l	i		ADLVGVSSQAIRDAEKAGRLPH
		1	1	ļ		PDMEIRGRVEQRVGYTIEQINH
		1	1			MRDVFGTRLRRAEDVFPPVIGV
		1	1			AAHKGGVYKTSVSVHLAQDLA
				i		LKGLRVLLVEGNDPQGTASMY
			i	1		HGWVPDLHIHAEDTLLPFYLGE
				1		KDDVTYAIKPTCWPGLDIIPSCL
		1		1		ALHRIETELMGKFDEGKLPTDP
		1				HLMLRLAIETVAHDYDVIVIDS
6851 6852	47219 47220	Α	16955	1	675 1032	
6852	47221	A	16956	3	978	HEAKHOMADDAGGSGGGPKA
0823	47221	Ι^	10937	3	910	LVGPGMG\NPVAFRRGF\GIVIR
		1				GPGSRPGGRGRGR\GRGARGSK
		1	1			
		1				\AEDKDW\MPVTKLG/RALVKD
						H*RSKFPWKEIYLFSLPH*RNQR
		1	ŀ			IIDF\FLGGLLSKDEGFE*LCPVQ
						EQDPCPASRTQASRPFVAIGGL
		ŀ				QMAHVGLGC*VLPRKVATGHP
					\	VGAIILAKLS\IVPVRR\GYLGNK
						VLAKP\HTVP\CKV\TGRCGSVL
						VRLIPAP\RGLGMVSAPVA\KKL
						LMMAGIDDCYT\SARG\CTATL
			1		1	GQIWPRATL*LPFLRTYKLP*PP
			1		1	DLWKGRLYLPSFPIKEFT\DHLV
		_				KDPHPESSVQQDSELQLVATT
16854	47222	В	16958	124	274	

SEQ ID NO:		Met	SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
NO:	of peptide sequence	hod	in USSN 09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	sequence	ĺ	09/340,217	sequence	or peptide sequence	deterior, · possible marroual macriton)
				L		
16855	47223	Α	16959	202	2264	KWPKMNPQQQRMAAIGTDKE
						LSDLLDFSAMFSPPVNSGKTRI
						TTLGSSQFSGSGIDERG\GTTSV
						GTSGQPSP\SYDSSRGFTDSPH\
						SDHLNDSRLGAHEGLSPTPFM:
	l .			1		SNLMGKTSERGSFSLYSRDTG
						PGCQSSLLRQDLGLGSPAQLSS
		1				SGKPGTAYYSFSATSSRRRPLH
				1		DSAALDPLQAKKVRKVPPGLF
						SVYAPSPNSDDFNRESPSYPSP
						PPTSMFASTFFMQDGTHNSSD
				1		WSSSNGMSQPGFGGILGTSTSF
						MSQSSSYGNLHSHDRLSYPPH:
		1				VSPTDINTSLPPMSSFHRGSTSS
	1	1		1	1	SPYVAASHTPPINGSDSILGTRO
						NAAGSSQTGDALGKALASIYS
				1		DHTSSSFPSNPSTPVGSPSPLTG
		1				TSQWPRPGGQAPSSPSYENSLI
		1				SLQSRMEDRLDRLDDAIHVLR
		1				HAVGPSTSLPAGHSDIHSLLGF
						HNAPIGSLNSNYGGSSLVASSR
		1				SASMVGTHREDSVSLNGNHSV
		1				LSSTVTTSSTDLNHKTQENYRG
		1				GLQSQSGTVVTTEIKTENKEKI
	1	1	1			ENLHEPPSSDDMKSDDESSQKI
		1			i	IKVSSRGRTSSTNEDEDLNPEQ
						KIEREKERRMANNARERLRVR
					i	DINEAFKELGRMCQLHLKSEK
						QTKLLILHQAVAVILSLEQQVF
						<b>ERNLNPKAACLKRREEEKVSA</b>
		İ				VSAEPPTTLPGTHPGLSETTNP
16856	47224	Α	16960	1190	1327	
16857	47225	A	16961	386	554	ATISFRYSQCK*AEQGCDSELG
						LFTKIRKSGYWGV*ATISFRYS
						CKALEIHLTAPVVPSALRIWGF
						QIPGFNQLSFHPSPESKGSFLPC
16858	47226	В	16962	499	915	
16859	47227	Α	16963	1	1785	
16860	47228	Α	16964	1	3036	
16861	47229	Α	16965	2	710	
16862	47230	A	16966	349	493	SS*VRWVSGR*HPQ*STLSAPL
L		L				ETSGCHQGGLHDLKIVVL
16863	47231	A	16967	1	1335	
16864	47232	Α	16968	83	426	
16865	47233	A	16969	93	345	APALCLQILLDCKSVRNRTSRF
		1	1	1	1	RPREVGIQQYKKGGGAAGKG
		1			1	TGNAPGFLLFSKDS*KDPTPLP
		L	L	1		PLLL*GQRDH*IQLHQE
16866	47234	A	16970	1	1302	
16867	47235	Α	16971	1	1174	
16868	47236	A	16972	274	1428	

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nuclcotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleofide insertion)
16869	47237	A	16973	411	629	HCLSHFQNTGPRGDVDFQQEL\
10007	1,725,	· ·	10770			FPVLMADIRKEERSHLCRSSRR
						TWTILDKS*IQGSRLSSKEQGW
1						GWGTSRK
16870	47238	Α	16974	618	1552	
16871	47239	Α	16975	I	558	
16872	47240	Α	16976	I	765	
16873	47241	A	16977	2	418	
16874	47242	Α	16978	130	1965	
16875	47243	Α	16979	1	1062	
16876	47244	A	16980	I	558	
16877	47245	Α	16981	37	676	
16878	47246	Α	16982	1	1014	
16879	47247	Α	16983	1	2964	
16880	47248	В	16984	259	1751	
16881	47249	Α	16985	1	987	
16882	47250	Α	16986	1	1047	
16883	47251	Α	16987	3	1413	GLHAARGPWVVQAWISITM\ER
	İ					KEVCYGQLGCFSDEKPWAGTL
l		l				QRPVKLLPWSPEDIDTRFLLYT
		Į.				NENPNNFQLITGTEPDTIEASNF
	l	l				QLDRKTRFIIHGFLDKAEDSWP
	1	1				SDMCKKMFEVEKVNCICVDWR
	ł	l				HGSRAMYTQAVQNIRVVGAET
		ĺ				AFLIQALSVKPCLGPVLWVGVR
	l	l				EGQGDAARGTALEDVHVIAHS
	ŀ	l				LGAHT/AAEAGRSWGPRGRITD
		l				DLGTA*YKVDGMG*ERRGVRF
		l				SI*P*GGGV*AGFGGERFR*RKN
		1				VGKSTAGWRM\GLDPAGPCFQ
		1				DEPEEVRLDPSDAVFVDVIHTD
	l	1				SSPIVPSLGFGMSQKVGHLDFFP
1		1	1	1		NGGKEMPGCKKNVLSTITDIDG
			1	1		IWEGIGGFVSCNHLRSFEYYSSS
1	1	1				VLNPDGFLGYPCASYDEFQESK
1		1				CFPCPAEGCPKMGHYADQFKG
						KTSAVEQTFFLNTGESGNFTSW
						RYKVSVTLSGKEKVNGYIRIAL
						YGSNENSKQYEIFK
16884	47252	В	16988	95	315	
16885	47253	С	16989	1	780	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
16886	47254	A	16990	2	1426	SGTLDRMLIFWTITLFLLGAAK GKEVCYEDLGCFSDTEPWGGT AIRPLKLIPWSPEKIGTRSTLLYT NENPNNFQILLIS.DPSTIEASNF QMDRKTRFIHGFIDKGDESWY MCSKLIFEVEEVNCIFVOWK KGSQATYTQAANNVRVVGAQ VAQMLDILLTEYSYPPSKUH GHSLGAHVAGEAGSKTPGLSK/ RLQGLDPVEASFESTFEEVELUL GTNQMGHLDFPPNGGESMFG GTNQOMGHLDFFPNGGESMFG CKKNALSQNUDLOGIWAGTRDF VACNHLRSYKYYLESILNPDGF AAYPCTSYKSFESOKCFFCPDQ GCPQMGHYJDKFAGKTSEEQQ KFFLNTGEASNFARWYGVSITI LGGRTATGGIKVALFGNKGNTT QYSIFRGILKPGSTHSYEFDAKL DVGTIEKVKFLWNNNINTLE KVGATKITVQKGEEKTVYNFCS
						EDTVREDTLLTLTPC
16887	47255 47256	A	16991 16992	954	1407 1663	EPSPDPAHAPSVALLHTGNQSK VLPWPRNPCMKRW*K*KMLKI SWVHEWYTSNWISTAVRSLRV FAPKNVFQ**ALGPSGWLVYC
16889	47257	A	16993	3	242	7,11,11,11,12,11,11,11,11,11,11,11,11,11,
16890	47258	A	16994	1	1815	
16891	47259	Λ	16995	1	375	
16892	47260	Α	16996	3	2005	
16893	47261	Α	16997	1	651	
16894	47262	Α	16998	114	275	
16895	47263	Α	16999	1	270	
16896	47264	A	17000	140	876	PPALVYGRROKSWIMFEQMISA WOKKLIKGIDRIYNPENLATLE NYVETOAKENAYDLEPNLAVP ESCTKFNPAFFQTNGSTAQDSC *KALTNLPHTDFTLJCKCMIRF GHIQBERPIPTDFCYLGGFOWE TWPFSRAP WESPGMKTYDLLW KV*LGFEDSVIRKFNCHVVGUT YQHIDRIWLLAEMLGDLFGQAS *RCWMSKYGWSADESGQIFIC SPREEHLTPRNIVEKIDFDSVSSI MASSQ

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		l		sequence		
16897	47265	A	17001	1	777	MSGENVTKVSTFILVGLPTAPG
10697	4/203	Ι^	17001	1	I'''	
		1				LQYLLFLLFLLTYLFVLVENLAI
		l				ILIVWSSTSLHRPMYYFLSSMSF
		l				LEIWYVSDITPKMLEGFLLQQK
		1				RISFVGCMTQLYFFSSLVCTEC
		1	i			VLLASMGYDRYVAICHPLRY\N
						LACTDFSTAELV/SFILAFIILVFP
	i					LLATILSYWHITLAVLRIPSATG
		1				CWRAFSTCASHLTVVTVFYTA
		l				LLFMYVRPQAIDSQSSNKLISA
		1				VYTVVTPIINPLIYCLRNKEFKD
						ALKKALGLGQTSH
16898	47266	A	17002	2	876	
16899	47267	Α	17003	I	894	
16900	47268	A	17004	377	501 823	
16901	47269 47270	A	17005 17006	3	823	
16902	47271	C	17007	156	287	
16904	47272	A	17007	1	1140	
16905	47273	A	17009	1299	3135	ISGSVCILLWLQLLPAYNLIIHT
1.0505	1,2,3	1	17007	1277	5155	WEHRHSPPGT/RMSRLAKRNA
						WEADR/YAEAKLAASRRGQPSS
						LMSSREGGWGEGSOSRNSSHG
					1	ALKEAOFIITNAEKSLKDLMEL
						KTMAQELRDECTSLSSRFDQLE
						EKVSVMEDEINEMKQEEKVRE
					l .	KRIKRNEOSLOEIWDYVKRPNL
		l			į.	HLIGVPESDRENGTKLENTLODI
		l			į.	
		l		l	1	IQENFPNLARQANIQIQEIQRMP
						QRYSSRRATPRHIIVRFTKVEM
						KEKMLRAAREKEIQTTIREYYK
						HLYTNKLENLEEMDKFLDTYS
	1					LPRLNQEEVESLKRPITGSEIGAI
	1					INSLPTKKSPGPDGFTAEFYQRY
	i					KKELVPFLLKLFQSTEKERILPN
	1	l				SFYEASIILIPKPGRDTTKKENFR
	l	1			1	PISLMNINAKILNKILANQIQQHI
l		1	1			EKLIHHDQVGFIPGMQGWFNIR
		1				KSINVIQHINRTNEKNHMIISIDA
		1	1			EKAFDKIQQPFMLKTLNKLGID
		1	1			GTYLKIVRAIYDKLTANIILNGQ
		1	1			KLEAFPLKTGTRQGCPLSPLLF
		1	1			NIVLEVLARAIRQEKEIKGIQLG
		l				KEQVKLSLFADDMIVYLENPIV
		1				SAQNLLKLISNFSKVSGYKINV
1		1	1			QKSQAFLYTNNRQTESQIMSEL
		L				PFTIASKRIK
16906	47274	C_	17010	189	457	
16907	47275	A	17011	2	2600	
16908	47276	A	17012	107	1493	l

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	eodon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequenee		
16909	47277	IA	17013	3	2209	IHTKTPSVCHHHQRPKVDKTTK
				[		MGKKOSRNTGNSKNOSTSPPP
		1				KECSSAPAMEQSWMENDFDEL
						REEGFRESNFSELTEEVRTHEK
1						EAKNLEKKIROM\VTRITNVEK
1						SLNDLMELKNMARELRDKCTS
		l				FSSRFDQLEERVSVIEDQMNEM
		l				KQEEKFREKRVK\RNEQSLQEIR
						DYVKRP\NLRLIGIPESDEENGT
l		1				KLENTLQDII\QENFPNLARQAN
				1	1	IOIKEIORMPORYSSRRATPROI\
						IVRFTEVEMREK\MLRAAREKG
1						RVTHKGKTIRLTVDLSAETIOA
				l		RRESTROKVNKDIQELNSAQHQ
1		i				ADLTDNYRTLHPKSTEYTLFSA
						PHHTYSKIDHIVGSKALLSKCK
İ						RTEIITNCLSDHSAIKLELRIKKL
						TONLSTTWKLNNLLLNDYWVH
						NEMKAEIKMLFETNENKDTTY
						ONLWDTFKAVCRGKYIALNAH
1						KRKOERSKIDTLTSOLKELEKO
					ľ	EQSHSKASRRQEITKIRAELKEI
1				l		ETOKTLOKINESRDWFFEKINKI
i .						DROLARLIKKKREKNOIDTIKN
				1		VLEFLAKAIRQDKEIKGIQLGKE
				ŀ		EVKLFLFAEDMIVYLENPIVSA
		1				ONLLKLISNFSKVSGYKINVOK
		1		ł		SQAFLYTNNRQTESQIMSELPFT
		l		ļ.		IASKRIKYLGIOLTRDMKDLFK
				i .		ENYKPLLNKIKEDTKKWKNIPC
						SWVGRINIMKMAILPKVIYRFN
		1				AIPIKLPMTFFTELEKTTLKFTW
16910	47278	A	17014	292	699	AIFIREFWITFTEEERTTERFTW
16911	47279	A	17014	269	803	ALGPCSEALPTWVNENGEEMA
1.0711	1	Γ.		[ · · ·		OEIDLSALKELEREAILOVLYRD
i					l	OAVONTEEERTRAAGN*KHTC
1						SISGGKGPKNTDWEHKEKCCA
1					l	RCQQVLGFLLHRGAVCRGCSH
1		l				RVCAQCRVFLRGTHAWKCTVC
1					1	FEDRNVKIKTGEWFYEERAKKF
1						PTGDNSV\RTSCTGKHETVGGQ
						LLQSYQK
16912	47280	A	17016	1	1173	
16913	47281	Α	17017	349	718	AGPEGTTTAECP/I/CQQQRPILS
		1			l	LRYGTISWG/DQSATWWQVDY
		1			l	IRTLLSWKWQSASAKTTIHGLT
		1				KCLIHHDIPHSIASD*GTCFMAK
1		1	1			EVWQWYCFSHSQDSRVQESRG
1			1			GIGSCTTHHHPCSFPN

Sequence	SEQ ID	SEQ ID NO:	Met	SEQ ID NO:		Nucleotide location of last	Amino acid sequence ( X=Unknown,
LAILSTDYNV-9PCFPAGAHOG	NO:		hed	in USSN 09/540,217	codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	16914	47282	A	17018	196	577	QPLAWPVPFLAWLSWQQKRC* KQQRSSRNLVDHRNPGWLHEE
16915   47283   A   7019   1   2523							
16917   47285   A   17021   1610   2004   VTWSAQQMPWAIKNCPTISPL	16915	47283	Α	17019	1	2523	
GQGCLPQPKM*VVQNDFQ*G* WTHCRKGIKGGRVQVVVWPWQ TQNRGKGTFLFLHSAVADAM LYAL*RGSDLDAAQTL_PTAAQ DALYAVVPGGEPTGQLQVRIN EFALGQ  16919 47287 A 17023 88 1871  16920 47288 A 17024 I 1299  16921 47288 A 17025 2 260  16922 47290 A 17026 144 1737  16923 47291 A 17027 I 1182  16924 47292 A 17028 262 1132  16924 47292 A 17028 12 1182  16924 47293 A 17029 I 484  16926 47294 A 17030 3 382	16916	47284	Α	17020	236	558	
16918   47286   A   7022   1   735	16917	47285	Α	17021	1610	2004	GQGCLPQPKM*VVQNDFQ*G* WTHCRKGIKGGQRVGVWPWQ TQNRGKGTFLTPLHSAVADAM LYAL*RGSDLDAAQTLPTAAQ DALYAVVPGGEPTGQLQVRHN
16919   47287   A   17023   88   1871	16019	47296	1_	17022	1	725	EFALOQ
16920   47288   A   7024   I   1299			-				
16921   47289   A   17025   2   260							
16922   47290							
16921   47292							
16925   47293   A   17028   262   1132			_				
16925   47293   A   17029   1   484					1.		
16926							
16927   47295	16926	47294	A	17030	3	382	GRKRKERALGRWQV*RSRCA* P/STPAALNAPLQGASHSPFRLR NCWKGRSVRASSLLRQLAKGG CAARRLSWNLCQIVQMYEGHS
16928   47296	16927	47295	A	17031	1	2022	XXXXXXXXXXXXXXXXXXXX
16929   47297   A   17033   213   1993     16930   47298   A   17034   1   378     16931   47299   A   17035   64   1180   SASHSGAPATSLYERGVCPPAL RRPPAVLVCRAAASCTILAMS DLQEEGKNANSPMSPALVDVP PEDTQLEENEERTMIDPTSKEDI KFKELGKVLLDWINDVLAEERI IVKQLEEDLYDQQVIQALIFREK NLAGLQSLNVAEVTQSEIGQKC KLQKVLEQLYDQVIQALIFREK NLAGLQSLNVAEVTQSEIGQKC KLQKVLEQHDLLRPRSWALR WUCINSHIGKNLVGNPQLLVSL AMHFRAPRLPEHTVQVVVV RKREGLHSSHISEELITTTEM MMGRFERDAFDTLFDHAPDKL SVYKKSLITEVNKHLINKLNEEV TELETQFADGVYLVLLMGLLE DYFYPLHHPYLTPESEDQKVIN VSFAFELTGFADGVYLVLLMGLLE DYFYPLHHPYLTPESEDQKVIN VSFAFELHGRIPSRNRVLVLK TWLTWDLKSPLEVLYNLFFKYL			_		209		
16930   47298	16929					1993	
16931 47299 A 17035 64 1180 SASHSGAPATSLYERGVCPPAL RRPPAVLVCRAAASCTLLAMS DLQEEGKNARNSPMSPALVDVV PEDTQLEENEER TMIDPTSKEDI KFKELGK VLLDWINDVLAEERI IIVKQLEEDLYDGQVLQKLFFEK NLAGLQSLAVAEVTQSEIGQKC KLQKVLEQLHDLJRRSWALR WLGNSHGKNLVGNPQLLVSL AMHFRAPRLPEHVTVQVVVV RKREGLHSSHISEELTTTTEM MMGRFERDAFDTLFDHAPDKL SVYKKSITFVNKHLNKLNLEV TELETGFADGVYLVLLMGLLE DYFVPLHHFYLTPESSFDQKVIN VSFAFELMLGRRPSRNPRLVLK TWLTWDLKSPLRVLYNLFTKYL TWLTWDLKSPLRVLYNLFTKYL	16930		_				
	110931	4/299	A	17/035	04	1100	RRPPAVLVCRAAASCTLLAMS DLQEEGKNAINSPMSPALVDVH PEDTOTLEENEERTMIDPTSKEDP KFKELGKVLLDWINDVLAEERI IVKQLEEDLYDGQVLQKLFFEK NLAGLQSLNVAEVTQSEIGGKQ KLQKVLEQLHDLLRPRSWALR IWLGRSHGKNLVGRPQLLVSL AMHERAPIRLPEHVTVQVVVV RKEGGLHSSHISEELTITTEM MMGRFERDAFDTLFDHAPDKL SVVKKSLITEVNKHLNKEV TELETQFADGVYLVLLMGLLE DYFVPLHHFYLTPESFDQKVHN VSSAFELMLGRRPSSNPRLVLK
	16932	47300	A	17036	3	764	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
16933	47301	Α	17037	I	1230	
16934	47302	A	17038	1	313	
16935	47303	Α	17039	145	263	IFLLYLKNKVQNK*EIKQHFLG KIMSRDNNTYLTWGTEN
16936	47304	A	17040	5	982	PTESAVATMESRAGVAGLSA WTLQPQWIQVRNMATLKDITR KLSIKNIQKITKSMKMYAAAK YARAERELKPARIYGIGSLALY EKADIKGPEOK KKHLLIGVSSD RGLCGAHSSIAKQMKSEVATL TAAGKEVMLVGIGDKIRGILVR THSDQFLVAKEWGRKPPTFGD ASVIALBLLNSGYEFDEGSIFN KFRSVISYRTEEKPIFSLNTIVAS ADQHGVSMTDIDADVAAKITQ EYNIWANIILLTLWESTTSGG ESARG*QPWDGQARIAFWRM DLDNLDIWTFNR\TRQAVITKE
16937	47305	A	17041	1334	1790	LIEIISGAASSVKKENSAS
16938	47306	A	17041	1334	930	
16939	47307	A	17042	2	477	SGLGRLPGPWQEAGSSRGPSSG DMAGVKALVALSFSGAIGLTF/ LHMLGCALEDYGVYWPLFVLI FHAISSIPHEIAKRYTYDSDATIS SACRELAYFFTTGIVVSCI.WISP VILARVALIKIWGACGLIVLAIG NAVIFPYNSRGFSLYLGRGDDF SWEQW
16940	47308	Α	17044	130	434	1
16941	47309	Α	17045	1	1365	
16942	47310	Α	17046	656	839	
16943	47311	В	17047	16	149	

SEQ ID NO:	SEQ ID NO: of peptide		SEQ ID NO: in USSN	Nucleotide location of first		Amino acid sequence ( X=Unknown, *=Stop eodon, /=possible nucleotide
	sequence	liou	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
16944	47312	Α	17048	1	1317	MTLNEHAAFKHLFNKAHLAPP
						LIHLTLSGHSTCFREHRVGVICS
						HFAQDLWPEQGREDSFQKVILR
						RYEKCGHENLQLKIGCTNVDES
						LTYKRIHTGEKPCKCEECDKAF
		1				SKFSILTKHKVIHTGEKHYKCE
		1				ECGKAFTRSSSLIEHKRSHAGE
						KPYKCEECGKAFSKASTLTAHK
ŀ		1				TIHAGEKPYKCEECGKAFNRSS
		1				NLMEHKRIHTGEKPCKCEECG
					1	KAFGNFSTLTKHKVIHTGEKPY
l						KCEECGKAFSWPSSLTEHKRIH
		ŀ		l		AGDKPYKCEECGKTFKWSSTL
		l				TKHKIIHTGEKPYKCEECGKAF
		l				TTFSSLTKHKVIHTGEKHYKCE
		l				ECGKVFSWSSSLTTHKAIHAGE
	1					KLYKCEECGKAFKWSSRLSEH
1		l				KRIHTGEKPYKCEECGKAFSW
		l				VSVLNKHKKIHAGKKFYKCEE
		l			1	CGKDFNQSSHLTTHKRIHTG\E
		l				KPYKCEECGKAFSKASTLTAHK
	ł	l				TIHAGEKPYKCEECGKAFNRSS
		l				NLMEHKRIHTGEKPCKCEECG
		1				KAFGNFSTLTKHKVIHTGEKPY
		l				KCEECGKAFSWPSSLTEHKRIH
		ı				AGDKPYKCEECGKTFKWSSTL
		1	ľ			TKHKIIHTGEKPYKCEECGKAF
						TTFSSLTKHKVIHTGEKHYKCE
		l				ECGKVFSWSSSLTTHKAIHAGE
		1				KLYKCEECGKAFKWSSRLSEH
		1			l	KRIHTGEKPYKCEECGKAFSW
						VSVLNKHKKIHAGKKFYKCEE
16945	47313	Α	17049	2	2183	

SEQ ID	SEQ ID NO:	Mct	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
16946	47314	Α	17050	3	1440	IKVLLGENRVPNTMAVWLAQ
						WLGKGASLTSFPPCPTASLLRR
						LGEHIOOFOESSAOGLGLSLGP
	1					GAAALPKVGWLEQLLDPFNVS
					Į.	DRRSHL\QRYWVNDQHWVGQ
l						DGPIFLHLHLTSPPPTHTLFTGH
						PAALAPAWGALVISLEHRFYGL
						SIPAGGRLALSRLFNISSSSPWIC
	l l					FGGSYAGSLPSHHAPTF\PRAOR
						IS*HFRIPSSAVRPQVVSRSLMS
						TAIGGSLE/CRRWGLVRGGLGG
						KRGLGCOGRGGPA*VLADIASC
						FPOCRAAVSVAFAEVERRLRSG
						GAAQAALRTELSACGPLGRAE
	İ					NOAELLGALQALVGGVVQYD
1	l					GOTGAPLSVROLCGLLLGGGG
	1			ľ		NRRGGIYVLCMYIVP*IVLHSLG
İ						OKCLSFSRAETVAQLRSTEPQL
	1					SGVGEAPIYLAPSYPFFPGDTDP
	l					WHYLSYTOALGSSESTLLIRTG
l	ŀ				1	SHCLDMAPERPSDSPSLRLGRQ
	1					NIFQQLQTWLKLAKESQIKGEV
16947	47315	В	17051	41	2709	
16948	47316	Α	17052	874	1024	
16949	47317	Α	17053	1	1602	MDSLWGPGAGSHPFGVHNSRL
						SPDLCPGKIVLRALKESGAGMP
						EQDKDPRVQENPGDQRRVPEV
					i	TGDAPSAFRPLRDNGGLSPFVP
	1					GPGPLQTDLHAQRSEIRYDQSS
	1					QTSWTSSCTNRNAISSSYSSTGG
						LPGLKRRRGPASSHCQLTLSSS
	ŀ	1				KTVSEDRPQAVSSGHTQCEKV
	İ					AEKAPGQTLALRNDSSRSEASR
	1	1		İ		PSTRKFPLLPHRRGEPLMLPPPV
						ELGYRVTAEDLDWEKEAAFQC
		1			ŀ	IKSALQVEDKAISDCRPSRPSHT
		l			1	LSSLATGAS\DSAQVTSLIPAPFP
1		l			ŀ	AASMDAGMRRTRPGTSAPAAA
	l					AAAPPPSTLNRTLGSLLEWMEA
						LHISGPQPQLQQVPRGQNQRSQ
		1	1			TSRTSSCPK/LKCHLELLQLYGR
		1	1			PPGTKAEEAPASSHCQLTLSSSN
						TVSEDGPEAVSSGHTQCEKTAD
		1	1			TAPGOTLGPRGGSPRSQSSRPR
		ľ				RHKFPLLPRRRGEPLMLPPPLEL
		1				GYWVTAEDLDREKEAAFORIN
		i				SALOVEDKAISDCRPSRPSHTLS
		l				SLATGASGLPAISKAPSMDAQQ
		1				ERHKS
16950	47318	Α	17054	1	1155	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		l		sequence		
		Ļ.	17055		1237	MDSLWGPGAGSHPFGVHNTRL
16951	47319	Α	17055	1	1237	SPDLCPGKIVLRALKESGAGMP
		i			\	
		l				EQDKDPRVQENPGDQRRVPEV
		ľ				TGDAPSAFRPLRDNRGLSPFVP
		l				GPGPLQTDLHAQRSEIRYNQTS
1						QISWTSSCTNRNAISSSYSSMGG
		l	1			LPGLKRRRGPASSHCQLTLSSS
		1			1	KTVSEDRPQAVSSGHTQCEKA
		l				ADIAPGQTLALRNDSSTSEASRP
1						STHKFPLLPRRRGEPLML\PPSL
					1	EVGVPGSLVKELDREKEAAF\Q
Ì		1				RINSALQVEDKAISDCRPSWPS
i		ĺ				HTLSSLATGTSGLPAISKAPSMD
1		1				AQQETHKSQDCLGLLAPLASA
		1				AGVPSTAPMSGKKHRPPGPLFS
		l				SSDPLPATSSHSQDSAQVTSLIP APFPAASMDVGMRRTRRGEPL
						MLPPPLELGYRVTAEDLDQEKE
		1				
16952	47320	ļ.	17056	132	835	AAFQRIKSALQVEDKAI
	47321	A A	17057	132	2947	MPEODKDPRVQENPDDQRRVP
16953	4/321	A	17037	1'	2947	KVTGDARSAFRPLRDNGVLSPF
		l				VPRPGPLQTYLHAQRSEIRYNQ
	1					TSONTWTSSCTNONAISSSYSS
l						VGGLLGLKWRRGPAGQESGAG
	1					MPEQDK\DPRV\QQNPDDHRTV
	l .					PEVTGDARSAFWPLRDNGGLSP
		1				FVPRPGPLQTDLHAQSSEIRYN
						OTSOTSWTSSSTKRNAISSSYSS
		ŀ				TGGLPGLKQRRGPASSRCQLTL
						SYSKTVSEDRPQAVSSGHTRCE
		1				KAADTAPGOTLAPR
16954	47322	c	17058	229	624	ILUIDIM OQIDALK
16955	47323	Ā	17059	1	1011	MVSTPATLPSLPKPALMASWG
10700		ļ.,	1	1		VPYDOLTKEEKTRVWFTDGSA
		l				RYAGTTOKWTAVALOPLSRTS
1		1		l		LKDSSEGKSSOWAELQAVYLV
						VHFAWKEKWPDVGLYTDSWA
1						VANGLAGWSETWEKODWKIG
						DKEIWGRGMWMDLSEWSKAV
1						KIFVSHVSAHQRVTSAEEEFNN
			1			QVDRPL/PVFTQWAHEQSGHSG
1				l		RDGGYSWAQQT\GLPFTKADL
1			1	I		AMATAECPICQQQRPTLSPLYS
				l		TIPQGDQPATWWQIDYIGPLPS
	1			I	1	WKGOKFVLTVIDTYSRYRFAY
				l		PAHNASAKTTIHGLIECLIHCYG
				1		IPHSIASDQSIHF/TTKEVQ*WAH
1						AHGIHWSYHVSHHPEAAGL
16956	47324	В	17060	10	597	
16957	47325	В	17061	6	297	

16958   47326   Day	SEQ ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
16958   47326   B   17062   1   474							
16958   47326   D   17062   I   474		sequence		09/540,217		of peptide sequence	deletion, \=possible nucleotide insertion)
16962   47332					sequence		
16960   47328   B   17064   I   738	16958	47326	В	17062	1	474	
16960   47328   B   17064   I   738			A			2712	
16961	16960	47328	В	17064	1	738	
ESQQRPLGFWSKALPSSANNY    FFKRQLLACYWVLVEIEHLTM    GHQVTMRPELPIINCVLSDPCS    KVGHAQQHSIIKWRWYIHYQA    QAGPEGTSNLHEEVAQMITYSS    TSATLPSLFEFTQMALWEVPY    DQFTEERETQAWFTDGSAHY    GTT*KWTVAALQPLSRTTLKD    CEGKSPHHPVIAQWAHEQSGH    GGRGGTYLWAQHGFPLTKAN    GGRGGTYLWAQHGFPLTKAN    DLAMATAECPICQQQKRTLNP    DDAMATAECPICQQQKRTLNP    DLAMATAECPICQQQKRTLNP    TSATLPSLFSTANIYAELGSK     GGRGGTYLWAQHGFPLTKAN    RINKRRLMKTMKVEACEDLSA    KYLRIQLPTGSPRRRSEAPEVC    FQGSSFSLVHPPLLSYPSARR     PQTPPRPPRRIPSLHPLHPPSAC    FGGSSFSLVHPPLLSYPSARR     FOTPRPPPRIPSLHPLHPPSAC    FGGSSFSLVHPPLLSYPSARR     FOTPRPPRPRIPSLHPLHPPSAC    FGGSSFSLVHPPLLSYPSARR     FTRALGTIGGSSSCRQQRRPTI    WVESTTILTAWSKRLQQLGPW    LQVTVAGQVNTLAGIQKTHA    HCNVTERPPTGHEALAPPCEQ    GPPQVLDSNAVAPTADCOYQL   STAINKNQELCGRRPAVSPSRK    ISPGSPILRPAVHPGHYCLQQR    SGGKSNRTTTGKSFGKLHVX    GTDASEELLFTKASLAVSTSVF    QPSTAKTPGHWMASATDLFYC    DPFAFPGGGPTLSLEGGPSVIL    GTDASEELLFTKASLAVSTSVF    QPSTGKIYTEWVQKNKSFSLS    HPTYPMASPVKGKHSTSLLQ    LNYRDRWQCLQEGAGLALS, HMKVPTGSKEPQAGKLPSK    HPTYPMASPVKGKHSTSLLQ    LNYRDRWQCLQEGAGLALS, HMKVPTGSKEPQAGKLPSK    GGKASPROPFRYSRDSKRRPP    HGEVGTVFTINKGGS9PATST    WEVQSACQKAPEAGFTPPST.   GDAGANALRQESEGNWGSE    KSPHVAEAGSWRPQCSCCHHI    HPPDKTKDAARKTHSPGDNGC    QPRPPRCKTLWSLSRI			A	17065	3	772	DPADPMVLEVSEADRDA\VPIS
FFKROLLACYWVLVEIEHLTM   GHQVTMRPELPIINCVLSDPCS   KVGHAQQHSIIKWRW1HYQQ   QAGPEGTSNLHEEVAQMPTVS   TSATLPSLPEFTGMALWEVPY   DQFTEEEKTGAWFTDGSAHY   GTT*KWTVAALQPLSRTTLKD   CEGKSPHHPVIAQWAHEQSGH   GGRDGGYLWAQQHGPLTKA   DLAMATAECPCQQKRTLNB   DLAMATAECPCQQKRTLNB   DLAMATAECPCQQKRTLNB   DLAMATAECPCQQKRTLNB   CEGKSPHHPVIAQWAHEQSGH   SRNKRRLMKTMKVEACEDLSA   KYLRIQLPTGSRRRSEAPEVC   FQGSSFSLVHPPPLLSYPSARR   PQTPPRPPPRIPELPHPSALV   PATRICAL   PATRICAL   CHARLES   PATRICAL   CHARLES   CANCEL   CHARLES   CANCEL   CHARLES   CANCEL   CHARLES   CANCEL   CHARLES   CANCEL   CHARLES   CANCEL   CHARLES   CANCEL   CHARLES   CANCEL   CHARLES   CANCEL   CHARLES   CANCEL   CHARLES   CANCEL   CHARLES   CANCEL   CHARLES   CANCEL   CHARLES   CANCEL	1.07.1						ESQQRPLGFWSKALPSSANNYS
KVGHAQQHSIIKWRWVIHYQQ QAGPGGTSNLHEEVAQMPTVS TSATLPSLPEPTQMALIWEVPY DQFTEEEKTGAWFTDGSAHY GTT*RWTVAALQPLSRT*LAD CEGKSPHHPVIAQWAHEQSGH GGRDGGYLWAQQHGFPLTKA DLAMATAECPICQQQKRTLNP   16962   47330   A   17067   1667   2012   LSPHWPFGLPFSALIVAFLGRS: RINKRRLMKTMKVEACEDLSA KYLRIQLPTGSPRRRSEAPEVC FGGSSFSLYHPPPLLSYPSARR POTPPRPPRPRISHESHEHLPIPSAC   VEPTILLTAWSFRLQGIGKTHA HCNVTERPPTGHEALAPPCEQ GPPQVLDSNAVAFTADCCYQ STAINRNQELCGRKPAVPSKR ISPGSPILRPAVHPGHYCLQGR SGQKSNRRTTQKSFQKLHVDK RKPENFSKESDHLLIVSREGNP VASLATPPGIWMMSATDLFYC DPFAFPGGGFTLSLERGPSVII GTDASELLFTKASLAVSTSVY QFSTGKIYTEWVWQKNKSFLS HFPTKPMASPVKGKHSTSLQI LLYYRDRWCLGCGGGALLIVSREGNP VASLATPPGIWMSATDLFYC DPFAFPGGGFTLSLERGPSVII GTDASELLFTKASLAVSTSVY QFSTGKIYTEWVWQKNKSFLS HFPTKPMASPVKGKHSTSLQI LLYYRDRWCLGCGGGALLIVS RKQPCHFTKSLASLAVSTSVY QFSTGKIYTEWVWQKNKSFLS HFPTKPMASPVKGKHSTSLQI LLYYRDRWCLGCGGGALLIS HMKVPTGSKEPQQAGKLPSKP RKQTTPFFKD   CSACPVSHPWLLPWQSGSAFS  PRALQRPPQHGHRLSKPMQSI RISVYLLPRWPRRP,PTDLLYPP TRGHIHLHDRHIGAPSVSRW GDKASPPQPFRYSRDSK/RRPP HGEVGTVFTNKGGQSPATSI WEVQSACQKAPEAGFTPST. GDAEGANALRGESEGNWGSE KSPHVAEAGSWRPQQSGCHH HPPDKTKDAARKTHSPEDDIGC QPRPPRCKTLWSLSRI		1			l		FFKROLLACYWVLVEIEHLTM
QAGPEGTSNLHEEVAQMPTVS							GHQVTMRPELPIINCVLSDPCSH
TSATLPSLPEFTOMALWEVPY					l		KVGHAQQHSIIKWRWYIHYQA
DQCFTEEEKTGAWFTDGSAHY					1		QAGPEGTSNLHEEVAQMPTVS
GTTYKWTVAALQPLSRTTLKD		Ì					TSATLPSLPEPTQMAL\WEVPY
CEGKSPHHPVIAQWAHEQSGH							D\OFTEEEKTGAWFTDGSAHYT
GGRDGYTLWAQOHGFPLTKA				i			GTT*KWTVAALQPLSRTTLKDS
16962					1		CEGKSPHHPVIAQWAHEQSGH
16962   47330   A   17067   1667   2012   LEPHWPFOLPPSALIVAFIGRS: RNKRRLMKTMKVEACEDLSA KYLRIQLPTGSPRRSEAPEVC FQGSSFSLVHPPPLLSYPSARR POTTPRPPPRHISHELPHEPSAC.   16963   47331   A   17068   5   1074   RISALGTGGSSSCRQQRRDT WVPETTILTAWSS/RLQQLGPW LQVTVAGQVNTLAGIQKTHAA HCNVTERPPTGHEALAPPCEQ GPPQVLDSNAVAFTADCGYQL STAINRNQELCGREAVSPSK/ISPGSPILRPAVHPGHYCLQQRI SGQKSNRRTTQKSFQKLHVVK RKPENFSKESDHLLIVSREGNP VASLATPPGIWMMSATDLFYC DPFAPPGGGPTLSLERQPSVIL GTDASEELLFTKASLAVSTSVF QPSTGKIYTEWWWQKNKSTLLY GPTASEVELFTKASLAVSTSVF QPSTGKIYTEWWWQKNKSTSLLQ LAYYRDRWCLGCGGGALLLS HMKVPTGSKEPQAGKLPSKF RKQTTPTFKD   16964   47332   A   17069   2   699   CSACPVSHPVLPWQSGSAFSI PPRALQRPQHGHRLSKPMOSI RISVYLLPRWFRRP, PTDLLYPP TGGHIHLIDRHGAPSVSRW GDKASPPQFFYSRDSK/RRPPGHGEVGTVFTINKGGQSPATSI WEWQSACQKAPEAGFTPPST. GDAEGANALRQESEGGNWGSE KSPHVAEAGSWRPQQSGCHHI HPPDKTKDAARKTHSPGDDGC QPRPPRCKTLWSLSRI							GGRDGGYLWAQQHGFPLTKA
RNKRRLMKTMKVEACEDLSA KYLRIQLPTGSPRRRSEAPEVC FCQSSFSLVHPPILSYPSARR FCQSSFSLVHPPILSYPSARR POTPPRPPRPRIFISLHPLHPPSAC RHSALGTIGGSSCRQORPROT WVESTILTAGICKTHA HCNVTERPPTGHEALAPPCEQ GPPQVLDSNAVAPTADCGYQL STAINKNQELCGKRPAVSPSKY ISPGSPILRPAVHPGHYCLQQR SGQKSNRRTTQKSFGKLHVOK RKPENFSKESDHLLIYSRGNP VASLATPPGIWMMSATDLFYC DPFAPGGPFTLSLERGPSVIII GTDASEELLFTKASLAVSTSVF QRSTGKIYTEWVQKNKSFLS HPPTKPMASPVKGKHSTSLQ LNYRDRWQCLQEGAGLALS, HMKVPTGSKEPQQAGKLPSK RKQTTPTFKD  16964 47332 A 17069 2 G99 CSACPVSHPWLPWQSGSAFSI PRALQRPQHCHGLSKPMQSI RISVYLRPWPRRP,PTOLLYPP TRGHIHLHDRHHGAPSVSRRW GDKASPQPFRYSRDSKRRPP HGEVGTVFTNKGGS9PATSI WEVQSACQKAPEAGFTPST. GDAEGANALRGGSSCHHI HPPDKTKDAARKTHSPGDNGC QPRPPRCKTLWSLSR	i						DLAMATAECPICQQQKRTLNP
RNIKRRLMKTMKVEACEDLSA KYLRIQL PTOSPRRSBAPEVO FQGSSFSLVHPPPLLSYPSARR PQTPPRPPRRISHELHPLHPPSAC FQGSSFSLVHPPPLLSYPSARR PQTPPRPPRRISHELHPPSAC RHSALGTIGGSSSCRQQRPROT WVESTILLTAGIGKTIHA HCNVTERPPTGHEALAPPCEQ GPPQVLDQNTAAGICKTIHA HCNVTERPPTGHEALAPPCEQ GPPQVLDSNAVAPTADCCYQL STAINKNQELCGRKPAVSPSRK ISPGSPILRPAVHPGHYCLQQRI SGGSKSNRTTINSFGKLHVOK RKPENFSKESDHLLIYSREGNP VASLATPPGIWMMSATDLFYG DPFAFPGGGFFTLSLERGPSVIL GTDASEELLFTKASLAVSTSVF QFSTGKIYTEWVQKNKSFLS HFPTKPMASPVSGKHSTSLQI LNYRDRWCLLGGGGGLALLS HMKVPTGSKEPQQAGKLPSKP RKQTTPTFKD  16964 47332 A 17069 2 G99 CSACPVSHPWLLPWQSGSAFSI PRALQRPPQHGHRLSKPMOSI RLSVLLRPWPRRP, PTDLLYP TRGHIHLHDRHHGAPSVSRRW GDKASPPQFRYSRDSKRRPP HGEVGTVFTINKGGSPATST WEVQSACQKAPEAGFTPST. GDAGGANALRGGSSGHHI HPPDKTKDAARKTHSPGDDGC QPRPPRRCKIL WSLSRI	16962	47330	A	17067	1667	2012	LSPHWPPGLPPSALIYAFLGRSS
FQQSSIESL VHPPPLLSYPSARR   PQTPPRPPPRHPSL VHPPLSAC     16963   47331   A   17068   5   1074   RHSALGTGGSSCRQQRPRT     WVPETTILTAWSSRLQQLGPW   LQVTVAGQVNTLAGIQKTIHA     HCNVTERPPTGHEALAPPCEQ   GPPQVLDSNA VAPTADCCYQL     STAINRNQELCGRKPAVSPSR   ISPGSPILRPAVHPGHYCLQQRI     SGQKSNRRTTQKSFQKLHVDW   RKPENFSKESDHLLIYSREGNP     VASLATPPGIWWMSATDLFYQ     GTDASEELLFTKASLAVSTSVF     QFSTGKIYTEWVQKNSKSIS.     HPPTKPMASPVKGKHSTSILQL     LNYRDRWQCLQEGAGIALLS     HMKVPTGSKEPQQAGKLPSKP     RKQTTPTFKD     GSACPVSHPWLLPWQSGSAFS     PRALQRPQHGHRLSKPMOSI     RISVYLRPWPRRP.PTDLLYP     TRGHIHLIDRHHGAPSVSRW     GGKASPQPPRYSRDSK/RRPP     HGEVGTVFTNNKGGQSPATS     WEVQSACQKAPEAGFTPPST     GDAGANALRQESEGNWGSE     KSPHVAEAGSWRPQGSCHHI     HPPDKTKDAARKTHSPGDDGC     QPRPPRCKILWSLSRI			1				RNKRRLMKTMKVEACEDLSAP
POTPREPPRIESLIPLIPESAGE						i	KYLRIQLPTGSPRRRSEAPEVCI
16963 47331 A 17068 5 1074 RIBALGTIGGSSSCRQQRRDT WVPETTILTAWSS/RLQQLGPW LQVTVAGQVNTLAGIQKTIHA HCNVTERPPTGHEALAPPCEQ GPPQVLDSNAVAFTADCGYQL STAINRNQELCGREAVSPSK/ ISPGSPILRPAVHPGHYCLQQRI SQGKSNRRTTIQKSFGKLHVVK RKPENFSKESDHLLIVSREGNP VASLATPPGIWMMSATDLFYC DPFAFPGGGFTLSLERGPSVIL GTDASEELLFTKASLAVSTSVF QPSTGKIYTEWVWQKNKSTSL-V LPTYRDRWCLGEGGGLALLS, HMKVPTGSKEPQAGKLFSKP RKQTTPTFKD CSACPVSHPWLPWQSGSAFSI PFRALQRPQHGHRLSKPMOSI RISVYLRPWPRRP,PTOLLYPP TGGHHLHDRHGAPSVSRW GDKASPPQFFRYSRDSK/RRPPG HGEVGTVFTNNKGGQSPATSI WEVQSAEQQKAPEAGFTPPST. GDAEGANALRQESEGGNWGSE KSPHVAEAGSWRPQGSCHHI HPPDKTKDAARKTHSPGDDGC QPRPPRCKTLWSLSRI			ŀ				FQGSS\FSLVHPPPLLSYPSARR*
WYETTILTAWSS/RLQQLGPW LQV/TVAGQVNTLAGIQKTHA HCNVTERPPTGHEALAPPCEQ GPPQVLDSNAVAPTADCGYQL STAINR/GELCGREPAVSPSRA' ISPGSPILRPAVHPGHYCLQQRI SQQKSNRRTTQKSFQKLHVDK RKPENFSKESDHLLYNSEGRPW VASLATPPGIWMMSATDLFYC DPFAFPGGGFTLSLERGPSVIL GTDASEELLFTKASLAVSTSYF QFSTCKIYTEWVWQKNKSFLS HPFTFMASSPVKGKHISTSLQ) LNYRDRWQCLQEGAGLALLS, HMKVPTGSKEPQAGKLPSKP RKQTTPFFKD GSVGKHISTSLQ) FRACUTPFFKD STAINLPWPRRPLPULTVYP TRGHIHLHDRHIGAPSVSRW GDKASPPOPRYSRDSKRRPP HGEVGTVFTNKGGQS/PATSI WEVQSAEQGKAPSAFST WEVQSAEQGKAPSAFST GDAGGANALRGSSEGNWGSE KSPHVAEAGSWRPQGSCHHI HPPDKTKDAARKTHSPGDDGC QPRPPRCKTLWSLSRI		i					PQTPPRPPPRHPSLHPLHPPSAQ
LQVTVAGQVNTLAGIQKTIHA HCNVTERPPTGHEALAPPCEQ GPPQVLDSNAVAPTADCGYQL STAINRNQELCGRKPAVSPSK/ ISPGSPILRPAVHPGHYCLQORI SGQKSNRRTTQKSFQKLHVDK RKPENFSKESDHLLIVSREGNP VASLATPPGIWMMSATDLFYC DPFAFPGGFTLSLERGPSVIL GTDASELLETKASLAVSTSVY QFSTGKIYTEWVWQKNKSFLS HFPTKPMASPVKGKHSTSLQI LMYRDRWCLQEGAGLALLS, HMKVPTGSKEPQQAGKLPSKP RKQTTPFKD I6964 47332 A 17069 2 699 CSACPVSHPWLLPWQSGSAFSI PRALQRPPQHGHRLSKPMOSI RISVYLLPPWRRPLPTDLLYPP TRGHIHLIDRHHGAPSVSRW GDKASPPQPFRYSRDSK/RRPP HGEVGTVFTNKGGQSPATSI WEVQSACQKAPEAGFTPPST. GDAEGANALRGESEGNWGSE KSPHVAEAGSWRPQGSGHHI HPPDKTKDAARKTHSPGDDGC QPRPPRCKTLWSLSRI	16963	47331	Α	17068	5	1074	RHSALGTGGSSSCRQQRPRDT
HCNYTERPPTGHEALAPPCEQ GPPQVLDSNAVAPTADCGYQL STAINRNQELCGRKPAVYPRSK ISPGSPILRPAVHPGHYCLQQRI SGGKSNRRTTGKSFGKLHVDK RKPENFSKESDHLLIYSREGNP VASLATPPGIWMMSATDLFYQ DPFAFPGGGPFTLSLERGPSVIL GTDASEELLFTKASLAVSTSVF QFSTGKIYTEWVQKNSKFISL HPFTKPMASPVKGKHSTSLLQ LNYRDRWCLQLGGAGLALLS, HMKVPTGSKEPQQAGKLPSKP RKQTTPTFKD  16964 47332 A 17069 2 699 CSACPVSHPWLLPWQSGSAFSI PFALQRPPQHGHRLSKPMQSI RISVYLRPWPRRP_PTDLLYPP TRGHIHLHDRHHGAPSVSRW GGNASPQPPRYSRDSKRRPP HGEVGTVFTNNKGGSPPATSI WEVQSAEQGKAPEAGFTPPST. GDAEGANALRGGSSGHHI HPPDKTKDAARKTHSPGDDGC QPRPPRCKTLWSLSRI		İ					WVPETTILTAWSS/RLQQLGPW
GPPQVLDSNAVAPTADCGYQI STAINRNQELCGRKPAVSPSR/I ISPGSPILRPAVHPGHYCLQQBI SGGKSNRRTTQKSFQKLHVDK RKPENFSKESDHLLYSREGMY VASLATPPGIWMMSATDLFYG DPFAFPGGFFTLSLERGPSVIL GTDASEELLFTKSLAVSTSVY QFSTGKIYTEWVWQKNKSFLS HFPTKPMASPVKGKHSTSLQI LLYYRDRWCQLQEGAGLALLS, HMKVPTGSKEPQQAGKLPSKP RKCYTPFFKD  47332 A 17069 2 699 CSACPVSHPWLLPWQSGSAFSI PRALQRPPQHGHRLSKPMQSI RI.SVLLRPWPRRPLPIDLLYP TRGHIHLHDRHHGAPSVSRW GDKASPPOPRYSRDSKRRPP HGEVGTVFTNKGGQSPATSI WEVQSACQKAPEAGFTPPST. GDAGANALRGESEGNWGSE KSPHVAEAGSWRPQQGSCHHI HPPDKTKDAARKTHSPGDDGC QPRPPRCKTLWSLSRI			l				LQVTVAGQVNTLAGIQKTIHAE
STANIRNOELCGRKPAVSPSK/ ISPGSPILRPAVHPGHYCLQQRI SGQKSNRRTTQKSFGKLHVVK RKPENFSKESDHLLIYSREGNP VASALTPPGIWMMSATDLFYC DPFAPFGGGFTLSLERGPSVIL GTDASEELLFTKASLAVSTSVF QFSTGKIYTEWVWQKNKSFLS HFPTKPMASPVKGKHSTSLLQ) LNYYRDRWCLQEGGGLALLS HMKVPTGSKEPQAGKLPSKP RKQTTPTFKD 2 699 CSACPVSHPVLLPWQSGSAFSI P*RALQRPQHGHRLSKPMOSI RISVYLRPWFRRP*PTDLTV*P TGGHHLHDRHGAPSVSRW GDKASPPQFFYSRDSK/RRPP HGEVGTVFTNNKGGQSPATSI WEVQSACQKAPEAGFTPFST. GDAGGANALRGESEGNWGSE KSPHVAEAGSWRPQGSGHHI HPPDKTKDAARKTHSPGDDGC QPRPPRCKTLWSLSRI			Į.				HCNVTE\RPPTGHEALAPPCEQ
ISPGSPILRPAVHPGHYCLQOR SGQKSNRRTTQKSFQKLHVDK RRPENFSKESDHLLVTSREGMP VASLATPPGIWMMSATDLFYC DPFAPGGPFTLSLERGPSVII GTDASEELLFTKASLAVSTSVF QRSTCKITYTEWVWQKNKSFLS HPPTFPMASPYCKGHISTILD) LNYRDRWQCLQEGAGLALLS, HMKVFTGSKEPQAGLALLS, HMKVFTGSKEPQAGKLPSKP RKQTTPTFKD  699 CSACPVSHPWLLPWQSGSAFSI P*RALQRPPGHGRLSKPMQSI RLSVLLRPWPRRPLPTDLLYP* TRGHIHLHDRHIGAPSVSRW GDKASPPOFRYSIDSVRRPP* HGEVGTVFTNNKGGQS/PATSI WEVQSAEQKAPEAGFTPPST. GDAEGANALRGESEGNWGSE KSPHVAEAGSWRPQQGSCHHI HPPDKTKDAARKTHSPEDDGC QPRPPRFCKTLWSLSRI	1		l				GPPQVLDSNAVAPTADCGYQL
SGGKSNRRTTOKSFOKLHVDK RKPENFSKESDHLLIYSREGNP VASLATPPGIWMMSATDLFYC DPFAFPGGFFTLSLERGPSVII. GTDASELLFTKASLAVSTSVF QFSTGKIYTEWVWQKNKSFLS HFPTKPMASPVKGKISTSILQI LLYYRDRWQCLQGAGLALLSV, HMKVPTGSKEPQQAGKLPSKP RKQTTPFTKD  47332 A 17069 2 699 CSACPVSHPWLLPWQSGSAFSI PRALQRPPQHGHRLSKPMQSI RISVYLLPRWPRRP,FTDLLYPP TRGHIHLHDRHHGAPSVSRW GDKASPPQPFRYSRDSK/RRPP HGEVGTVFTNNKGGQSPATSI WEVQSACQKAPEAGFTPPST. GDAGGANALRGESEGNWGSE KSPHVAEAGSWRPQGSGHHI HPPDKTKDAARKTHSPGDDGC QPRPPRCKTLWSLSRI							STAINRNQELCGRKPAVSPSR/G
RRPENFSKESDHLLIYSREGNP VASLATPRGIWMMSATDLFYG DPFAFPGGOFFTLSLERGPSVIL GTDASEELLFTKASLAVSTSVF QFSTGKIYTEWVQKNSKFLS HFFTKPMASPVKGKHSTSLLQ LNYRDRWCLQLOGAGLALLS, HMKVPTGSKEPQQAGKLPSKP RKQTTFTTKD  2 699 CSACPVSHPWLLPWQSGSAFSI P*RALQRPQHGHRLSKPMQSI RISVYLRPWFRRP, PTDLLY*P TRGHIHLHDRHHGAPSVSRRW GGNASPQFFRYSRDSKRRPP HGEVGTVFTINKGGS9PATSI WEVQSACQKAPEAG*FTPSTL GDAGANALRGGSEGNWGSE KSPHVAEAGSWRPQGSCHHI HPPDKTKDAARKTHSPGDDGC QPRPPRCKTL WSLSRI			1				ISPGSPILRPAVHPGHYCLQQRL
VASLATPPGIWAMSATDLFYC DPFAFOGGPFTLSLERGPSVIL GTDASEELLFTKASLAYSTSVF QFSTCKIYTEWVWQKNKSFLS HPFTFMASPVKGKHISTSLQ) LNYRDRWQCLQEGAGLALLS, HMKVPTGSKEPQAGKLPSKP RKQTTPFFKD  699 CSACPVSHPWLLPWQSGSAFS P*RALQRPPQHGHRLSKPMQSI RI.SVLLRPWPRRPLPTDLLY*P TRGHIHLHDRHIGAPSVSRW GDKASPPOPFRYSIDSVRRPP HGEVGTVFTNKGGQS/PATSI WEVQSACQKAPEAGFTPPST. GDAGANALRGESEGNWGSE KSPHVAEAGSWRPQQGSCHHI HPPDKTKDAARKTHSPGDDGC QPRPPRCKTLWSLSRI							SGQKSNRRTTQKSFQKLHVDK
DPFAPGGGPTLSLERGPSVII. GTDASEELLPTKASLAVSTSVF QPSTGKIYTEWVWQKNSKSIS. HPPTKPMASPVKGKHSTSLLQ) LNYNDRWGCLQEGGGLALLS. HMKVPTGSKEPQQAGKLPSKP RKQTTPTFKD  2 699 CSACPVSHPWLLPWQSGSAFSI P*RALQRPQHGHRLSKPMOSI RISVYLRPWPREP,PTOLLY*P TRGHIHLHDRHGAPSVSRW GDKASPPQFPRYSRDSK/RRPP HGEVGTVFTNNKGGQSPATSI WEVQSACQKAPEAGPTPPST. GDAGANALRQESEGGNWGSE KSPHVAEAGSWRPQGSGHHI HPPDKTKDAARKTHSPGDDGC QPRPPRCKTLWSLSRI	1		1				RKPENFSKESDHLLIYSREGNPD
GTDASEELLFTKASLAVSTSVF QRSTGKIYTEWVWQKNKSFLS HFPTKPMASPVKGKHSTSLLQ) LNYRDRWQCLQEGAGLALLS, HMKVPTGSKEPQAGKLPSKP RKQTTPTFKD  16964 47332 A 17069 2 699 CSACPVSHPWLLPWQSGSAFSI P*RALQRPPOHRLSKPMQSI RLSVLLRPWPRRPLPTDLLY*P TRGHIHLHDRHIGAPSVSRW GDKASPPOFPRYSDSKRRPP HGEVGTVFTNNKGGQSPATSI WEVQSACQKAPEAGPTPPST. GDAEGANALRGESEGNWGSE, KSPHVAEAGSWRPQQSSCHHI HPPDKTKDAARKTHSPEDDNGC QPRPPRFCKTLWSLSRI			1				VASLATPPGIWMMSATDLFYG
QFSTGKIYTEWVWQKNKSFLS HFPTKPMASPVKGKHSTSLQI LNYRDRWQCLQEGAGLALLS, HMKVPTGSKEPQQAGKLPSKP RKQTTPTFKD  47332 A 17069 2 699 CSACPVSHPWLLPWQSGSAFSI P*RALQRPQHGHRLSKPMQSI RISVYLLRPWRFRP,PTDLLYP* TRGHIHLHDRHHGAPSVSRW GDKASPQPFRYSRDSK/RRPP HGEVGTVFTNNKGGQSPATSI WEVQSACQKAPEAGFTPPST. GDAEGANALRGESEGNWGSE KSPHVAEAGSWRPQGSGHHI HPPDKTKDAARKTHSPGDDGC QPRPPRCKTLWSLSRI							DPFAFPGGGPFTLSLERGPSVIL
HPFTKPMASPVRGKHISTSLLQI LNYRDRWQCLQEGAGLALS, HMKVPTGSKEPQQAGKLPSKP RKQTTPTFKD  CSACPVSHPWLLPWQSGSAFSI P*RALQRPQHGHRLSKPMQSI RISVYLRPWPRRP,PTDLLYP* TRGHIHLHDRHHGAPSVSRRW GDKASPQFPRYSRDSK/RRPP HGEVGTVFINKGGGS/PATSI WEVQSAEQUKAPEAGFTPPST. GDAEGANALRQESEGNWGSE KSPHVAEAGSWRPQGSGHHI HPPDKTKDAARKTHSPGDNGC QPRPPRCKTL WSLSR!			ı				GTDASEELLFTKASLAVSTSVF
LNYRDRWQCLQEGAGLALLS, HMKVPTGKEPQQAGKLPSKP RKQTTPTFKD  16964 47332 A 17069 2 699 CSACPVSHPWLLPWQSGSAFSI P*RALQRPPQHGHRLSKPMQSI RLSVLLRPWPRRPLPTDLLYP* TRGHIHL-HDRHHGAPSVSRW GDKASPPQFRFXSDSK/RRPP HGEVGTVFTNNKGGQS/PATSI WEVQSACQKAPEAGFTPPST. GDAGANALRGESEGGNWGSE KSPHVAEAGSWRPQQSGCHHI HPPDKTKDAARKTHSPGDNGC QPRPPRFCKTLWSLSRI			l				QFSTGKIYTEWVWQKNKSFLSP
HMKVPTGSKEPQAGKLPSKP RKQTTPTKD  16964 47332 A 17069 2 699 CSACPVSHPWLLPWQSGSAFSI P*RALQRPQHCHRLSKPMOSI RISV*LLRPWRFRP,PTOLLYP* TRGHIHL.HDRHHGAPSVSRW GDKASPQFPRYSRDSK/RRPP HGEVGTVFTNNKGGQSPATSI WEVQSAEQQKAPEAGFTPPST. GDAEGANALRQESEGNWGSE KSPHVAEAGSWRPQGSCHHI HPPDKTKDAARKTHSPEDDNGC QPRPPRCKTLWSLSRI			1				HFPTKPMASPVKGKHSTSLLQR
RKOTTPTEKD  16964 47332 A 17069 2 699 CSACPVSHPWLLPWQSGSAFSI PPRALQRPPQHGHRLSKPMGSI RISVLLRPWPRRPLPTDLLY*P TRGHIHLHDRHHGAPSVSRRW GDKASPPQFPRYSRDSK/RRPP HGEVGTVFTNNKGGQSPATSI WEVQSAECQKAPEAGPTPPST. GDAEGANALRQESEGNWGSE. KSPHVAEAGSWRPQGSCHHI HPPDKTKDAARKTHSPEDDIG QPRPPRFCKTLWSLSRI	1		l				LNYRDRWQCLQEGAGLALLSA
16964 47332 A 17069 2 699 CSACPVSHPWLLPWQSGSAFSI PFRALQRPPQHGHRLSKPMQSI RI.SVLLRPWPRRPLPTDLLYPP TRGHIHLHDRHHGAPSVSRRW GDKASPPOPRFXSRDSKRRPP HGEVGTVFTNNKGGQSPATSI WEVQSACQKAPEAGFTPFST. GDAEGANALRGESEGNWGSE KSPHVAEAGSWRPQQSGCHHI HPPDKTKDAARKTHSPGDNGC QPRPPRCKTLWSLSRI			l	1			
P*RALQRPPQHGHRLSKPMQSI RI.SVLLRPWPRRPLPTDLLY*P TRGHIHL HDRHHGAPSVSRRW GDKASPPQFRYSRDSK/RRPP4 HGEVGTVFTINKGGQS/PATSI WEVQSAEQUKAPEAGFTPPST GDAEGANALRQESEGNWGSE KSPHVAEAGSWRPQQSCHHI HPPDXTKDAARKTHSPGDNGC QPRPPRPCKTLWSLSRI							
RISVL\RPWPRRPLPTDL\Y*P TRGHIHLHDRHIGAPSVSRRW GDKASPPOPFRYSRDSK/RRPP HGEVGTVFTNNKGGQ9PATSI WEVQSAECQKAPEAGPTPPST. GDAEGANALRQESEGNWGSE. KSPHVAEAGSWRPQQSCHHI HPPDKTKDAARKTHSPGDNGC QPRPPRRCKTLWSLSRI	16964	47332	Α	17069	2	699	
TRGHIHLHDRHHGAPSVRRW GDKASPPOPRYSRDSK/RRPPI HGEVGTVFINNKGGGS/PATSI WEVQSAEQKAPEAGFIPPST. GDAEGANALRGESEGNWGSE KSPHVAEAGSWRPQGSCHHI HPPDKTKDAARKTHSPGDNGC QPRPPRPCKTLWSLSRI			1				
GDKASPPQFPRYSRDSK/RRPPG HGEVGTVFTNNKGGQSPATSI WEVQSAEQQKAPEGAFPPST GDAEGANALRQESEGNWGSE KSPHVAEAGSWRPQQSSCHHI HPPDKTKDAARKTHSPGDNGC QPRPPRPCKTL WSLSRI			1				
HGEVGTVFTNNKGGQS/PATST WEV QSAECQKAPEAGFTPPST. GDAEGANALROESEGNWGSE KSPHVAEAGSWRPQQSCHHI HPPDKTKDAARKTHSPEDDNGC QPRPPRFCKTLWSLSRI	l		1				
WEVQSAECQKAPEAGPTPPST. GDAEGANALRGESEGNWGSE. KSPHVAEAGSWRPQQGSCHHL HPPDKTKDAAKTHSPGDNGC QPRPPRPCKTLWSLSRI	1		1				
GDAEGANALRQESEGNWGSE. KSPHVAEAGSWRPQQSSCHHI HPPDKTKDAARKTHSPGDNGC QPRPPRPCKTLWSLSRI			1			1	
KSPHVAEAGSWRPOQOSCHHI HPPDKTKDAARKTHSPGDNGC QPRPPRCKTL WSLSRI					l	I	
HPPDKTKDAARKTHSPGDNGC QPRPPRPCKTLWSLSRI						1	GDAEGANALRQESEGNWGSEA
QPRPPRPCKTLWSLSRI	1				1		KSPHVAEAGSWRPQQGSCHHL
					1	1	HPPDKTKDAARKTHSPGDNGC
16965 47333 A 17070 223 1611	L		L				QPRPPRPCKTLWSLSRI
	16965						
16966 47334 A 17071 12 310	16966	47334	Α	17071	12	310	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
16967	47335	A	17072	31	430	LQAVRLFTLPTTSSGL*KLRTVP
10907	41333	l^	17072	13.	1730	TWPSPPSCFPHFOSGPRTTRAPT
		1				PSTINGSGYSGSYSGPPSLCPRTS
		1			ŀ	RRAPPRHRVPAGRERI.HIRVPP
		1			i	YPRPERHLLRVSRRGILGNNRV
1	l	1				
	ļ	ļ.		ļ		GRLPESRAIAGRKEEKTDTK
16968	47336	Λ	17073	1	474	
16969	47337	Α	17074	153	1224	RVFSESVCSPVRNLEFLWRFAF
		1	1			PLAPAGRCPPGVPLQTSPRDTD
					l .	AHRSSPLPPARASPGQVAAAYR
		1	1			WARCPGCGGRKPRSSGSWQLC
	1		1	İ		RCPTLPPPPRGSRSSGRC/RTWP
				1		SPPSCFPHFQSGPRTTRAPTPSTI\
		1				PGYSGSYSSGPGR*GLSPLHAA/
						VSPPLPPGGP*GSWARAGLGSI
		1			l .	ASAHSPCPLCRSLIRSRS*QTCT
1		1				RSPT*NCEVPPSAP*AASPLRTM
		1			l	FALVRTAGLKVHLLPLGYCTT
		1				MS*SSSMPQTVPVVVKVSNIPS
i i				1		VHPP*PCCKDCTISRSRSIFTRSPI
		1				CNPPGFLLPFCSPSTGO*SL*KEP
		1				PLASWTHFRSDVLLLFSVSMNG
		1				STLSLGCPSOKAVIALVOVT
16970	47338	A	17075	215	1246	OTESEGEI SQUETTIAE TQTT
16971	47339	A	17076	566	675	OPCROO/CLOPGSPPRFHARTLT
10771	7/337	l^	17070	1500	l <sup>0</sup> /3	VTLVHTRTHTHAHAH
16972	47340	A	17077	184	584	VIEVIIIKIIIIIAIIAII
16973	47341	A	17078	1	1167	
16974	47341	A	17079	849	2266	
16974	47342	A	17080	1505	1891	DAEKAFDEIQQ/PFMIKILSRISI
16975	4/343	I <sup>A</sup>	1 /080	1505	1891	
1		1				QGTYLNVIKTIYDKPTANTILN
1		1				VEKLKTFPLRTGTRQGCPLSAL
ł		1			i	LFNMVLEVIARAIRQEKGIKGIQ
ł		1				ISKKEVKLSLFADDMIVHIENPK
		_				DSSRKLLELIKEFSKV
16976	47344	Α	17081	1	842	
16977	47345	Α	17082	155	531	GNLWSVDLRPGTPLRQNFRGTI
l		1				RQQHSRFTKNHCSQTPLLIPRQ
l				i		TGSGVDLSKLQQTCS*GSCLVC
1		1				TIDLANAFFSIPVHKA/HQKQFA
		1				FSWQ\YTFTVLPRLTWLQPC*V
1	1	1				PNLPAAETNTEPSNGT
16978	47346	A	17083	1	1773	
16979	47347	В	17084	598	1428	
16980	47348	A	17085	3	227	
16981	47349	A	17086	li -	207	
10701	7/347	ı^_	1,000	1.	1207	L

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleatide togetion of tast	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1.0.	sequence	1100	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	,			sequence		
16982	47350	Α	17087	1	789	RDLQPFTSVTVHCRKGNDQTF
						GGPLDAGSELTLIPGDPKHHCG
						PPVKVGAYGGQVINGVLA\HPL
						IWLVQKTDGS/WRMTVDYCKL
		1				NOVVIPIAAAVSDVVSLLEQINT
		İ	l			SPGTWYAAIDLANAFFSIPVHK
		1			1	AQOKOFAFSWOGOQYTFTVLP
		1	İ			OWYINSPALCHNLIRRDLDCFS
		l				LPLDITLVHYIDDIMLIGSSEQE
		1			1	
		ı				VANTLDLFVRHLRARGWEINPT
1		l			i	KIQGPSTSVKFLGFQWCGACQA
		<u> </u>				IPSKMRDKLLHLVPPTTKKEAQ
16983	47351	Α	17088	1	435	
16984	47352	A	17089	2	808	PLIWLVQKTDGS/WRMTVDYC
		1		\		KLNQVVIPIAAAVSDVVSLLEQI
		ł				NTSPGTWYAAIDLANAFFSIPV
1	l	ŀ		ł		HKAQQKQFAFSWQGQQYTFTV
		1			l	LPQWYINSPALCHNLIRRDLDC
		ı				FSLPLDITLVHYIDDIMLIGSSEQ
	1	1				EVANTLDLFVRHLRARGWEINP
		l				TKIQGPSTSVKFLGFQWCGACQ
1		l				AIPSKMRDKLLHLVPPTTKKEA
		l				QCL\QLLACY/WALVETEHLTIS
		l				HOVTMRPELPIMNWVLFDPSSH
		İ			1	KVGCAQQHSIIKWKWYVHDW
						ARAGPEGT
16985	47353	A	17090	2	544	AKAGIZOT
16986	47354	A	17090	1	633	MTVDYRKFNOVVTPMAA/AVP
10,00	47334	<u>۱</u> ^	17031	l'	033	DAVSLLEQINTFPGTWYAAIDL
		1			1	ANAFFSIPVHEAHOKOFAF\LPO
		1				GYINFPALCHNLIRRELDFFLLL
					I	QDITLVHYIDDILLIGSSEQEVV
1					1	NTLDLLIHKRSKEAEHTAASRIR
						VSCLPEQKSHEQTLPWEQVPSS
1						GDIKEYFPNAFVLLTTASLQGQ
1						DNTSQLQLTWKAPEDIKMSKT
						DADADEEIEALRG
16987	47355	Α	17092	1	3228	MVTSSLTVAITSLVVVITSLVVII
1		ı	l	1	1	TSFVVVTTSLVVVITSLVVVITSI
1		l				AIAIATLVVVLTFTVVVLTSLV
1	1	l	1	1		VVTTSLVMVITPPFAVITSLGVV
		1				ITSLVVIITCLVLVITALGVVITS
1		l		1	1	LGVVVTSLVMVITPLVAVITPL
1		l				GVVITSLVVVITSLVMVITSLTV
1		l	1	I	1	VITSSIVVITPLVMVITSLTVIITS
1		1		1		LFVVITPLVMVITFLIVVNTSLV
1		1		1	1	VVLITLIVSPPPSLCSLVVVITFL
1		l				
		<del>  -</del>		l		VVAITSLVVVITSLVVVITSL
16988	47356	A	17093	1	471	
16989	47357	Α	17094	1	1590	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
16990	47358	A	17095	332	1704	RGYVFCSWKKTDGSWRMTVY VCKLNQVVIPIAAAVSDVVSLL EQINTSPGTWYAAIDLANAFFSI PYHKAQQKGFAFSWQGQQYTT TVLPQWYINSPALCINLIRRDL DCFSLPLDITLYHYIDDIMLIGH RQLLACY/WALVETEHLISH VTMRPELPIMNWVLFDPSSHKV GCAQQHSIIKWKWYVHDWAR AGPEGTTIPYISQWPHEQCGHG GRDGGYAWAQQCRLPITKAD LINTATAKRPIQQQRPTLSPQY GTIPQGDQPATWWVDYMGS LINSWKQRRVLTGIDTYSGYGF AYPACNASAKTAICGLTECLIH HIDIPHSIASDGGTHFMAKEW QWAHDHGIHWSYHVSHIPEA AGLIEWWNGLKSQLQCQLGD NTWQGWGKVLQKVYALNOH PYGTVSPIAKIHRRYADSLKGG SGSWWGFSTLAALDNDLGTF
16991	47359	В	17096	1	2061	
16992	47360	Α	17097	1	1623	
16993	47361	Α	17098	1	741	
16994	47362	A	17099	213	679	
16995	47363	A	17100	33	853	
16996	47364	Α	17101	3	1249	
16997	47365	A	17102	17	770	
16998	47366	Α	17103	130	469	
16999	47367	Α	17104	1	1425	
17000	47368	A	17105	1	882	

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hođ	in USSN 09/540.217	location of first codon for pentide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/340,217	sequence	or peptide sequence	deservat,possible nucleotide inscrition)
17001	47369	A	17106	227	1519	VTLIKMNAMLETPTLS\AVSDG
1,001	117507		17700			VKLSAVAAVLYVIVRCMNLKS
						ATAAPDLYLQDSGLSRFLLKSC
		ı				PLLTKEYIPPLIWGKSGHIOTAL
		1				YGKMGRVRSPHPYGHRKFITM
		1				SDGATSTFDLFEPLAEHCVGDD
						ITMVICPGIANHSEKOYIRTFVD
						YAOKNGYRCAVLNHLGALPNI
		l				ELTSPRMFTYGCTWEFGAMVN
		l				YIKKTYPLTQLVVVGFSLGGNI
		1				VCKYLGETOANOEKVLCCVSV
						COGYSALRAQETFMOWDOCRR
						FYNFLMADNMKKIILSHROALF
		1				GDHVKKPQSLEDTDLSRLYTAT
				1	1	SLMQIDDNVMRKFHGYNSLKE
		1				YYEESCMRYLHRIYVPLMLV
		l				NAADDPLVHESLLTIPKSLSEKR
		İ				ENVMFVLPLHGGHLGFFEGSVL
		l				FPEPLTWMDKLVVEYANAICQ
						WERNKLQCSDTEQVEADLE
17002	47370	Α	17107	21	385	SRSSSVVRQEPGRADGQRRRRR
	1					GGPGLRSPGERQQPRPARPCRR
						AHHPGDPAGAQ/PPPKTGKTCG
						APKATTRSTRCSISR*PPFPRSSC
	ĺ	1				PTSPRATPS\$SASSTAAMRRWL
17003	47371	A	17108	158	423	VTCRMPNWRA
17003	47371	A	17108	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1851	
17004	47373	A	17110	1	1104	
17005	47374	A	17111	66	432	
17007	47375	A	17112	103	3531	
17008	47376	A	17113	1	1311	
17009	47377	A	17114	1	750	
17010	47378	Α	17115	183	373	QPQATTLVHPVHVA*LF*VHW
						QNRYRAPDNQGYRHWRCLLPA
		1		1		LPDAGR/VRLSASC*KPPNSRG
17011	47379	Α	17116	344	480	SPKDQEPSISKKV***TSLPTSSR
		l _				SLCLPPARMHFWVLAALLSFA
17012	47380	Α	17117	3	3565	HEARRGLKMAACGRVRRMFRL
		1				SAALHLLLLFAAGA\RNSPARA
						SHSQGQGPGANFVSFVGQAGG
		1				GGPAGQQLPQLPQSSQLQQQQ
	1	1				QQQQQQQPQPPQPPFPAGGPP
		1				ARRGGAGAGGGWKLAEEESCR
						EDVTRVCPKHTWSNNLAVLEC
		1			1	LQDVREPENEISSDCNHLLWNY
						KLNLTTDPKFESVAREVCKSTIT
		1			1	EIKECADEPVGKGYMVSCLVD
		1		1		HRGNITEYQCHQYITKMTAIIFS
	l	1				DYRLICGFMDDCKNDIN

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540.217	Nucleotide location of first codon for peptide	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown,  *=Stop codon, /=possible nucleotide deletion, \==possible nucleotide insertion)
	sequence		05/540,217	scquence	or permit requests	sections t possible national insertions
17013	47381	A	17118	1	495	PDRRRGCPALSGS*SGPAPRL/C
		l			İ	LCNPTLTFHPGSVIGVCL*RHW
l			ŀ			LCRANTRHPSYRGRLSSR
17014	47382	A	17119	1	1479	
17015	47383	В	17120	67	8652	
17016	47384	В	17121	67	9183	
17017	47385	A	17122	ı	1440	
17018	47386	A	17123	1	422	FRWKELLDRPLEPSPETAQPPPP
						WLQK/NPTAVERANLLNMAKL
			ł			SIKGLIESALSFGRTLDSDYPPL
1						OOFFVVMEHCLKHGLKVRKSF
i		1				LSYNKTIWGPLELVEKLYPEAE
						EIGASVRDLPGLNEFYEYHALM
i						MEEEGAVIVG
17019	47387	A	17124	2	587	WMGSCGLHRAWLQMRWWPE
						SAWKELLDRPREPPPETAOPPPP
						WLOK/NPTAVERANLLNMAKL
						SIKGLIESALSFGRTLDSDYPPL
}		1	l			OOFFVVMEHCLKHGLKVRKSF
	1	1				LSYNKTIWGPLELVEKLYPEAE
		1				EIGASVRDLPGLKTPLGRARAW
		1	l			LRLALMOKKMADYLRCLIIOR
		1	Ì		ŀ	DLLSEFYEYHALMMEEEGAVI
17020	47388	A	17125	312	493	
17021	47389	c	17126	102	278	
17022	47390	Α	17127	2	140	KAHNCSGLERPPLDNPSVSNRL
		l l				FASFLSPRDLKGR\ICSD*SQVL
17023	47391	Α	17128	1	2051	
17024	47392	Α	17129	I .	498	
17025	47393	A	17130	2	340	
17026	47394	A	17131	140	396	
17027	47395	A	17132	703	912	
17028	47396	В	17133	201	912	
17029	47397	A	17134	1	1382	
17030	47398	Α	17135	2	431	
17031	47399	В	17136	99	1151	
17032	47400	A	17137	1	891	
17033	47401	Α	17138	15	2722	

			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
17034	47402	I A	17139	476	2934	TEPKTKTT*LSO*MOKKPLTKF
17054	7/402	n	1,,13,	170	2734	NNPSC*KLSIN/IVLEVLARAIRO
		l				EKEIKGIOLGKEEVKLSLFADD
						MIVYLENPIVSAONLLKLISNFS
		l				KVSGYKINVOKSOAFLYTNNR
		1				OTESOIMSELPFTIASKRIKYLGI
						OLTROVKOLFKENYKPLLKEIK
	1					EDTNKWKNIPCSWVGRINIVK
						MAILPKVIYRFNAIPIKLPMTFF
						TELEKTTLRFIWNOKRARIAKA
						LSQKNKAVGITLPDFKLYYKAT
						VTKTAWYWYONRDIDOWNRT
						EPSEITPLIYNYOIFDKPEKNKO
						WGKDSLFNKWCWDNWLAICR
						KLKLDPFLTPYTKINSRWIKAL
						NLRPKTIKTLEENLGITIODIGTO
						KDFMTKTPKAMATKDKIDKW
						DLIKLKSFCTAKETTIRVNRLPT
						KWEKIFATYSSDKGLISRIYNEL
						KQIYKKKTNNPIKKWEKDMNR
						HFSKDDILAAKKHMKKCSSLAI
						REMQIKTTMRYHLTPVRMAIIK
						KPGNNSQKDIPDWRNGPKRKD
						RQITTFRGPTKLQVVVPTLGAA
l						PGRGCPWPRRPRCPGREGEELH
						PALGGERGQRQAAGSGGARRL
						APSAGDGLCVGPVEDTGETQT
				1		WKTGQPGLREPWWGWRPTEPF
						PAPSSHSEEWPRRPPVRRAPRP
						AGEHAGEGGAAVADTTAFSPW
						LPRVGGWHLQVHRGGRSCAGA
						RRFGGSRGWDLGDLSSAPVASL
17035	47403	Α	17140	1	2298	
17036	47404	Α	17141	3	482	
17037	47405	Α	17142	1	1026	
17038	47406	Α	17143	1	623	
17039	47407	Α	17144	25	392	ESLKGADPKFLRNMRFANKHN
						KKGLKKMQANSARATSARAD
						AIKALVKPKEGKPDIPKGVSRK
						LDPLAYIAHP\RLGKCAHSCIAK
						GLKLCRLQAKDKDQTKAQAA
						APA*APKGARTPTKASE
17040	47408	Α	17145	1	507	

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
17041	47409	A	17146	2	811	YRFSGPTIRSIONHTTHNOGRK
11/041	4/409	I <sup>A</sup>	1/140	4	011	WHKKGIKKPRAQRYESLKGPE
		1		1	İ	V*PSGOGVTCLLRADWLSPLLG
			l			SGTY\VGPKFLRNTRFAKKHNK
	l					
		l				KGLKKMQANNAKAMSAR\AE
1						A\IKALVKPKEVKPKIPKGG\SR
1		l				KLRSTLPDIVHP\KLGKSARAPY
						LPRGFRLCLPNANAKSISSQGQ
		l		l		GQGQGQGSNQGPGFKPQLQVP
		1				ASGVPNVPRALTKGFQSRYSLA
		i		ļ		QHEGQERTWVRPPTPRPWGYH
	1	ŀ		l		FAWGWGSPVAICTNKPEAGKR
						RNEKEKLCQGDGY
17042	47410	A	17147	I	636	
17043	47411	Α	17148	169	410	
17044	47412	Α	17149	385	1359	QTNSPNCVRGRVSPPVLPGSSS
l				ļ		MDVLASYSIFQELQLVHDTGYF
		l				SALPSLEETWQQTCLELERYLQ
	İ	l				TEPRRISETF\GEDLD\CFL\HAFP
l		1		1		SPCIEESFRRLDPLLLPVEAAICE
l		1				KSSAVDILLSRDKLLSETCLSLQ
1		1				PASSSLDSYTAVNQAQLNAVTS
			İ			LTPPSSPELSRHLVKTSQTLSAV
			l			DGTVTLKLVAKKAALSSVKVG
		l				GVATAAAAVTAAGAVKSGQS
		1				DSDQGGLGAEACPENKKRVHR
		1	Ì	1		CQFNGCRKVYTKSSHLKAHQR
		1				THTGEKPYKCSWEGCEWRFAR
		1				SDELTRHYRKHTGAKPFKCNH
		_				CDRCFSRSDHLALHMKRHI
17045	47413	Α	17150	1	948	
17046	47414	A	17151	400	446	PSFLR*PSFWSREFH
17047	47415	A	17152	7212	10914	ADSGCKL/PSSC*HVLCA/WVTY
1	l	1				MVMAAILHKLDQLDASRGRAI
	l	ļ				PFCGQRGRFKYEILVKTGWGR
		1	l			GSGTTAHVGIMLYGVDSRSGH
		1				RHLDGDRAFHRNSLDIFRIATP
ŀ		1				HSLGSVWKIRVWHDNKGLSPA
1	l	1	l	l	1	WFLQHVIVRDLQTARSAFFLVN
1		1	l	l		DWLSVETEANGGLVEKEVLAA
1	l		l	l		SDAALLRFRRLLVAELQRGFFD
				l		KHIWLSIWDRPPRSRFTRIORAT
				1		CCVLLICLFLGANAVWYGAVG
				1		DSAYSTGHVSRLSPLSV
17048	47416	В	17153	T	14934	
1,040	1	1-	1.,123	r	1.75	L

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /~possible nuclcotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
			100.54	999	3009	ADSGCKL/PSSC*HVLCA/WVTY
17049	47417	Α	17154	1999	3009	
			l			MVMAAILHKLDQLDASRGRAI
		i				PFCGQRGRFKYEILVKTGWGR
		i				GSGTTAHVGIMLYGVDSRSGH
						RHLDGDRAFHRNSLDIFRIATP
		1				HSLGSVWKIRVWHDNKGLSPA
		l				WFLQHVIVRDLQTARSAFFLVN
						DWLSVETEANGGLVEKEVLAA
		ŀ		ĺ		SDAALLRFRRLLVAELQRGFFD
1					1	KHIWLSIWDRPPRSRFTRIQRAT
						CCVLLICLFLGANAVWYGAVG
		l				DSAYSTGHVSRLSPLSVDTVAV
		l				GLVSSVVVYPVYLAILFLFRMS
		l				RSKVAGSPSPTPAGQQVLDIDS
						CLDSSVLDSSFLTFSGLHAEVRT
1		1				LLGVLGWAGGPAALAQLGLKT
		1				LCTSQQAFVGQMKSDLFLDDS
		ł				KSLVCWPSGEGTLSWPDLLSDP
1		1				SIVGSNLRQLARGQAGHGLGPE
1		ĺ				EDGFSLASPYSPAKSFSASDEDL
1		1				IOOVLAEGVSSPAPTODTHMET
		l				DLLSSLCAEVHTALPLHCSCLQ
1		l				DSVQWHAVQGLPAFCRGDPVT
		ı				OEAOETA RPA A ONL VLIPLHA A
1		1				PHOAVAEIDALYDVYLDVIDK
1	ĺ	1				WGTDDMLFLGDFNADCSYVR
1		1			1	AODWAAIRLRSSEVFKWLIPDS
I			1			ADTTVGNSDCAYDRIVACGAR
1			1			LRRSLKPQSATVHDFQEEFGLD
1		l				OTOASGPWGGAGLGSPPPGRT
		l				QAAGRALAISDHFPVEVTLKFH
17050	47418	Α	17155	242	363	TKROENGRKKODRTPTEOOLR
		l				VK*KSRSTKKRRKQSRSES
17051	47419	В	17156	1	12879	
17052	47420	Α	17157	3	596	NLLFPVRSERGPHRPTPLSWLW
1		1			1	LRPCELNKLAAGGLAAGSSRA
1		1			1	GALYLLIYIPRRPARAAPLCPAA
1		1				ATGAPGASAGSASPASARPPGL
1		l				ARAAPGPLRGRRPRSPRTPFCV/
1		1				WLGVSLLLS\YQHYFAEPFESFQ
		1				VCCRHCGILCLTIRVHFPCLSAN
1		1				PFHFSQLHLGPRPGKACHSVGL
	1	1				OIYNSOAHSHPSOOEROLFC
17053	47421	A	17158	1	235	FFFVLYNLFLFVITSIPLOKVSIL
1		Γ.	1			TOROLVAEENVKCCTV\PEPO**
	1	1				*LSNYPIFVEMGFCHVGPGWSR
	1					TPTPKSVSR
	L	_				

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
17054	47422	A	17159	256	4064	ADSGCKL/PSSC*HVLCA/WVTY
						MVMAAILHKLDQLDASRGRAI
						PFCGORGRFKYEILVKTGWGR
						GSGTTAHVGIMLYGVDSRSGH
						RHLDGDRAFHRNSLDIFRIATP
						HSLGSVWKIRVWHDNKGLSPA
						WFLQHVIVRDLQTARSAFFLVN
				ł		DWLSVETEANGGLVEKEVLAA
				ŀ		SDAALLRFRRLLVAELQRGFFD
				l		KHIWLSIWDRPPRSRFTRIQRAT
				1		CCVLLICLFLGANAVWYGAVG
						DSAYSTGHVSRLSPLSV
17055	47423	A	17160	2	347	LTSRGP/LCCVLLICLFLGANAV
		1	ŀ			WYGAVGDSAYSTG/LCVQAEP
						AERRHSRCWPGVQRGCLSRLP
						GHPLSLPDVPEQGGWEPEPHTC
l				ł		RAAGAGRRQLPGLNPCWTAPS
				1		SRSEASTLR
17056	47424	Α	17161	9415	9994	ADSGCKL/PSSC*HVLCA/WVTY
				1		MVMAAILHKLDQLDASRGRAI
		1				PFCGQRGRFKYEILVKTGWGR
						GSGTTAHVGIMLYGVDSRSGH
						RHLDGDRAFHRNSLDIFRIATP
						HSLGSVWKIRVWHDNKGLSPA
		l	l		İ	WFLQHVIVRDLQTARSAFFLVN
		1				DWLSVETEANGGLVEKEVLAA
						SKASFRVPTPSRSPVALPAPAGG
17057	47425	A	17162	1030	1222	
17058	47426	A	17163	2	2762	
17059	47427	Α	17164	25	115	
17060	47428	A	17165	1	383	W - DO - OF DWG CFD G G D D G D I G D I
17061	47429	Α	17166	120	596	IKAPCASFPTSGFPGQRRSFVGR
		l				SSSTPEECGHSELGRNEDKASR
				l		GRIRQQ/PFAVLKYLLFCSLRW*
				1		YPGKQGLEWTSSKLQQTCRKY
						RERHKDTPQEEQLQDT*LSG/V
		1				TK/G*NEGKNVKGSQRERSGYS
		1		1		QREAHQTNSRSLGRNSTSQKRV
	L	L	L	L		GASIQRS

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nuclentide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop eadon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequenee		
17062	47430	A	17167	1	2236	RPSGPQPLPGSVRHPRPVLRRPL
		l				PRAQGSSSSFRPRPPFAPDTMD
1						KFWWHAAWGLCLVPLSLAQID
						LNITCR\FAGVFHVEKNGRYSIS
		l		ł		RTEAA\NLCKAFNSTLPTMAQM
		I				EKALSIGFETCRYGFIEGHVVIP
		ł				RIHPNSICAANNTGVYILTSNTS
				İ		QYDTYCFNASAPPEEDCTSVTD
1		ļ.				LPNAFDGPITITIVNRDGTRYVQ
1	1	l		1		KGEYRTNPEDIYPSNPTDDDVS
	ł	1				SGSSSERSSTSGGYIFYTFSTVH
1		1		1		PIPDEDSPWITDSTDRIPATSTSS
		1				NTISAGWEPNEENEDERDRHLS
		1	1			FSGSGIDDDEDFISSTISTTPRAF
	ŀ	1				DHTKQNQ\DW\TQW\NPSH\SNP
1		1				EVLL\Q\TTTRMTDVDRNGTTA
						YEGNWNPEAHPPLIHHEHHEEE
						ETPHSTSTIQATPSSTTEETATQ
	1					KEQWFGNRWHEGYRQTPREDS
İ				l		HSTTGTAAASAHTSHPMQGRT
	1	1				TPSPEDSSWTDFFNPISHPMGRG
	i	l				HQAGRRMDMDSSHSTTLQPTA
		l				NPNTGLVEDLDRTGPLSMTTQ
1		ļ				QSNSQSFSTSHEGLEEDKDHPT
1						TSTLTSSNRNDVTGGRRDPNHS
		1				EGSTTLLEGYTSHYPHTKESRT
						FIPVTSAKTGSFGVTAVTVGDS
					1	NSNVNRSLSGDQDTFHPSGGSH
	l					TTHGSESDGHSHGSQEGGANTT
						SGPIRTPQIPEWLIILASLLALALI
		1			1	LAVCIAVNSRRRCGQKKKLVIN
					1	SGNGAVEDRKPSGLNGEASKS
17063	47431	Α	17168	1	1980	

SEQ ID NO:		Met	SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop eodon, /=possible nucleotide
NO:	of peptide sequence	hod	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion
	sequence		07/340,217	sequence	pepulae sequence	position in position indicated inscriton
17064	47432	IA.	17169	362	2551	EDFSTSATTPSSSPRELPSGOG
17004	47432	A	1/109	302	2331	WLCWLELLPSFTRNGVVHTG
		1			ĺ	C*GLC*RWQLSPQPSLPSNFGN
		1				
						KISDMATLITTVPAA/FSSSSDV
						NTPAPTQSPEEVRRLHLCTSF
						DMLKVGGQGEGAAAGLVQN
						SGHALGCLDSAASGISDPSVA
						LLENVPNQRGESLRCVPVYLC
						WNCSKETGMDSGQFGEEKG/
		ŀ				DPSPTYYHACLSTQWWPSPES
		1				YPQPSGPQVKEPRNPGKSISM
						CLWIRYHAADSGSSRAKLPLE
		1			1	RLRPFSPTHDCLAFPLPLEKRP
		1				GNVGSRCPSGTKLPEEGSGSN
						CCSAIFPVLQPPLVIPRQTRSG
						DLQQTPTDLQLRDLTDRSSLP
						MEQSWIENDFDELNRSRLQK.
		l				NKLENLEETDKFLDTYTLPRL
		1				QEETESLNRPITGSEIEAIINNV
		1				TKKSPGPDGVTAKFYQRYKE
		1				LRTVNKNHMIISIDAEKAFDN
	İ	1				QPFMLKTLNKLGIDATYLKIII
		1				IDDKPTANIILNGQKLEAFPLK
		1		l		GTRQGCPLSPLLFNIVLEVLA
		1		1		AIRQEKEIKGIQLGKEEVKLSL
		1	1	1		ADDMIVYLENPIVSAQNLLKI
		1		1		NNFSKVSGYKINVQKSQEFLY
		1				NNRQTENQIMSELPFTIASKRI
		1				YLGIQLTRDVKDLFKENYNPI
		1				NEIKKDTNKWKNIPCSWIGRI
		1		1		MKMAILPKSGPSAARLLEFAC
		Ļ.		ļ	100	PLQTLFAWVSPEEAAEQQILP
17065 17066	47433 47434	A	17170	52	483 321	
17067	47435	A	17172	274	393	
17068	47436	A	17173	304	415	
17069	47437	A	17174	321	796	
17070	47438	A	17175	1	198	
17071	47439	A	17176	2	454	CRPVPAATNGRCFPATPRDPG
1,0,,	177	Γ.	1	1	1.5.	RMRRACA WGRSKGAGRCLR
		1				ATRRDKMAKKESILDLSK\YII
		1				KTIRVKFQGGRK\ASGILKGFE
		1			1	NLL\NLVLTVTI*YMRDPDDQ
		1		l		KLTED\TRQLG\LVVFRG\TSL\
						VICPQDGMEAIP\NPFIQQQDA
17072	47440	Α	17177	ı	1806	
17073	47441	Α	17178	1215	2065	
17074	47442	Α	17179	217	441	
17075	47443	A	17180	117	296	DWSDIQKLG*SLSLSKEIFQL*
		1		1		SPPALHPAKLLHRSA*LSVPQI
	1	1	I	i	1	RECQGCGWTAMC

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ 1D NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X-Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17076	47444	Λ	17181	2	138	LRTAPEFPGRRFRGCAAAAAES VAALL*STPPCRSGDSLCGKSR
17077	47445	Α	17182	222	760	
17078	47446	A	17183	192	244	YIQPVF*GWTLGCCQFF
17079	47447	A	17184	1	990	
17080	47448	A	17185	1	2196	
17081	47449	A	17186	459	1387	
17082	47450	A	17187	2	454	
17083	47451	A	17188	1	957	
17084	47452	A	17189	398	553	
17085	47453	Α	17190	2	293	
17086	47454	В	17191	53	182	
17087	47455	A	17192	3	1114	
17088 17089 17090 17091	47457 47458 47459	A A A	17194 17195 17196	2 185 3	291 307 392	SVVEFIPSCAVVLWSVLLSPV  LISYLSGYPOHPMEDSMDML  MSPLRPHNYLFGCELKAGQDY  HFKVDNDENEHQLSLRTVSLG  GAKDELHIVEAEAMYYEGS  IKV/THLATLKMSVQFTVSLG  GHLVAVEEDAESEDEEEDVY  LSLSISGKRSAPNGGSKYPQKE  KTCMLMKDDDDVDDEEDGYJ  EDDVDDDDDDDDDEDEEBEKJ  EDDVDDDDDDDDDEDEEBEKJ  ERNLYNDTPAKNAGKSNON  KDSKPSSTPRSKGQESFKKQEI  TRKTPKGPSSVEDIKAKMGASI  VRGGQAFRQRPAPPLPVTRSAI  RGRRPTRASQPSLFIILLLREGK
17092 17093	47460 47461	СВ	17197 17198	76 1803	378 11905	MSESSSKSSQPLASKQEKDGTE KRGRGRPRKQP\PVSPGTALVC SQKEPSEVPTPKRPRGRPKGSK NKLEKEEEEGISQESSEEEQ
17094	47462	A	17199	1	416	
17094	47463	A	17200	30	407	
17096	47464	A	17201	1	993	
17097	47465	A	17202	i -	1287	
17098	47466	A	17203	1	2004	
17099	47467	A	17204	i	1368	
17100	47468	В	17205	1	3035	
17101	47469	В	17206	i	981	
17102	47470	Ā	17207	1	2017	-
17103	47471	A	17208	1	1069	
	47472	A	17209	i	2463	
17104						

SEQ ID NO:	SEQ ID NO: of peptide	Met	SEQ ID NO: in USSN	Nucleotide location of first	Nuclentide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
NO.	sequence	1100	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence	,,,,,,	
17106	47474	I A	17211	51	1528	GREASKMAOTOGTRRKVCYY
						YDGDVGNYY*G\QGHPMKP\H
		l				IRMTHNLLLNYGLYRKMEIYR
		1				HKANADEMTKYHSDDYIKFLF
		l				SI/RVPDNIVGSTSKQMQRFNV
	l					EDFPSIPMACFEFCQLSTGGSV/
		1	l			KCL*NFNKQQTDIAVNWAGGL
			l			HHAKKSEASGFCYVNDIVLAII
						ELLKYHQRVLYIDIDIHHGDGV
						EEAFYTTDRVMTVSFHKYGEY
						FPGTGDLRDIGAGKGKYYAVN
		1				YPLRDGIDDESYEAIFKPVMSK
						VMEMFQPSAVVLQCGSDSLSG
	1	1				DRLGCFNLTIKGHAKCVEFVKS
		1				FNLPMLMLGGGGYTIRNVARC WTYETAVALDTEIPNELPYND
					1	FEYFGPDFKLHISPSNMTNONT
		l				NEYLEKIKQRLFENLRMLPHAI
						GVQMQAIPEDAIPEESGDEDED
		l	l			DPDKRISICSSDKRIACEEEFSD:
	ł					EEEGEGGRKNSSNFKKAKRVK
						TEDEKEKDPEEKKEVTEEEKTI
						EEKPEAKGVKEEVKLA
17107	47475	Α	17212	1	492	
17108	47476	Α	17213	1	1851	
17109	47477	A B	17214	1	753	
17110	47478 47479	В	17215	427	614 711	
17111	47480	A	17217	750	1173	
17113	47481	A	17217	1	1224	
17114	47482	A	17219	1242	1743	
17115	47483	A	17220	423	1739	
17116	47484	A	17221	117	1183	
17117	47485	A	17222	1	377	FRRGAW/VPLLTRWGFRPRGG
		l				ISNDSPRRS/IHYRETKPEPPVR1
		ı				CARGLQRTPSAGHRAVLRMPR
						RGRTRPGAPQGGAALGGPARE
						RECACAGRGAQTFALRKNCVC
						KMPSGRGRTCSKNFSYFPS
17118	47486	A	17223	178	1134	
17119 17120	47487 47488	A	17224	178	1200	
17121	47489	A	17226	85	3360	
17121	47499	A	17227	8	930	
17122	47490	A	17228	1	765	
17123	47491	В	17229	120	509	
17125	47493	A	17230	232	3187	
17126	47494	A	17231	1	999	
17127	47495	A	17232	1	325	
17128	47496	В	17233	1	535	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	ŀ	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		l		sequence		
	1.5.000	In.	17235	201	523	
17130	47498	В		301		
17131	47499	Α	17236	1	1185 497	
17132	47500	Α	17237	178	497	LPVPAYELNGSQQLPLLLGAAA
						IGYLAYKRFYVKDHRNKAMIN
		1				LHIQKDNPKIRHAFDME\DLGD
ŀ		l				KAV\YCRCWRSKKFPFCDGAHT
						KHNKE\TGDNVGPLIIKKKET
17133	47501	В	17238	184	395	
17134	47502	Α	17239	1	103	PAWHEGQPQPESECPPQRQCIC
		1				SHGRGTPARCGVSY*ART/PAG
l	1					ESP*TQQDLRAS*LGTRANHSQ
		1				RASARHKDSASAVTGAGHQRD
						AE
17135	47503	Α	17240	447	667	HRPRRRFQIKPQSQVPEHAPLPL
		l			1	PTASDPP/AHSPRCPSESRLSPGG
	ł	1				QRLGFPSSVLNCSKCSWQLAAC
		l				MGFSF
17136	47504	Α	17241	265	890	
17137	47505	Α	17242	1	1374	
17138	47506	Α	17243	1	6189	
17139	47507	Α	17244	1	8277	
17140	47508	Α	17245	178	1177	
17141	47509	Α	17246	1	447	
17142	47510	Α	17247	1	465	
17143	47511	Α	17248	3	3910	
17144	47512	Α	17249	2	1871	
17145	47513	Α	17250	1	666	
17146	47514	Α	17251	1	635	FPGRRFRRAVWCTHCCAPTPSG
		l			i	PVLPHSAAMSFLKSFPPPGPAE
		İ				GLLRQQPDTEAVLNGKGLGTG
		ĺ				TLYIAESRLSWLDGSGLGFSLE
	1	l				YPTISLHALSRDRSDCLGEHLY
ĺ		l				VMVNAKFEEESKEPVADEEEE
	1					DSDDDVEPITEFRFVPSDKSAF*
l	1	1	1		l	FPCSVEAMFTAMCECQALHPD
	1					PEDEDSDDYDGEEYDVEAHEO
	1					GOGDIPTFYTYEEGLS
17147	47515	A	17252	1	2796	
11,141	17,515	11.	11222	l'	2770	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
17148	47516	A	17253			MEIRGALDLRKRQVLIFLVILL LSRAGTESAHYSVABETEIGSI ANLARDLGLGVEELSREARY VSDDNKKYLHI.DLLTGNLLLI EKLDRDEL.GGSTEPCVLHFQU EKLDRDEL.GGSTEPCVLHFQU EKDPLQFFRELCVKDINDHSI FLOKELI IKISEGTTVGATFLM SAQDLDVGSNSLQNYTISPNS FYIKIPDSSDRKIVPELVLDRA DYEQEAELRJTLTAVDGGSPS SGTTI.VLIKVLDINDNAPEC LYEVQVPEDRPL.GSWIATISAI DLDAGNYGKISYTFFHASEDI LYEVQVPEDRPL.GSWIATISAI DLDAGNYGKISYTFFHASEDI KYTEINIQATDGGGLSGKCTLLI KYMDINDNPEVTISSITKPI NASETLVALFSILDQDSGDNG MICSIQDNLPFFLKPTFKNFFT: VSEKALDRESQAEYNITTVTI GTPRLKTEYNITVLLSDVNDN TPITOTSYTLTVERENNSPALHI SVSATDRDSGTNAQVNYSLLF QDRHLPLASLVSINADNGHLF LRSLDYEALQEFERVGATDR SPALSSEALVRULVLDANDNI LRSLDYEALQEFERVGATDR SPALSSEALVRULVLDANDNI LRSLDYEALQEFERVGATDR SPALSSEALVRULVLDANDNI EGYLVTKWVAVDGDSGQNA WLSYQLLKATEPGLFGVWAH GEVRTARLLSERDAAKHLVY LVKDNGEPPRSATATLHYLLL LVKDNGEPPRSATATLHYLLL LVKDNGEPPRSATATLHYLLL LVKDNGEPPRSATATLHYLLL LVKDNGEPPRSATATLHYLLL LVKDNGEPPRSATATLHYLLL LVKDNGEPPRSATATLHYLLL LVKDNGEPPRSATATLHYLLL LVKDNGEPPRSATATLHYLLL LVKDNGEPPRSATATLHYLLL LVKDNGEPPRSATATLHYLLL LVKDNGEPPRSATATLHYLLL LVKDNGEPPRSATATLHYLLL LVKDNGEPPRSATATLHYLLL LVKDNGEPPRSATATLHYLLL LVKDNGEPPRSATATLHYLLL LVKDNGEPPRSATATLHYLLL LVKDNGEPPRSATATLHYLL LVKDNGEPPRSATATLHYLLL LVKDNGEPPRSATATLHYLLL LVKDNGEPPRSATATLHYLL LVKDNGEPPR
17149	47517	A	17254	89	1283	TVYLVVALASVSSLFLLSVLL
17150	47518	A	17255	1	276	
17151	47519	Α	17256	2	259	WQGGILGSDPTPPLTSPNLLQ ACFREERDV/RRERGQPLGDH ALCLPRRGVPVPCDGLLCWW PPDAAEPLRGPSPARAGPVLP
17152	47520	Α	17257	624	4055	
17153	47521	A	17258	3	1784	
17154	47522	A	17259	1	1272	
17155	47523	A	17260	3	576	
17156	47524	A	17261	1	1017	
17157	47525	Α			1107	
17158	47526	Α	17263	256	634	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	eodon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
17160	47528	Α	17265	1659	2107	NLLCCTCSPFSSPVSAPQTCTSN
						CIALLVHQQQWLVSSHLQKHF
		l		į .	1	LHLHIFLA\LIVFNFSLHSF*IFDF
				l		DPWKLPP*PISPTLSSLPSNRHIA
		1		1		LILPCSCMTEDFDFKMPPAVAR
		1				YMTSPQAVHIIAVCPFKASRKV
		1		1		SHSSLKIWLFKSV
17161	47529	Α	17266	248	540	KFFSLRMLNINPHCLLACRVSA
		l				ERSAVSLMGFPLCISRPFSLAAL
İ						NIFSFISTLVNLMIISLGVALLEE
		1				YLCGILCIS*IGMLACLARLGKF
						SWIIR
17162	47530	Λ	17267	4880	5121	
17163	47531	Α	17268	468	602	CLQLCSFGLGLTW*CGLFFYST
						*TLK*FFPIL*RMMVVF*WGLH
17164	47532	Α	17269	359	462	
17165	47533	Α	17270	457	600	LWWFNALFLCWLTSFLTTTLLE
l						LHECLPVWRD*TRRHLTGWSK
						GSCTN
17166	47534	Α	17271	2405	2830	TPVFRFIALSYTFADSDGEYF*IL
		1				LSENPQRFFKCCFNMRSNKIPW
						DTFANSIKGAEFSGKHFITEFISS
						SESESESESTRFRDFRGLETSSSL
		1				SLDSFSLLGDDFLSFLLSFTIDA
						VSSKRLSKEIRKARLCWRFPRI
17167	47535	Α	17272	1	2172	
17168	47536	В	17273	446	625	
17169	47537	В	17274	1	2604	
17170	47538	A	17275	1	3039	
17171	47539	В	17276	1	1383	
17172	47540	Α	17277	1	993	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nuclcotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
17173	47541	A	17278	3	2494	RSTROKVNKDTOELNSALHOA
		1				DLIDIYRTLHPKSTEYTFFSAPH
						HTYSKIDHIVGSKTLLSKCKRTE
					l .	IITNYLSDHSAIKLELRIKNLTOS
						RSTTWKLNNLLLNDYWVHNE
						MKAEIKMFFETNENKDTTYON
		1				LWDAFKAVCRGKFIALNAYKR
						KOERSKIDTLTSOLKELEKOEO
1						THSKASRROEITKIRAELKEIET
						OKTLOKINESRSWFFERINKIDR
1		İ	1			PLARLIKNKREKNOIDTIKNDK
						GDITTNPTEIQTTIREYYKHLYA
			i			NKLENLEEMOTFLOTYTLPRLN
1						QEEVESLNRPITGSEIVAIINSLP
						TKKSPGPDGFTAEFYQRYKEEL
						VPFLLKLFQSIEKEGILPNSFYE
		1				ASIILIPKPGRDTTKKENFRPISL
i	į.	l l				MNIDAKILNKILANRIQQHIKKI
		1		ļ		IHHDOVGFIPGMQGWFNIHKSI
1		1		I		NVIQHINRAKDKNHMIISIDEEK
1		1	ļ			AFDKIQQPFMLKTLNKL\G/DKI
		ı			1	PRNPTYKGCEGPLQGELQTTAC
1		1		1		GNKRGHKOMEEHSMLMGRKN
		1		1	1	QYHENGHTAQG/IL*IQCHPHQ
		1	ì			ATNOFLHRIGKNYFKVHMEPK
ľ		1		ł		KSPHRQVNPKPKEQSWRHHTT
		1				*LQTILQGYSNQNSMVLVPKQR
		1				YRSMEQNRALRNNAAYLQLSD
		1		1		L*QP*EKQAMGKGFPI**MVLG
		1		1		KLASHM*KAETGSLPYTLYKN
l .		1		ł		QFKMD*RFKR*T*NHKNPRRKP
						RHYHSGHRHGQGLHVQNTKSN
17174	47542	A	17279	285	502	
17175	47543	A	17280	I	3189	
17176	47544	В	17281	1	1235 3139	
17177	47545	A_	17282	1	1779	
17178	47546	В		1		
17179	47547 47548	A	17284	1	3127 3325	
17181	47549	A	17286	i i	3145	
17182	47550	A	17287	1	1095	MIMGDFNTPLSTLDRSTROKVN
17102	47330	<u> </u> ^	1/20/	ľ	1093	KDIQELNSALHQADLIDIYRTLH
				1		PKSTEYTFFSASHLTYSKIDHIV
						GSKALLSNCKRTEIITNYLSDHS
				1		AIKLELKIKKLTPNRSTTWKLN
1	1	1		1	1	NLLLNDYWVHNEMKAEIKMFF
1		1		1	1	ETNENKDTTYQNLWDTFKAEC
1	1	1		1	1	RGKFIALNAHKRKQERSKIDTL
		1		1		TSQLKELEKQEQTHSKASRRQE
1		1			I	ITKIRAELKEMETQK\TLQK\INE
		1				SRG/WKKFLEKLCFIELS*ARRI
i	1	1	1	1	I	DIVOLM VILLEVICLIETO, WKKI

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
17183	47551	Α	17288	1	3229	
17184	47552	Α	17289	1	1205	7
17185	47553	Α	17290	1	986	
17186	47554	Α	17291	1	3170	MGDFNTPLSTLDRSMRQKVKK
		l				DTQELNSALHQADLIDIYRTLH
		l				PKSTEYTFFSAPHHTYSKIDHIL
		1			İ	GSKALLSKCKRTEIITNYLSDGS
		1				AIKLELRIKNLTQNRSTTWKLN
		l				NLLLNDYWVPNEMKAEIKMFF
						ET\NENKDTTYQNLWDTFKAV
		l				CRGKFIALNAHKRKQERPKIDT
		1		1		LTSQLKELEKQEQTHSKASRRQ
		l				EITKIRAELKEIETQKTLQKIN*S
		l		1		QSWFFERVKKIDRPLARLIKKK
						REKNQIDTIKND
17187	47555	В	17292	1	2148	
17188	47556	A	17293	1	1416	LOW WITH ON PROTECTION
17189	47557	Α	17294	1	3099	MGELITPLSTLDRSTRQKVNKD
		1				TQELNSALHQGDLIDIYRTLHP
						KSTEYTFFSAPHHTYSKIDHILG
		1				SKALLSKCKRTEIITNYLSDHSA
		1				IKLELRIKNLTQNRSTTWKLNN LLLNDYWIHNEMKAEIKMFFET
						NENKDTTYQNLWDAFKAVCR
		1		1		GKFIALNAHKRKQERSKIDTLT
		l	ŀ	1		SQLKELEKQEQTHSKASRRQEI
į.						TKIRAELKEIETOKTLOKINESR
	1					SWFFERINKIDRPLARLIKKKRE
						KNQIDTIKNDK
17190	47558	A	17295	1	3345	
17191	47559	В	17296	1	3122	
17192	47560	A	17297	1	2118	
17193	47561	A	17298	965	4091	
17194	47562	В	17299	15	2762	
17195	47563	Α	17300	1	3049	MTVKVRITVTSGKKPPWLIPRQ
1		1			1	TGYGVDLWQTPTDLQLRVLTV
		1				RRKTNKQKGHPHQNPICTSPSS
						KTKDRSTRQKVNKDIQELNSAL
l		1			1	HQEDLIDIYRTLHPKSTEYTFFS
1		1				APHHTYSKIDHIVGSKALLSKW
		1				KRTEITANCLSDHSAIKLELRIK
1		1	l		1	KLTQNWSATWKLNNLLLNDC
	1	1				WVHKEMKAEIKMFFETK\ENK\
l		1	l		1	DTTYQNLWDAFKA\VCRGKFIA
1		1	1			LNAHKRKQERSKIDTLTSQLKE
L _		L	L			LEKQEQTHSKASRR

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon,/=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1				sequence	' '	
		L				
17196	47564	Α	17301	3	4101	PLSTLDRSTRQKVNKDIQELNS
						ALHQVDLIDIYRTLHPKSTEYTF
i						FSVPHHNYSKIDHIVGSKALLS
						KCKRTEIITNCLSDYNAIKLELR
		1			l	TEKLTONRSTTWKLNNPLLND
		1				YWVHKEMKAEIKMFFETNENK
		1				DTTYONLWDAFKAVCRGKFIA
	1					LNAHKRKQERSKIDTLTSQLKE
		1			i	LEKQEQTHSKATRRQEITKTRA
		1				ELKKIETQKTLQKINESRSWFFE
						KTNKIDRLLATLIKKKREKNOI
						GARKNDEGAITTN
17197	47565	A	17302	1	3234	MANKNNOCREVLKGPDELKT
1,112,	4,303	l^	1,302	Ι'	J2.57	MAREPHDKCTSFSSQFDQLEER
1	1	l	1	1	ł	VSAMEDOMNEMKREEKFREK
1		1		l		
		1				RIKRNEQRLQEIWDYVKRPNLC
	l					LIGVPESDGENGTKLENTLQDII
		l			1	QENFPNLARQANIQIQEIQRMP
		l			İ	QRYSLRRTTPRHIIVRFTKVEM
		1			ì	KEKMLRAAREKGRVTHKGKPI
						RLTADLSAETLQARRESTRQKV
		1		i		NKDIQELNSAQHQADLTDNYR
		1				TLHPKSTEYTLFSAPHHTYSKID
						HIVGSKALLSKCKRTEI
17198	47566	Α	17303	1	3390	MLTLNHNRLTDAILNISTCLSR
		1				HLDLNTGGKKRISYKRNYLME
	1	1				EHLEGLCSNEFTWENSTIMTDS
	l	l	l			QMLMHREEPGSLPNIPILSIVFT
		1				NNRSKRQKVNKDIQELNSALH
	İ					QADLIDIYRTLHPKSTEYTFFSA
	i	1				PHHTYSKTDRIVGSKALLSKCK
						RTEHTNCLSDHSAIKLELRIKKL
						TQNCSTTWKLNNLLLNDYWV
		1				HNEMKAEIKMFFETNENKDTT
		1				YQNLWDTFKAVCRGKFIALNA
						HKRKQERSKIDTLTS
17199	47567	В	17304	1	2427	
17200	47568	A	17305	1	4257	
1720I	47569	A	17306	1	3726	MVVKTNARELRDECTSLSSPFN
1	1	1				QLEERVSVMENQMNKMKQEE
		1				KFREKRIKRNEQSLQEIWDYVK
1		1			1	RPNLCLIGVTESDGENGTKLEN
					1	TLODITOENFPNLARKANIQIQE
1		1				TORTPORYSSRRATLRHIIVRFT
		1			l	KVEMKEKMLRAAREKDFTPTK
		1		I	I	
		1	l	I	1	IKRDKEGHYIMVKGSIQQEELTI
		1	l	l		LNIYAPNTGAPRFIKQVLSDLQ
		ı	ĺ	I		RDLDSHTLIMGDFNTSLLTLDR
		1		I		SMRQKVNKDTQELNSSLHQAD
		_				LIDIYRTLHPKSIE
17202	47570	Α	17307	1	1059	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nuclcotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
17203	47571	A	17308	130	1092	
17203	47572	A	17309	1	924	
17204	47573	A	17310	1	1206	
17205	47574	В	17311	1	1257	
17207	47575	A	17312	1	685	MEHLRICKLTISKELLDSGSSRL
17207	4/3/3	n	17512	Ι'	005	TMTHYKHRYFSHSAEEQIISEEL
						NESEMICOHHHTAENDFDELRE
1						EGFRRSVITNFSKLKEDVOTHF
						KEAKNLEKRLDEWLTRINSVEK
						TLNDLM*LKTVA*ELRDTYTSF
						NSRFDQVEERVSVIEDQMNEM
						EREEKFREKRV*RNEQS/LQEIW
						NYVKRPNLHLIGVSEIDRENGT
						KLENTLQDIFQENFTYLARQAN
l						IQIQEI
17208	47576	В	17313	70	1227	IQIQEI
17209	47577	В	17314	640	751	
17210	47578	Ā	17315	1	2328	MGVSGAQPGRSCWHRSSTGSQ
17210	47376	^	17313	ľ	2320	GLGPVPEPADCGGEAAGRARE
		1				EGTVSLTMGTADSDEMAPEAP
1					İ	OHTHIDVHIHOESALAKLLLTC
1						CSALRPRATOARGSSRLLVASW
		1				VMQIVLGILSAVLGGFFYIRDY
1				•	i	TLLVTSGAAIWTGAVAVLAGA
1						AAFIYEKRGGTYWALLRTLLTL
						AAFSTAIAALKLWNEDFRYGYS
						YYNSACRISSSSDWNTPAPTQSP
						EEVRRLHLCTSFMDMLKVGGO
						GEGAAAGLVONPSGHALGCLD
				}		SAASGISDPSVAVLLENVPNOR
		l				GESLRCVPVYLGOWNCSKETG
						MDSGQFGEEKGAHDPSPTYYH
		ı		ļ		ACLSTOWWPSPESPYPOPSGPO
		1				VKEPRNPGKSISMLCLWIRYHA
		1		1	İ	ADSGSSRAKLPLEERLRPFSPTH
		1				DCLAFPLPLEKRPEGNVGSRCP
		1				SGTKLPEEGSGSNICCSAIFPVL
1					İ	QPPLVIPRQTRSGVDLQQTPTD
						LQLRDLTVRRKTNKQKGHPHQ
	1		1	I		NPMCTSPSSKTKELKEDVRTHH
						KEAKNLEKRLDKM\VNRINSVE
		1		l		KTLNDPMELKT\QARELHDKCT
						SFSSRFDQLEERVSVTEDQMNE
				l		MKREEKFREKRVK\RNEQSLQE
	1	1		1		IRDYVKRPNLCLTGVPESDGEN
		1		l	l	ETKLENTLQDNIQENFPNLARQ
				1	l	ANIQIQEIQRTPQRYSSRRATPR
		1		1	l	HIIVRFTKVEMKEKMLRAAGE
				l	l	KGQVTHKGKPITLTADLLAETL
17211	47579	A	17316	508	666	
17212	47580	A	17317	622	780	

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
17213	47581	В	17318	1	777	
17214	47582	A	17319	1	508	MSGFEKOYKKIRLDKTLDSENE
	17502	1	1	ľ		GLELPVPAKRSNLGVRLYACC
						GLLLCPAYPOHFAHGYVDKIPG
		l				YPGRAGTLTGLHPMQVCRCRR
		1				OAPCLKSNNALIVILGTVTLDA
		1				VGIGLVMPVLPGLLRDIVHSDSI
						ASHYGVLLALYALMOF\LCAPK
1						YKLPSENTTNTSMQIN
17215	47583	В	17320	310	1047	
17216	47584	Α	17321	1	1101	
17217	47585	Α	17322	577	735	
17218	47586	Α	17323	337	642	
17219	47587	Λ	17324	2	653	
17220	47588	Α	17325	2	935	
17221	47589	Α	17326	532	729	
17222	47590	Α	17327	1	675	
17223	47591	A	17328	1	684	
17224	47592	Α	17329	2	641	
17225	47593	Α	17330	1	808	
17226	47594	Α	17331	562	675	
17227	47595	A	17332	2	1687	DTGNNEWKQQEGLSHNNWLG
ĺ						LGCLFGPETPIFYPATLGHTSSIY
					i	YERKKEDKNGMKEEHDTSVA
					1	MFFTLFNFQISVENIRKGPMVV
						GESIAQSYLNVVQEIFRSRNHQ
						LLQDLTRDLCDNLKTCHTSHGS
						VMAETAVINHKKRKNSPRIVQS
		1				NDLTEAAYSLSRDQKRMLYLF
						VDQIRKSDGTLQEHDGICEIHV
						AKYAEIFGLTSAEASKDIRQAL
1						KSFAGKEVVFYRPEEDAGDEK
						GYESFPWFIKQRSNLGVRLYAC
1						CGLLLCPAYPQHFAHGYVDKIP
						GYPGRAGTLTGLHPMQVCRCR
						RQAPCMKSNNALIVILGTVTLD
1						AVGIGLVMPVLPGLLRDIVH\SD
						SIASHYGVLLALYALMQFLCAP
						VLGALSDRFGRRPVLLASLLGA
				I		TIDYAIMATTPVRGHSVLKGKQ
1	1	1			1	HKSVENLQPDNVIEKKIPFSGEK FKPAAEICKSNRELNVNHODNG
		1			1	
	1	1			I	ENVSRACQRPLLQPLPSQAWRF
1				I	1	RRKNWFCGPGPWSPFSVQSRD
						LVPCVPAAPALTKRGQGTAQA
1				1		VASEGGSPKPWQLPHGVEPAG
17228	47596	В	17333	12	60	AQKSRAEVWEPPPRFQKM
17228	47597	В	17334	253	2103	
11229	71371	10	1.,554	1222	12.00	L

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: io USSN 09/540,217	Nucleotide location of first codoo for peptide sequence		Amino acid sequence (X=Unkoown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17230	47598	A	17335	469	2512	PTSAYERGORFASRLOMNLLEY FLRWLMAKIFFO, POMKSNNA LIVILGTVTLDAVGIGLVMPVL PGLLEDIVHSDSIASHYGVLLAL YALMOFLCAPULGALSDRER RPVLLASLLGATIDYAIMATTP VLWYPLVNVSKSDDTLKINGV EDHKTIFEGDOKTYONVOOFID EGNYTSGDNHTLRDPHYVEDK GHKYLVFEANTGTENGYOGE SLFNKAYYGGGTNFFRKESQKL QQSAKKRDAELANGALGIIEL MOYTLKKVMKPLITSNTVIDE ERANVFKMRGKWVLFTDSRGS KMTIDGIKLNDIYMLGFVSNSL TGPYKPLINKTGLVLQMVLDPN DVTFTNFYLFGPQAKANMWLL OAHDKKSFSRIKGTGPAAL
17231	47599	Α	17336	2393	2945	
17232	47600	Α	17337	980	1732	

2183

SEO ID	SEQ ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon,/=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		ı		sequence	1	
17233	47601	Α	17338	I	2400	GRPFPRPPRLCÖRRLRGGGRMK
		1				MTGDFEECLKDSPRFRAALEEV
		1				EGDVAELELKLDKLVKLGIAMI
						DTGKAFCVANKQFMNGIRDLA
					1	QYSSNDAVVETSLTKFSDSLQE
		l				MINFHTIL/L*PNSEINLRHSFSN
						FVKEDLRKFKDAKKQFEKVSE
					1	EKENALVKNAQ VQRNKQHEVE
		ł				EATNILTATRKCFRHIALDYVL
			l			QINVLQSKRRSEILKSMLSFMY
		l				AHLAFFHQGYDLFSELGPYMK
		l	1		1	DLGAOLDRLVGDAAKEKREME
						QKHSTIQQKDFSRDDSKLKYNV
		l				DAANGIVMEGYLFKRASNAFK
						TWNRRWFSIQNNQVVYQKKFK
						DNPTVVVEDLRLCTVKHCEDIE
		l				RRFCFEVVSPTKSCMLQADSEK
		l				LRQAWIKAVQTSIATAYREKG
						DESEKLDKKSSPSTGSLDSGNE
						SKEKLLKGESALQRVQCIPGNA
		l				SCCDCGLADPRWASINLGITLCI
		1				ECSGIHRSLGVHFSKVRSLTLDT
1						WEPELLKLMCELGNDVINRVY
		1				EANVEKMGIKKPQPGQRQEKE AYIRAKYVERKFVDKYSISLSPP
		1				
			l			EQQKKFVSKSSEEKRLSISKFGP
			l			GDQVRASAQSSVRSNDSGIQQS
			i			SDDGRESLPSTVSANSLYEPEG
		l				ERQDSSMFLDSKHLNPGLQLYR
		l	1			ASYEKNLPKMAEALAHGADVN
		l				WANSEENKATPLIQAVLGGSLV
						TCEFLLQNGANVNQRDVQGRG
17234	47602	Α	17339	1	782	
17235	47603	Α	17340	1	475	
17236	47604	A	17341	1	852	
17237	47605	A_	17342	432	696	
17238	47606	A	17343	3	296	ETEIEALKEELLFLKKNQEEEV
		1	1			KGLQAQIAISGLTVEVDVPKSQ
						DLAKIMADIWAQ*DELEDGEDF
		1				SLRDALDSSNSMQTIRKTTTRPI
		L				VsGwqsGV
17239	47607	A	17344	2	292	SQKKGLVGALTLNPPHFCPCHL
	1	ı				*EVKGLQAQIASS\GLTVEVDAP
1		l	l			KSQDLAKIMADIRAQYDELAR
1						KNREELDKYWSQQVREGKGM
						GCQGVGGRQTE
17240	47608	Α	17345	1	908	

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	nf peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
17241	47609	A	17346	1	1452	TGPEFHDRLRVRRRPOSLSPVL
	., .,	1		[	l	LLSSPDSMSFTTRSTFSTNYRSL
	ŀ					GSVQAPSYGAGPRRAARPASY
		1				AGAGGSGSRISVSRSTSFRGGM
						GSGSL\ATG\IAGG\LAGMG\GIQ
		1			ľ	NEKETMOSLNDRLASYLDRVR
		1		ŀ		SLET\ENRRL\ESKIRE\HLEKKG
ł		1				PQ\VRDWSHYFKI\IEDLRA\QIF\
l		1				ANTV\DNARIVL\QI\DNAPSCVR
1		1		l		DDFR\VKY\ETELA\MRQSCWRT
					Į.	DIHGAPQGPFDDTNYHTDLQL/
						EKTEIRGSSRRELLFQ*RRNHEE
		1		1		
		1		1	ŀ	ÆKLKGLQAQIAQFLGLTRGRL
						DCPQIFRDLRQDSWADIRGPIID
		1		l		ELASEEPRGSLDKY\WSQQI\EE
		1		l		STTVVTTQF\AEVEAAETT\LTE
		1		1		LRRTVQSLEI\DLDSMRNLKAS\
		1		1		LENSLREG*RPAYALQ\MEQLN
		1				GI\LLHLESELAQTRAEGQRQA
		1		1		QEYEALLNIKVKLEAEIATYRR
		1				LLEDGEDFNLGDALDSSNSMQ
						TIQKTTTRRIVDGKVVSETNDT
17242	47610	Α	17347	467	843	
17243	47611	Α	17348	114	1363	
17244	47612	A	17349	2	281	
17245	47613	Α	17350	1	588	
17246	47614	Α	17351	184	354	
17247	47615	c	17352	391	657	
17248	47616	Α	17353	1	2010	
17249	47617	Α	17354	2	443	VPDLPPSHRGFRAAQGGLPPKN
	1	1	1	1		KVAALPSWGSANQNSSARWEL
l						VSPPIHRGGS*GPGETGDLDGSS
						IQRAVELRLVQAFVVPKSSLRD
		1		1		PSREGRGGWAG*VQTKGA*AR
		1		1		PTLLWAPKR/DRGGKAAPTSTW
		_				NSPKAGCPSARSSPAPP
17250	47618	Α	17355	1	1359	
17251	47619	Α	17356	260	380	
17252	47620	A	17357	153	273	LIVE OT COOR LE CLUMP L'EVE
17253	47621	Α	17358	270	484	AKYRGTGSSRKALGAHWVPKQ
		1			l	PIPAWQHKDPSGGRPEEQGVKL
		1				YREKEFSS*TL*/RI*TGPDAWA
L		-	ļ			YAWADAW
17254	47622	A	17359	2	941	
17255	47623	A_	17360	1	615	
17256	47624	A	17361	911	1472	
17257	47625	A	17362		442	
17258	47626	В	17363	76	235	
17259	47627	A	17364	38	190	
17260	47628	A	17365	134	523	
17261	47629	В	17366	1	1776	

NO:	TAVAVEERQS TTTTGIIPALL DWLIERPKG PLPQHCGSD AASFHSDDDL LCIHSSKEALE FSK  CQGKNTPERS
17262   47630   A   17367   394   554	TAVAVEERQS TTTTGIIVPALL DWLIERPKG PLPQHCGSD RASFHSDDDL LCIHSSKEALE FSK CQGKNTPERS RADLGPAGH
17263   47631   A   17368   22   831	ITTTGII\PALL DWLIERPKG PLPQHCGSD RASFHSDDDL LCIHSSKEALE FSK  CQGKNTPERS R\ADLGPAGH
17264   47632   C   17369   1   1191	ITTTGII\PALIL DWLIERPKG PLPQHCGSD RASFHSDDDL LCIHSSKEALE FSK  CQGKNTPERS R\ADLGPAGH
17265   47633   A   17370   199   647   PSVPTEGSRNRTT DGSGSLSPGKLQT HITGAPVSSDFAL GRRAELSIRSLAL NDWPLQUELLSS GFGAYRRLALHI LNTTQPVTFLNAI   17266   47634   A   17371   1   2697   17267   47635   B   17372   25   1698   ASLRSSPFSRSLR GLPKALFCTKPSR RRPLPSVQPG*AII LTNR   17269   47637   A   17374   2   2543   2543   17270   47638   A   17375   198   403   PQALREHSPSV*T KDCTCQRGRDV	ITTTGII\PALIL DWLIERPKG PLPQHCGSD RASFHSDDDL LCIHSSKEALE FSK  CQGKNTPERS R\ADLGPAGH
DGSGSLSPGLQ  HTGAPVSSDFRL GRRAELSIRSLAL NDWIPLQLRLLSR GFGAPKRLLAHI LNTFQPVTFLNAI   17266 47634 A 17371   2697     17267 47635 B 17372 25 1698     17268 47636 A 17373 2 218 ASLRSSPFSRSLR GLPKALFCTKPSS RRPLPSVQPG*AIL LTNR   17269 47637 A 17374 2 2543     17270 47638 A 17375 198 403 PQALREHSPSV*T KDCTCQRQRDV	ITTTGII\PALIL DWLIERPKG PLPQHCGSD RASFHSDDDL LCIHSSKEALE FSK  CQGKNTPERS R\ADLGPAGH
17266   47634   A   17371   1   2697	CQGKNTPERS R\ADLGPAGH
17267   47635   B   17372   25   1698	R\ADLGPAGH
17268   47636   A   17373   2   218   ASLRSSPFSRSLRG GLPKALFCTKPSR RRPLPSVQPG*AII LTNR   17269   47637   A   17374   2   2543   17270   47638   A   17375   198   403   PQALREHSPSV*T KDCTCQRQRRDV	R\ADLGPAGH
17270 47638 A 17375 198 403 PQALREHSPSV*T KDCTCQRQRRDV	
KDCTCQRQRRDV	
HISSPQGLNSFPA'	/DSVQGKRRL VSLKLEHNV
17271	GRHDYAAAA GTRGSGAPHS GVSICFLFSLK LGPVLGNNSC GLGFPKMCT*
17272 47640 A 17377 14 701	
17273   47641   A   17378   91   309   GRKQFPHLATGK   PCVTVELIFPAPA   PRTAPS*LHCLPV   ARHAAWV	GAAVPRRP*L
17274 47642 A 17379 2 2625	
17275 47643 A 17380 I 1752	
17276 47644 A 17381 3257 3412	
17277 47645 A 17382 1 1091	
17278 47646 A 17383 233 1148	
17279 47647 A 17384 I 1716	
17280 47648 C 17385 162 356	

SEOID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide inscrtion)
		1		sequence		
		<u> </u>		I .		A LUCIONA DE LA PROPERCIONA DEL PROPERCIONA DE LA PROPERCIONA DE LA PROPERCIONA DE LA PROPERCIONA DE LA PROPERCIONA DEL PROPERCIONA DE LA
17281	47649	A	17386	836	2106	AKKFRKRWPLEEQEQNVPDGG
		1				AAPVTALRKRVTSQRCSLEFLE
l		ł		l		DAVGCAPAQRYTPPSAPSSTTP
1	l	l				LGLPLT/TCGARGSWEEKSDLC
		l				PLPCRTKHTSGSPRHKGLKKTH
		l				FIKNMRQYDTRNSRIVLICAKR
		l	ŀ	l		SLCAAFSVLPYGEGLRISDLRV
		l	ľ	l		DSQKQRHPSGGVSVSSEMVFEL
						EGVELGADGKVVSYAKFLYPT
						NALVTHKSDSHGLLPTPRPSVP
		l				RTLPGSRHKPAPTKSAPASTEL
					l .	GSDVGDTLEYNPNLLDDPQWP
		l		1		CGKHKRVLIFASYMTTVIEYVK
		l				PSDLKKDMNETFREKFPHVKLT
1					İ	LSKIRSLKREMRSLSEECSLEPV
						TVAMAYVYFEKLVLQGKLIKQ
						NRKLCAGACVLLAAKISSDLRK
ŀ		l				SGVTQLIDKLEERFRFNRRDLIG
		1				FEFTVLVALELALYLPENQVLP
17282	47650	Α	17387	1	2531	
17283	47651	A	17388	1	1506	
17284	47652	Α	17389	34	576	
17285	47653	Α	17390	112	1840	EELRVREHVTGGICGGSQMMV
		1				DLLGATTLELVAVAPWVMSAA
		i				AGGKNLKSPHKVEVDIIDDNFI
		l			ł	LRWNRSDESVGNVTFSFDYQK
		l			l	TGMDNWIKLSGCQNITSTKCNF
		1			l	SSLKLNVYEEIKLRIRAEKENTS
		l				SWYEV\DSFTPFRKAQIGPPEVH
		1			l	LEAEDKAIVIHISPGTKDSVMW
		1	ļ		1	ALDGLSFTYSLLIWKNSSGVEE
1		1			1	RIENIYSRHKIYKLSPETTYCLK
		1		1		VKAALLTSWKIGVYSPVHCIKT
		1				TVENELPPPENIEVSVQNQNYV
		l				LKWDYTYANMTFQVQWLHAF
		1				LKRNPGNHLYKWKQIPDCENV
				1		KTTOCVFPONVFOKGIYLLRVO
	1					ASDGNNTSFWSEEIKFDTEIQAF
	l	1				LLPPVFNIRSLSDSFHIYIGAPKO
						SGNTPVIODYPLIYEIIFWENTS
		1		1		NAERKIIEKKTDVTVPNLKPLT
		1		1	1	VYCVKARAHTMDEKLNKSSVF
		I		1		SDAVCEKTKPGNTSKIWLIVGI
		I		1		CIALFALPFVIYAAKVFLRCINY
		1		1	l	VFFPSLKPSSSIDEYFSEOPLKNL
	1	1		1		LLSTSEEQIEKCFIIENISTIATVE
		I		1		
		1		1		ETNQTDEDHKKYSSQTSQDSG
17206	17664	١.	17201	12	222	NYSNEDESESKTSEELQQDFV
17286	47654	A_	17391	3	373	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
	L	<u> </u>		[	Luca	L PRICE CONTROL OF TH
17287	47655	Α	17392	1	432	LPRFVGQQPRPLGPLRGSGSEG
į .						CRAPGEAVRAPDYAFPIPGTRA
		1				S/PLNRFPLGGTAWPQAHPTNP
		l				KPAPAPGAQLDDPPRYSRHGLS
					l	RWGLPLQSLVLLPPLQRPMLPQ
		l				AAAPNTPWWPWTLRAGRREN
		ᆫ				AHAQRKLHLWAGKVE
17288	47656	Α	17393	98	376	
17289	47657	A	17394	1	364	
17290	47658	A	17395	1	1230	
17291	47659	A	17396	892	2004	RRMSFMSSEVLVGELMSPFDQS
		1				GLGA\EESLGLLDDYL\EVAKHF
		1				KPHGFSSDKAKAGLLPNGLAV\
		1		ì		DGLVSPSNNSKE\DAF\SGTDW
			ļ	1		DVGRKWVLKEFDFGCPCLGIE*
						PWETIARLTFLTTFGIDICDSLLP
				ŀ		P*FQGRLIKAAPPRRLNPIG\HLP
						QKFLTKPRPGLAPFTF\LQPL\PL
1						SPGVL\SSTPDSFPFSFRSWGS*K
	1	1				WDIH*KGD*/RKPDYTAYVA\MI
		l				PQCIKE\EDTPSD\ND\SGI\CMSP
						ES\YLGSPQHSPST\RGSPNRSLP
		l	ŀ			SPGVLCGSARPKPYDPPGEKMV
			Ì		İ	AAKVKGEKLDKKLKKMEQNK
						TAATRYRQKKRAEQEALTGEC
		1				KELEKKNEALKERADSLAKEIQ
						YLKDLIEEVRKARGKKRVP
17292	47660	Α	17397	43	1300	DSCCIQGTMRLSRTQQRPGVEG
		1			ł	SLKQHQRLHSNFSSINESVFIVS
		l				FSLNTIGSGGRGAEGEP/GREPL
İ		l				SRPQPPAGPLGGALPAPP\SLMP
		ł				QL*SE*GRLLQLLYLLLQ/PAVC
		1				SCSRCSAPRSRCVARPAARTGL
		1				PTPAPASSP/CSRSLSSSRSLSSSC
		1	1			RVSCCHSLSSCCRSLSCSRSSST
		1			1	SSRSSSTSSSSLSLSSSLSCSSCRL
		l				SCSNSFSTSSSSLSLSSSLSCSSC
		1			1	CLSCSNSFSTSSSSLSLSSSLSCS
		ı				SCRLSCSNSFSTSSSSLSCPGSFS
		l				CSHSLSSCSRSLSSCSHSLSSCSR
		1		l		SLSSCSHSLSSCSRSLSSCSHSLS
		1		l		SCSRSLSSCSHSLSSCSRSLSSCS
		l	1			CSLSSCSRSLSSCSHSLSSCSHSL
						SSCSRSLSSCSCSLSSCSRCLSSC
		l				SCSLSSCSRSLSSCLLFRRLNI
17293	47661	A	17398	288	574	COLOCONSESSORE RICENT
17293	47001	A	17398	1200	J/4	

SEO ID	SEO ID NO:	late.	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
17294	47662	A	17399	230	648	VIAPGI.WMMAADIPRVTTPLSS
17274	177002	1.	.,,,,,	1200	0.0	LVQVPQEEDRQEEEVTTMILED
	l	1				DSWVOEAVLOEDGPESEPFPOS
		1	i			AGKGGPOEEVTRGPOGALGRL
						RELCRRWLRPEVHTKEOMLTM
						LPKEIOAWLOEHRPESSEEAAA
	1					LVEDLTOTL*DSWVQEAVLQE
l						DGPESEPFPQSAGKGGPQEEVT
		1				RGPOGALGRLRELCRRWLRPE
		i				VHTKEQMLTMLPKEIQAWLQE
						HRPESSEEAAALVEDLTQTL
17295	47663	Α	17400	105	381	SSGFWPLRFPLDVIKAVSTIAVH
				1		EKEESLWPRVAVFSTLAP/ESPP
l	1	1				WGEAPQSAGR*SGVPEDHVHL
						RYRGTLSLACCSSRHHPPAQLS
			į			HYKN
17296	47664	Α	17401	1023	1915	
17297	47665	Α	17402	3	277	QVLLQGALLLLITVAQAGRVLK
				l		LGVSREFQDLLILWGKETFRR/C
						PGPCSPALHLQPGSSIP/SSQQLL
				į.		*YLAAEQPQLHRGPPRTPAPVS
						GAE
17298	47666	Α	17403	3	299	
17299	47667	С	17404	46	398	
17300	47668	Α	17405	171	403	GKNSTLQQFNNLLHYSSITVAV
		1	l			NNPTLGNSVSVFPLYILFTGIHQ
	1					LVKVILRKLGK*RFGLELASLSL
		<del>  -</del>			100	LFLPPVSLF
17301	47669	A	17406	291	467 395	DHAYVFLGRTACYLMKAYRK
17302	47670	A	17407	2	393	VNPRVIFSSNTIETHPKDLLHSC
	1	1				DHPFAEKTQFTVSTLDDVKNSG
		1				SIRDNYCRTSEISAVHIDTECVS
		1				VMLQAGTPPLQVK*RKNFQQR
1		1				KQG*KMKWDPSDISNSMAEVL
17303	47671	A	17408	1	149	EKEIPGPWLLGAMRFRFCGDLD
17303	4/6/1	^	17408	11	149	CPDWVLAEISTLAK\IPL*SCGCS
		1		1		AARY
17304	47672	A	17409	555	1156	OFYNKTPSRSECPNLLHHMRTE
17304	47072	l^	17409	1777	11130	GPPGGVDQPDGHQAGWPPPEP
i	i		1			AGOORGROSGCHLLOGGASPR
		1	1			PSCGTVHARACTPPASCPPCHR
		ł		l		YRSHLQRGKWWPK/GLPQHTR
				1		LDHTEVLGAAEGSTVSAVPSAT
1		1	1			RAARDHVRRLQTRKCFCKGAL
1	1	1	1	1		LLLITAARAGRVLFGQPQLLQF
						TGQGFAIDTVLGRTGEDETQHC
				1		HCGLHIA
17305	47673	A	17410	3	366	
17306	47674	A	17411	408	1702	
17307	47675	A	17412	1	2661	
		10.0			L	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ 1D NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, V=possible nucleotide insertion)
17308	47676	A	17413	2	2288	
17309	47677	Α	17414	1	1992	MGDFNTPLSTLDRSMRQKVNK
		l		1		DIQELNSAVHQVDLIDIYRTLHP
						KSTEYTFFLAPHRTYSKIDHIVG
	ŀ	l				SKALLSKCKRTEIIRNCLSDHSA
		1				IKLELRINKLTQNCSTTWKLNN
		1				MLLNDYWVHNEMKAEIKMFF
						ETNENKDTTYKNLWDTFKAVC
		l				RGKFIALNAHKRKQERSKIDTL
		l				TSQFKELEKQEQTHSKASRRQE
	1					ITKIRAELKEIETQKTLQKINESR
	ı					SWFFEMISKIDRPLARLIKKKRE
	l	1				KNQIDTIKNDKGDIITDPTEIQTT
						IREYYKHLYAIKLENLEEMDKF
	l					PYTNTLPRLNEEEIESLNRTITGS
						EIEAIIKSLPTKKSPGPDGFTAKF
						YQRYKEELVPFLLKLFQSIEKE
						GILPNSFYEASIILIPKP/DVGSSS
	1	1				QGNQAGERNKGYSFRKRGSQI
		1				VPVCR*YDCTFRKSHFLSPKSP*
	1					ADKQLQQSLRIQNQCAKITSIPI
						HHQQTNREPNHE*TPIHNCFKE
		1				NKIPRNPTYKGCEGPLQGELQT
	i	1				TAQ*NKKGHKQMEEHSMLMD
		1				RKNQYRENGHTAQGNLQIQCH
		1				PHQATNDFLHRIGKNYFKVHM
		1				EPKKSPHCQDTPKQKE*SWRH
	1	1		[		HAT*LQTILQGYSNQNSMVLVP
		1				KQRYRPMEQNRALRNNTTHLQ
	1	1			1	QSDL*QT*QKEEMGKGFPI**M
		1				VLGKLASHM*KAETGSLLYIL
17310	47678	A	17415	ı	1677	

SEQ ID	SEQ ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
17311	47679	A	17416	1	2178	MGDFNTPLSTLGRSTROKVNK
17311	1,0,,	ľ`		ľ	[	DTQELNSALHQADLIDIYGTLH
						PKSTEYTFFSAPHHTYSKIDHIV
	İ					GSKALLSKCKRTEIITNCLSDHR
						AIKLELRIKKLTONRSTTWKLN
		1				NLLLNDYWVHNEMKAEIKMFF
						ETNENKDTTYONLWDTFKAVC
1	İ					RGKFIALNAHKRKOERSKIDTL
ļ					İ	TSQLKELEKQEQTHSKASRRQE
		1				ITKIRAELKEIETOKTLOKINESR
						SWFFERINKIDRPLARLIKEKRE
					1	KNQIDATKNDKGDITTDPTEIQ
						TTIREYYKTLYANKLENLEEMD
			1			KLLDTYTLPRLNQEEVESLNRPI
						TGSEVVAIINSLPTKNSPGPDGF
			l			TAKYYQRYKEELVPFLLKLFQS
						TEKEGILPNSFYEASIILIPKPGR
						DTTKKENFRPISLMNVDAKILN
				l	ł	KILANRIQQHIKKLIHHDQVGFI
						PGMQGWFNICKSINVIQHINRT
						KDKNHMIISIDAEKAFDKIQQPF
				Į.		MLKTLNKLVLEVLARAIRQEKE
						IKGIQLGKEEVKLSLFADDMIV
						YLENPIISAQNLLKLISNFSKVS
ĺ						GYKINVQKSQAFLYTNNRQTES
					i	QIMSELPFTIASKRIKYLGIQLTR
			İ		1	DVKDLFKENYKPLLNEIKEDTN
					1	KWKNIPCSWIGRINIVKMAILPK
						VIYRFNAIPIKLPMTFFTELEKTT
				1		LKFIWNQKRARITKSILSQKNK
					1	AGGITLPDLKLYYKAIVT\KTA
						WYCYQNRDIDQWNRTEPSEIM
17312	47680	A	17417	1	1770	
17313	47681	Α	17418	1	1101	
17314	47682	A	17419	1	1614	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17315	47683	^	17420	1		MVLALTGNKADLASKRPLEFQ EAQAYADDSWLFMETSAKG AMNVNEIFMAIAEKLPKNYD NAAGAPDRNQGYLSACEFSGR KLPKQTTKHIKQSLRTKLCGAS SGYDLQQTPTDLQLWVLTVRK SGYDLQQTPTDLQLWVLTVRK SGYDLQQTPTDLQLWVLTVRK KOKKQKGYPHQNPICMLPSKX KDFKPTKIKRDKDGHYIMVKG SIQQEELTYLNINAPNTGAPRI TRALDRSTRQKVNKDIQEL SALHQADLIDIYRTLHPRSKDY TFFSAPHHTYSKIDHIVGSKALL AKCKRTEITRNCLSOHSAIKLEI KIKKLTQKCSTTWKLNNLLLNI YWYHNEMKABIKMFETNEN DTTYQNLWDTFKAVCRGKFIA LNAHKKKERKSCRSKIDILTSQLKE KINKLIDQKCSTTWKLNNLLLNI KEIKTGKTLYGKNESSEL KINKLIDQKLARLIKKKREKNQI AIKNDKKGDITTDPTEIQTTIREY YKHLYGKLSKELEEMDKFLDT YLPRLNQEEVESLNRPITGSEI
						QRCEKELAQFLLRLFKSTEKEG LPNSFYEDSIIL/ILPKPGRDTTK KENFRPISL
17316	47684	Α	17421	1	1761	
17317	47685	A	17422	1	1875	
17318	47686	Α	17423	1	1611	
17319	47687	A	17424	1	4539	
17320	47688	В	17425	1	6294	
17321	47689	A	17426	2	1913	
17322	47690	Α	17427	1	1026	
17323	47691	A	17428	1	2112	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
17324	47692	Α	17429	I	1884	MENGFDELREEGFRRSNYSELQ
		l			ŀ	EEIQTKGKEVKNIEKNLDECITR
	l	ı	l			IPNTEKCLKKLMELKTKARELR
		l			ł	EECISLRSRCDQLEESVSVMED
	ŀ	l			1	EMHEMKREGKFREKRIKRNEQ
		ı			ŀ	SLQEIWDYVKRPNLRLIGVPED
		l				RSMRQKVNKDTQELNSALHQA
						DLIDIYRTLHPKSTEYTFFSAPH
		l				HTYSKIDHIVGSKALLSKCKRT
		l				EIITNYLSDHSAIKLELKIKKLTO
					1	NFSTTWKLNNLLLNDYWVHN
				1		KMKAEIKMFFETNENKDTTYO
			ł			NLWDTFKAVCRGKFIALNAYK
				ļ	ľ	RKQERSKIDTLTSQLKELEKQE
						OTHSKASRROEITKIRAELKEIE
		l			ŀ	TQKTLQKINESRSWFFERINKID
						RPLARLIKKKREKNOIDAIKND
		l			ŀ	KGDITTDPTEIQTTIREYYKHLY
		1				TNKLENLEEMDKFLDTYTLPRL
		ı				NOEEVESLNRPITGSEIVAIIHSL
		l				PTKKSPGPDGFTAOFYORYKEE
		l				L/RNKIPRNPTYKGCEGPLOGEL
				1		QTTAQGNKRGDKQMEEHSML
		l				MGRKNOYRENGHTAOGNLOIO
		1				
		l				CHPHQATNDFLHRIGKNYFKV
1						HMEPKKSPHRQVNPKPKEQSW
1		l		1		RHHAT*FQIILQGYSNQNSMVL
						VPKQRYRSMEQNRALRNNATY
						LQLSDL*QT*EKQAI
17325	47693	Α	17430	1	1695	
17326	47694	Α	17431	1	3779	MELKTKARELREECRSLRSRRN
						QLEERVSAMEDEMNEMKREG
		1				KFREKRIKRNEQSLQEIWDYVK
		1		l	ŀ	RPNLRLIGVPESDAENGTKLEN
		l		ļ		TLQDIIQEDFPNLARQANVQIQE
		l	İ		1	IQRTPQRYSSRRATPRHIIVRFT
		l			ł	KVEMKQKMLRAAREKDFKPT
		1				KIKRDKEGHYIMVKGSIQQEEL
		1	l	l	l	TILNIYAPNTGAPRFIKQVLSDL
1			1	l	l	QRDLDSHTLIMGDFNTPLSTLD
1			1	l		RSTRQKVNKDTQELNSALHQA
1		l			l	DLIDIYRTLHPKSTE
17327	47695	Α	17432	1	735	
17328	47696	Α	17433	1	2541	
17329	47697	Α	17434	1	1461	
				ــــــــــــــــــــــــــــــــــــــ	ь	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
17330	47698	Α	17435	2	429	AACAAAMSLVIPEKFQHILRVL
		1				NTNIDGRRKIAFAITASSSSSSSS
					1	SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS
		l				SSSSSSSSSVNLLSNGLYL/VKG
		1				VGRRYAHVVLRKADIDLTKRA
		l			ŀ	GELTEDEVERVITIMQNPRQYKI
		ı				PDWFL
17331	47699	Α	17436	1	615	
17332	47700	В	17437	264	556	
17333	47701	A	17438	1	406	FFFFFLQKVGIYLHIKTFQQHRL
		l				WVTSAAFLSLSSMAAVGTSSSL
		l			i	SENSGPGHGGKQTF*GP/EGTDI
		l				PEGRHHFSAQAFSVVAGRGTA
		ı				AALLHGSHVPQGR\SRIGSRSGG
		ı				PPSHPDTCSGSSHSAGRSCPHSC
		1				TG
17334	47702	Α	17439	3	3484	
17335	47703	В	17440	42	367	
17336	47704	В	17441	203	382	
17337	47705	Α	17442	22	266	YRDLPHFLLNSDLIFNMSTSLRE
		l				TMILIRTLSRVPL/PLHGVIQPIS
ĺ		l				KIQGLVLNALNQVQESIFQVSF
						NLFPDAFQHVIRA
17338	47706	Α	17443	1	1137	
17339	47707	Α	17444	1218	1482	QSPWPSLLRGDVSITPNLIFSCL
		l				SIGWPFCLV/SFC*PKK*TFQGV
		l				GSEVYDVKHFASCVLCHKQMN
		_				KLNLYFRNTYFVALLSTELFEN
17340	47708	Λ	17445	2	377	
17341	47709	Α	17446	1	211	
17342	47710	A	17447	2	732	CSSPSN/TILGVQKLNSQWRLA
ĺ	1	l			1	QDFRLINEAVIPLYPVVPNPYTL
	1	l				LSQIPEEAESFTVLDLKDAFFCIP
		l				LHSDSQFLFAFEDPTDHNSQLT
	1	l				WMVLPQGFRDSPHLFGQAQAQ
	i	1				DLVHFSSPGTLVVQYMDDLLL
		1				ATSSEASCQQATLDLLNFLANQ
		l				GCKRVGIALGVLTQTHGTTPQP
				ľ		VAYLSKETDVAAKGPLTAILLL
		l		ł		LAFGPCIFNLLVKLVSSRIDAIK
l	1	1	1	1	I	LQMVLQMEPQMSSTNNFYRGP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	location of first codon for peptide	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				sequence		
17343	47711	Α	17448	I	3003	MPGAQDLQPTMPEPPHPQWAP
						TWPEPPRRVPPPAPRRPVPLTA
						QGLSVDQSRLGKFSDDPDRYID
						VLQGLGQTFDLTWRDVMLLLD
		ŀ		l		QTLAFNEKNAALAAAREFKDT
		l				WYLSQVNDRMTAEERDKFPSG
		1				QQAVPSMDPHWDLDSDYGDW
		1				SHKYLLTCVLEGLRRIRKKPMN
		1				YSMMSTITQGKEENPAFLEQL
						WEALRKYIPLSPKSLEGQLILKD
		l				KFITQSAADIRGKLQKQSLVPE
		<u> </u>				QNLEALLNLATSVFYNRDQ
17344	47712	Α	17449	5	624	IQPILAYPHPKTLKQLWGFLGIT
					i	/GFCPVWIPRCSKIAKSLYTLIKE
		1				TQRANTHLVEWEPEAETAFKT
		1			i	LKQALVQAPTLSLPTGENFSLY
	1				l	VTERAGIALGVLTQTRGTTPQP
						VTYLKDGEPMKCDCQQIIVQTY
		1		1		ATQDDLLEVPLANPDLNLYTD
						GSSFVENGIRRAGYAIVSDVTIL
		l				ESKPLPPGTSAQLAELVALTRA
10045	40010		17450	626	2620	LELGKGKE SNDRTEDDCGKHPFMSSPP\TEP
17345	47713	A	17450	636	2628	WVCLIEGOEIDFLLDTGTTFSV
	ł					LIPCLGRLSSRSVTIQGILGQPVT
	ļ					RYFSHLLSCNWETLLFSHAFLV
						MPESPTPLLGRDILAKAGAIISM
	1	l				KTGNKLPICCPLLEGINPEVWA
	1	l				LEGOFGRAKNAHPLOIRLKDPI
		l				SFPYOROYPLRPEAHKGLODIV
		1				KHLKAQDSVRKCSSPCNTPILG
						VOKLNSOWRLVODLRLINEAVI
					l	PLYPVVRNPYTLLSOVPEEAEW
						FTVLDLKD
17346	47714	Α	17451	2	568	CSSPSN/TILGVQKLNSQWRLA
1,340	1	l' 1	1.,,,,,	Γ		ODFRLINEAVIPLYPVVPNPYTL
	1	1				LSQIPEEAESFTVLDLKDAFFCIF
	I				1	LHSDSQFLFAFEDPTDHNSQLT
1	1		1		1	WMVLPOGFRDSPHLFGOAOAO
	1	1			1	DLVHFSSPGTLVVQYMDDLLL
	1	1	1		I	ATSSEASCOQATLDLLNFLANO
					1	GCKRVGIALGVLTOTHGTTPOP
		1	I			VAYLSKETDVAAK

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
		_				
17347	47715	Α	17452	254	849	LQPESLEIAGILVQ*MIE*QPKK
					\	GTNSIPVSKPSP/GVQKPNGQW
			Ì			RQVQDLRLISDAVIPLYPAVSNF
						YTLLSQILEEAEWFTVLDLKDA
						FFCIPLRSDSQFLLAFEDPTDHT
1						SQLTWTVFTQGFMDTPHLFGQ
ŀ						SLAQDLGHFSSPGTLVLQYVDD
İ		1				LLLAKQQATLDLLNFLANQGY
1 2 40	40014	١	17452		369	KLSKLKAQLCELLVFSSCARMH
17348 17349	47716 47717	A	17453 17454	1	1632	
17350	47718	A	17454	636	1837	SNDRTEDDCGKHPFMSSPP\TEP
1/330	4//10	^	17433	030	1007	WVCLIEGOEIDFLLDTGTTFSV
		1				LIPCLGRLSSRSVTIQGILGQPVT
1		i				RYFSHLLSCNWETLLFSHAFLV
l						MPESPTPLLGRDILAKAGAIISM
						KTGNKLPICCPLLEGINPEVWA
						LEGOFGRAKNAHPLOIRLKDPI
		1				SFPYOROYPLRPEAHKGLODIV
ŀ						KHLKAQDSVRKCSSPCNTPILG
		1		l		VQKLNSQWRLVQDLRLINEAVI
		1				PLYPVVRNPYTLLSQVPEEAEW
		l				FTVLDLKDAFFCIPLHSDSQFLF
		ı				AFEDPTDHTSQLMWMVLPQRF
		ı				RDSPHLFGQAQAQDLGHFSSPG
1	1	ı				TLVLQYSEIAKTLYTLIKEMER
		ı				ANTHLVEWEPEAETAFETLKQ
		l				ALVQAPALSLPTGQNFALYVIE
1		l				RAGIALGVLTQTHRTTPQPVAY
17351	47719	A	17456	2	52	EISFVENGIQRAGYAIVSDVTVL
		l				ESKPLLPGTSAQLAELVALTRA
		l				FELGKGKRINANTDSKYAYLIL
		l				HALAAIWKEREFLISGGTPIKYH
		l				KEIMELLHAMQKPKEVAVLHC
		Ь				QSHQKG*EWDTKGRLCHS
17352	47720	Α	17457	1625	2505	PGVQKP/GQWRLVQDLRLINEA
		l			•	VIPLYPVVPKPYTLFSQIPKEAE
		l				SFTVLDLKDAFFCIPLHSDSQFL
		l				FAFEDPTDHTSQLTWTVLPQRF
		1				RDSPHLFGQALVQDLGHFSSPG
		ı		l		TLVLQFVDDLLLAASSEASCQQ
						ATRDLLNFLANQGYKASKSKA OLCLOOVKYLGLILARGTRALS
						KKRIQPILAYPRPKTLKQLRGFL
		1	l			GITSFCRLQIPGYSKMARPLYTL
		l				IKETORANTHLVEWEPEAETAF
			1			KSLKQALVQAPALSLPTRQNFS
		1				LYVRERAGIALEVLTQTHGTTL
						OPVAKG
17353	47721	A	17458	1	2415	V
11333	7//21	<u></u>	1.7450	l.	~T10	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
		<u> </u>				TO COLUMN OTTO DO VIDA VA VIDA VIDA
17354	47722	Α	17459	2646	5167	KNSGHILGTCPGYRYAKGKET
					1	GKEIIKGPQNPPGYRLCPLQAV
						GGGEFGPTQVHVPFSLSDLKQI
		1				RVDLGKFSDDPDRQYPLRPEAH
					1	EGLQDILRYLKVQGLVRKCSSP
						CNTRILGVQKPKGQWRLVQDL
						RFINEAVIPLHSVVPNSYTLLSQI
						PEEVEWFTVLDLKDAFFCIPLH
						SVCQFLFAFEDPTDIITSQFTWT
						VLPQGFRDSPHLFGQILAQDLG
						HFSSPGTLVLQYVDDLLLATSL
	l	1				EASCQQATLDLLNLLANQGYK
	i	1				ASKPKAQLCLQQVKYLDLSLA
1		1				RVTRALSKERIQPILACPRPKTL
				ì		KQLRGFLGITNFCQLWIPGYSE
						MARPLYTLIKETQRANSHLVER
						EREAETAFKTLKQALVQALALS
						LPTGQNFSLYARERAGIALGILT
1						OTHGTTPOPVTYLRKLIYSFVE
1						NGMRRAGYAIVSDVTVPESKPL
						PPGTSTQLAELVVLTQALELRK
						KKRINVNTDSKYAYLILHAHAA
						IWKEREFLTSGGTPNKYHKEIM
		1				ELLHAVQKPKEVAVIPCQSHQK
						GEEK/EAEGNRRADAE\AKIAA
				1	i	RRNLPTEIPMEGPLVWNNPVQE
		l				IKPOYSLTKTEWGLSOGHSFLP
						LGWLTTLEGKAGRATPNPRNV
		l		l		YFPLHLRGLRTGRLPLSOSTRA
		1				QEMTLVRPRPSSSPPPEKAAEG
		1				RGRRCSSETKLRHRRLFRPLRTP
		1				LCATAPLAASVAAVLAAAPAA
17355	47723	В	17460	l .	2208	
17356	47724	A	17461	2	168	·
17357	47725	A	17462	890	1034	
17358	47726	A	17463	386	619	TFITGDCLGTKN/HIFDGCGVLS
1.556		1		1		EVGLVLDCSNQRFKAGPA*LCQ
		1		I	1	SPFKNIL*ESLPMCMCROLEKH
	1			I		AHPOGLCHTOVT
			l——			40504 . 1

SEQ ID	SEQ ID NO:		SEQ ID NO:		Nucleotide location of last	
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				bequeue		
17359	47727	Α	17464	123	2169	DLGHRGSREMASVA\LEDVAV
		İ				NFTREEWALLGPCQKNLYKD\
						MQETIRNLDCVGMKWKDQNII
				1		DOYRYPRKNLRCRMLERFVES
				1		KDGTQCGETSSQIQDSIVTKNT
	l .	1				LPGS/VGPYESRMSGEVIMGHS
		1				LNCYIRVGAGHKPHEYHECGE
		ı		1		KPDTHKQRGKAFSYHNSFQTH
		1				ERLHTGKKPYDCKECGKSFSSI
	-	1				GNLQRHMAVQRGDGPYKCKL
		1				CGKAFFWPSLLHMHERTHTGE
		1			l	KPYECKQCSKAFSFYSSYLRHE
		1				RTHTGERPYECKQCSKAFPFYS
	1	1		1		SYLRHERTHTGEKPYKCKQCS
		1				KAFPDSSSCLIHERTHTGEKPY
	İ		1			CKQCGKAFSVSGSLQRHETTH
						AEKPYACQCGKAFHHLGSFQ
			1			RHMIRHTGNGPHKCKICGKGF
						DCPSSLQSHERTHTGEKPYECK
	1				1	QCGKALSHRSSFRSHMIMHTG
	1	1			1	DGPHKCKVCGKAFVYPSVFQF
		1				HERTHTAEKPYKCKQCGKAYF
						ISSSLRRHETTHTGEKPYKCTLO
	Į.					KAFIDFCSFQNHKTTHTGEKPY
						ECKECGKAFSRFRYLSRHKRTI
						TGEKPYECKTCRKAFGHYDNL
						KVHERIHSGEKPYECKECGKA
						SWLTCFLRHERIHMREKSYECE
		1	1			QCGKAFTHSRFLQGHEKTHTG
		1				ENPYECKECGKAFASLSSLHRI
	1					KKTHWKKTHTGENPYECKEC
		1				KAFASLSSLHRHKKTHWKKTH
17360	47728	Α	17465	1	1317	
17361	47729	Α	17466	1	336	
17362	47730	С	17467	51	353	
17363	47731	Α	17468	190	348	YAIHIMDVHTVRSLYYFNCFR
		1	•			*ACYCCHYLTDIPEITKLSGCSY
		_				GGTSLIWG
17364	47732	Α	17469	I	1716	
17365	47733	Α	17470	I	840	
17366	47734	Α	17471	699	1283	LLTARLTWVSARLMSYVLLM
						*LFPRLLSCLTTPPHCSFSICFVI
						C/FKNVDLKGFEPDVRILLTKY:
						NSNGSQSPWMEEQIRDAGERV
l		1				HSAFSLNWGKPLVFEKDRPYS
		1				SVFIGLFLPMAEKTGPLKGNPG
		1		1	1	GEFLLFLRQIQLVWLPAAGIMT
	1	1	1	1		EHYFPITATQALEINNAISTIME
	1	1				
		L				FPTVSFASQWITASFSV
17367 17368	47735 47736	A	17472	300 I	461 2451	FPTVSFASQWITASFSV

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*-Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide sequenee	of peptide sequence	deletion, \=possible nueleotide insertion)
17369	47737	Α	17474	2	3542	
17370	47738	Α	17475	1	1156	
17371	47739	Α	17476	Ĭ	1176	
17372	47740	Α	17477	1	257	
17373	47741	A	17478	295	1353	
17374	47742	Α	17479	3	1772	
17375	47743	Α	17480	2	284	
17376	47744	Α	17481	1	141	
17377	47745	Α	17482	1	506	PHSPLWKTLCSPSSGVCCGFVT
						LFCNDRFACLFQLTPPPSPAWM
						TAAASLLASLLPALPPLNLQDA
						KFVEERRKQLQNYLRTVMNKV
						IQMVPEFAASPKKETLIQLMPFF
						VMGLQVGMYGLFHFGVMMDQ
						PQPSLTRADESPCDRVLSPCAA
	1		l			HRKQRDCCLSWKAEPE*FLVK*
	1	1				KTLCSPSSGVCCGFVTLFCNDR
	1				i	FACLFQLTPPPSPAWMTAAASL
	1			ł		LASLLPALPPLNLQDAKFVEER
	İ	l				RKQLQNYLRTVMNKVIQMVPE
						FAASPKKETLIQLMPFFVMGLQ
				l	ļ	VGMYGLFHFGVMMDOPOPSLT
		l		1		RADESPCDRVLSPCAAHRKQR
						DCCLSWKAEPE
17378	47746	Α	17483	1	741	
17379	47747	Α	17484	1	993	
17380	47748	В	17485	277	416	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence		09/540,217		of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
17381	47749	A	17486	686	2400	TGMSVDEKPDSP\MYVYESTVH
1/361	47749	^	17480	000	2400	CTNILLGLNDORKKDILCDVTLI
		l				VERKEFRAHRAVLAACSEYFW
	Ì	1				QALVGQTKNDLVVSLPEEVTA
						RGFGPLLOFAYTAK\LLLSRENI
						REVIRCAEFLRMHNLEDSCFSF
		ļ.				LQTQLLNSEDGLFVCRKDAAC
						QRPHEDCENSAGEEEDEEETM
1		ļ.				DSETAKMACPRDQMLPEPISFE
}						AAAIPVAEKEEALLPEPDVPTD
		[				TKESSEKDALTQYPRYKKYQL
				İ		ACTKNVYNASSHSTSGFASTFR
1	l					EDNSSNSLKPGLARGQIKSEPPS
			i			EENEEESITLCLSGDEPDAKDR
1				1		AGDVEMDRKQPSPAPTPTAPA
1		1			ŀ	GLCLERSRS/GNYGQPH/VGQK
1		l				EVSNFTMGS/PLRGPGLEALCK
		l				QEGELDRRSVIFSSSACDQVSTS
		l	İ			VHSYSGGARFLATEHQEPGLM
						GDGMYNQVRPQIKCEQSYGTN
						SSDESGSFSEADSESCPVQDRG
i				ŀ		QETGSTSDLRLSTKLQSCSGPM
						FKGPTATVAATESWGTVLQNIP
1						LGCAGTGEEVTYTNPPPRGRAA
1		1		l		LVPRSPLTVYSSSLPEHQTSLKQ
1						CAQAGPGVCLLVHNHWQLLEG
17382	47750	Α	17487	1	1089	
17383	47751	С	17488	295	348	
17384	47752	Α	17489	1	711	
17385	47753	A	17490	1	1248	
17386	47754	Α	17491	135	259	
17387	47755	Α	17492	434	506	
17388	47756	Α	17493	3	227	
17389	47757	С	17494	3	236	
17390	47758	С	17495	25	153	

17391   47759   A   17496   1   1   1   1   1   1   1   1   1	ISEO ID		Met	SEQ ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence ( X-Unknown,
17391   1759   A   17496   I   1557   MASPEAVASQINDGFSQRPP   PLFASRSVINELKSQRTPRGEV   SVTDGEKTDGSWRMTVDYCK   NQVVTPIAAAVPDVVSLLEQII   TSPDITLVHYIDDIMLNGSSEQ   VINTLDLLVRHLCATTWEINE   KIQGSSTSVKFLGVQWCGDCR   DVPSKVKDKLLHLAPPTIKKE   QPL.TGLFGFRRKYIPYLGVLL   PIYQVTRKAASPQWRPEGEKA   QQVQAAMQAAPLGPYDPAA   WILEIAVADTEAVWGHWHS   SFPSHPCHCPMGP*TKWP*WQ   WRLCMGSATWTSTHEG*PGY   HQ*VPNLPAAETNTEPAI*HHS   SRRSASVLAG*I,VWTSCIME   AEHILLWWCLSCMQCFCQD   YPPRHSQHPPLWYSTQLCI   PPRHSLYH*STSNIFASCFYGTTC   WSRGLSRGRNAATRRQNNSI   LVPCSPSS*SSRVDRTVERPFEI   TTMPTSQESRVCPSGSGGSGT   THHHPF*STSNIFASCFYGTTC   WSRGLSRGRNAATRRQNNSI   L*VKIATWTLWAPPTISKL   PHYTGGESRGGSGGT   WSRGLSRGRNAATRRQNNSI   L*VKIATWTLWAPPTISKL   PHYTGGESRGGSGGT   WSRGLSRGRNAATRRQNNSI   L*VKIATWTLWAPPTISKL   PHYTGGESRGGSGGF   WSRGLSRGRNAATRRQNNSI   L*VKIATWTLWAPPTISKL   PHYTGGESRGGGSGG   WSRGLSRGGRNAATRRQNNSI   L*VKIATWTLWAPPTISKL   PHYTGGESRGGGGGT   WSRGLSRGGRNAATRRQNNSI   L*VKIATWTLWAPPTISKL   PHYTGGESRGGGGGT   WSRGLSRGGRNAATRRQNNSI   L*VKIATWTLWAPPTISKL   PHYTGGESRGGGGGT   WSRGLSRGGRNAATRRQNNSI   L*VKIATWTLWAPPTISKL   PHYTGGESRGGGGGT   WSRGLSRGGRNAATRRQNNSI   L*VKIATWTLWAPPTISKL   PHYTGGESRGGGGGT   WSRGLSRGGRNAATRRQNNSI   L*VKIATWTLWAPPTISKL   PHYTGGESRGGGGGT   WSRGLSRGGRNAATRRQNNSI   L*VKIATWTLWAPPTISKL   PHYTGGESRGGGGT   WSRGLSRGGRNAATRRGNNSI   L*VKIATWTLWAPPTISKL   PHYTGGSRGGGT   WSRGLSRGGRNAATRRGNNSI   L*VKIATWTLWAPPTISKL   PHYTGGSRGGGT   WSRGLSRGGRNAATRRGNNSI   L*VKIATWTLWAPPTISKL   PHYTGGSRGGGGT   WSRGLSRGGRNAATRRGNNSI   L*VKIATWTLWAPPTISKL   PHYTGGSRGGGT   WSRGLSRGGRNAATRRGNNSI   L*VKIATWTLWAPPTISKL   PHYTGGSRGGGT   WSRGLSRGGT   PHYTGGSRGGGT   WSRGLSRGGT   PHYTGGSRGGT   PHYTGGSRGGGT   WSRGLSRGGT   WSR	NO:	SEQ ID NO:		in USSN			*-Stop codon, /-possible nucleotide
17391   47759   A   17496   1   1557   MASPEAVASQINDGFSQKPF   PLFASRSVNRLKSQRTPRGEV  SVTDGEKTDGSWRMTVDYCK   NQVYTPIAAVPDVSLLEGG  NGVYTPIAAVPDVSLLEGG  NGVYTPIAAVPDVSLLEGG  NGVYTPIAAVPDVSLLEGG  NGVYTPIAAVPDVSLLEGG  NGVYTPIAAVPDVSLLEGG  NGVYTPIAAVPDVSLLEGG  NGVYTPIAAVPDVSLLEGG  NGVTSPATRICAGGE  NGVGSTSVKFLGVQWCGDCF   DVPSKVKDKLLHLAPPTTKKE   QHLTGLEGFREKYIPYLGVLL   PLYQVTRKAASFQWRPEGEKA   QQVQAAMQAALPLGPYDPAG   MVLEIAVADTEAVWFW WG   WRLCMGSATWTSTHEG*PGY   HQ*VPNLPAAETNTEPAI*HIS   SRRSASVLVAG*I,VMSCGMS   VLPCSPSS*SSRVDRTVERPFE  TTMPISOESR VCPSSGGSGSG   THHPP*STSNIFASCFYGITFC   WSRGLSSRGRNAATRQNNSI   L*VKIATWTL WAPPTSKL   PHYDGESR VCPSSGG   THHPP*STSNIFASCFYGITFC   WSRGLSSRGRNAATRQNNSI   L*VKIATWTL WAPPTSKL   VGCSWNSI   VLPCSPSS*SSRVDRTVERPFE  TTMPISOESR VCPSSGGSGSGS   THHPP*STSNIFASCFYGITFC   WSRGLSSRGRNAATRQNNSI   L*VKIATWTL WAPPTSKL   VGCSWNSI   VLPCSPSS*SSRVDRTVERPFE  TTMPISOESR VCPSSGGSGSGS   VLPCSPSS*SSRVDRTVERPFE  TTMPISOESR VCPSSGGSGSGS   VLPCSPSS*SSRVDRTVERPFE  TTMPISOESR VCPSSGGSGSGS   VLPCSPSS*SSRVDRTVERPFE  TTMPISOESR VCPSSGGSGSGS   VLPCSPSS*SSRVDRTVERPFE  TTMPISOESR VCPSSGGSGSGS   VLPCSPSS*SSRVDRTVERPFE  TTMPISOESR VCPSSGGSGSGS   VLPCSPSS*SSRVDRTVERPFE  TTMPISOESR VCPSSGGSGSGS   VLPCSPSS*SSRVDRTVERPFE  TTMPISOESR VCPSSGGSGSGS   VLPCSPSS*SSRVDRTVERPFE  TTMPISOESR VCPSSGGSGSGS   VLPCSPSS*SSRVDRTVERPFE  TTMPISOESR VCPSSGGSGSGS   VLPCSPSS*SSRVDRTVERPFE  TTMPISOESR VCPSSGGSGSGS   VLPCSPSS*SSRVDRTVERPFE  TTMPISOESR VCPSSGGSGSGS   VLPCSPSSGGSGSGS   VLPCSPSSSSSS VCPSSSSSSS VCPSSSSSSSS VCPSSSSSSSSS VCPSSSSSSSSSS				09/540,217		of peptide sequence	deletion, \=possible nucleotide inscrtion)
PLFASRSVNELKSORTPRGEV    SVTDGEKTDGSWRMTVDYCK    SVTDGEKTDGSWRMTVDYCK    NQVYTPIAAAVPDVVSLLEQI    TSPDITL VHYIDDIMLINGSSEQ     VTNTLDLLVRHILCATGWEINS    KIQGSSTSVKFLGVQWCGDCR    CQUYGAMQAALPLGYPPPAC    MVLEIAVADTEAVWGHAVHS    SFPSHPCHCPMGP*TKWP*WQ     WRLCMGSATWTSTHEG*PGYV     HQ*VFNLPAAETNTEPAI*HHS    SRRSASVLVAG*I,VMTSCMEIN     AFHIL WWWC1.SCMQCPCOD     YHPWTHGMPYPPLWYSTQLC    **PRISLYH*RSVAVCSCSWNSI    VLPCSPSS*SSRVDRTVERPFEI     TTMPTSQESR VOSGSOS     THHHP**STSNIRASCFYGITFC     WSRGLSSRGRNAATRRQNNSI     L*VKIATWTLWAPPTSKL     WSRGLSSRGRNAATRRQNNSI     L*VKIATWTLWAPPTSKL     QVQAVQAALPLGPPPADPM     VQATQKAASFEWGPEGEKAL     QVQVAVQAALPLGPPPADPM     VQATQKAASFEWGPEGEKAL     QVQVAVQAALPLGPPPADPM     VGCGFWRGHFHIGALLW     VQATQKAASFEWGPEGEKAL     QVQVAVQAALPLGPPTKWPWWQF     LEEA*LENW*QRNLGKRYDC     PL*VVKNWKDICIPECSPTGD     SRGGF**SSG*DDPFCGHHASSI     PSHCCRPMGP*TKWPWWQF     RLCMDSATWTSTHGS*PDYSH     C*VPNLPAAETNTETSIWHHS     G*SASYLLAG*LH*TSSIMEKAI     VSPHWNKIISLUWVCLSSMQ     FCQOYHEWTHSMPYELSWYST     QHCLSLQRERHSLVR*RSAAVC     ACS     T3393   47761   A 17498   I 998     T3395   47765   A 17501   I 1332     T3397   47765   A 17505   I34     4477     PLFASSTONSSTORE     SPHOCR TO STORE     SVENTEN	1	1	1		sequence		· ·
PLFASRSVNELKSORTPRGEV    SVTDGEKTDGSWRMTVDYCK    SVTDGEKTDGSWRMTVDYCK    NQVYTPIAAAVPDVVSLLEQI    TSPDITL VHYIDDIMLINGSSEQ     VTNTLDLLVRHILCATGWEINS    KIQGSSTSVKFLGVQWCGDCR    CQUYGAMQAALPLGYPPPAC    MVLEIAVADTEAVWGHAVHS    SFPSHPCHCPMGP*TKWP*WQ     WRLCMGSATWTSTHEG*PGYV     HQ*VFNLPAAETNTEPAI*HHS    SRRSASVLVAG*I,VMTSCMEIN     AFHIL WWWC1.SCMQCPCOD     YHPWTHGMPYPPLWYSTQLC    **PRISLYH*RSVAVCSCSWNSI    VLPCSPSS*SSRVDRTVERPFEI     TTMPTSQESR VOSGSOS     THHHP**STSNIRASCFYGITFC     WSRGLSSRGRNAATRRQNNSI     L*VKIATWTLWAPPTSKL     WSRGLSSRGRNAATRRQNNSI     L*VKIATWTLWAPPTSKL     QVQAVQAALPLGPPPADPM     VQATQKAASFEWGPEGEKAL     QVQVAVQAALPLGPPPADPM     VQATQKAASFEWGPEGEKAL     QVQVAVQAALPLGPPPADPM     VGCGFWRGHFHIGALLW     VQATQKAASFEWGPEGEKAL     QVQVAVQAALPLGPPTKWPWWQF     LEEA*LENW*QRNLGKRYDC     PL*VVKNWKDICIPECSPTGD     SRGGF**SSG*DDPFCGHHASSI     PSHCCRPMGP*TKWPWWQF     RLCMDSATWTSTHGS*PDYSH     C*VPNLPAAETNTETSIWHHS     G*SASYLLAG*LH*TSSIMEKAI     VSPHWNKIISLUWVCLSSMQ     FCQOYHEWTHSMPYELSWYST     QHCLSLQRERHSLVR*RSAAVC     ACS     T3393   47761   A 17498   I 998     T3395   47765   A 17501   I 1332     T3397   47765   A 17505   I34     4477     PLFASSTONSSTORE     SPHOCR TO STORE     SVENTEN	15201		-	T17496	11	1557	MASPEA VASODNINGES OF PRO
SVTDGEKTDGSWRMTUDYCK   NQVVTPIAAAVPDVVSLLEQIT   TSPDITLVHYUDDIM.NGSSEQ   VTNTLDLLVRH.CATGWENN   KIQGSSTSVKE,GVQCGDCE   DVPSKVKDKLLHLAPTTKKE   QHL.TGLFGFRKYPYLGVLL   PLYQVTRKAASFQWRPEQEKA   QQVQAAMQAALPLGFYDPAG   MVLEIAVADTEAWGHWHS. SFPSHPCHCPMGP*TKWP*WQ   WRILCMGSATWTSTHEG*PGV   HQ*VPNLPAAETNTEPA1*HIS   SRRSASYLVAG*1,YWTSCIME  AEWHLLWIWVCLSMQCFCQD   YHPWHIGMPYPPLWYSTQLC   *PRRISLYH*RSVAVGSCSWNSI   VLPCSPSS*SSRVDRTVERPEI   TTMPTSQESRVQSRGGSGGT   THHIP**STSNIFASCFYGTTC   WSRGLSSRGRNATRRQNNSI   L*VKIATWTLWAPTTSKL   WGATQKAASFEWGPEQEKAL   QQVQAVQAALPLGFYDPADPR   VLEWSVADRDAVWSLWQAPIE   GQRQFGFWSKALPSSTDNY; GFRCAINY*NRGCQ*FGWNSL   GPRCAINY*NRGCQ*FGWNSLAPSSTDNY; GFRCAINY*NRGCSWNSLAPSSTDNY; GFRCAINY*NRGCSWNSLAPSSTDNY; GFRCAINY*NRGCSWNSLAPSSTDNY; GFRCAINY*NRGCSWNSLAPSSTDNY; GFRCAINY*NRGCSWNSLAPSSTDNY; GFRCAINY*NRGCSWNSLAPSSTDNY; GFRCAINY*NRGCSWNSLAPSSTDNY; GFRCAINY*NRGCSWNSLAPSSTDNY; GFRCAINY*NRGCSWNSLAPSSTDNY; GFRCAINY*NRGCSWNSLAPSSTDNY; GFRCAINY*NRGCSWNSLAPSSTDNY; GFRCAINY*NRGCSWNSLAPSSTDNY; GFRCAINY*NRGCSWNSLAPSSTDNY; GFRCAINY*NRGCSWNSLAPSSTDNY; GFRCAINY*NRGCSWNSLAPSSTDNY; GFRCAINY*NRGCSWNSLAPSSTDNY; GFRCAINY*NRGCSWNSLAPSSTDNY; GFRCAINY*NRGCSWNSLAPSSTDNY; GFRCAIN	17391	47759	^	1,7.50	1	1337	
NQVYTPIAAA VPDVYSLLEQNT   TSPDITLVHYIDDIM.NGSSEQ	1	1	1	1		1	
TSPDITLYHYIDDIMINGSSEQ	1	1	1	1		l	
VINTLDLVRHLCATGWENN   KIQGSTSVKFLGVQWCGDCR   DVPSKVKDKLHLAPPITKKE   QHLTGLFGFRRKYIPYLGVLL   PHYQVTRKAASFQWFEQEKA   QQVQAAMQAALPLGPYDPAG   MVLEIAVADTEAWGHMHS.   SFPSHPCHCPMGPTKWP*WQ   WRLCMGSATWTSTHEG*PGY-HQ**VPNLPAAETNTEFPAI*HIS   SRRSASYLVAG*LYWTSCIMEI   AEHILLWIW*CLSCMQCPCQD   YHPWHTIGMBYPLWYSTQLCL   *PRRISLYH*RSVAVGSCSWSI   VLPCSPS*SSTAVDTVERPEI   TTMPTSQESR VQESRGGSGGT   THHHP**STSNIFASCFYGITFC   WSRGLSSRGRNAATRQNNSI   L*VKLATWTLWAPPTSKL   PSKVEKLLHLAPPTIKKEAGR   LVQCJGFWRQHPHLGALLW   YQATQKAASFEWGPEQEKAL   QVQVAQAALPGTPDAAPP   VLEVSVAADRDAVWSLWQAPIC   ESQQPLGFWSKALPSSTDNYS   CFRCAIIV*FMGCCQ*FGWINT   LEEA*LENW*QRNLGKRYVDC   PL*VVNIWKDICIPCECSTGOD   SRGGF**SSG*DDPFCGHISASI   PSHPCCRPMGP*TK WPWWQE*RLCMSATWTSTHQS*PDYSH   C*VPNLPAAETNTETSIWHHS   G*SASYLLAG*H*TSSIMEASH   VSPHWKHSLWIWVCLSSMQCQOYHUMTHSSIMEASH   VSPHWKHSLWIWVCLSSMQCQOYHUMTHSSIMEASH   VSPHWKHSLWIWVCLSSMQCQOYHUMTHSSIMEASH   VSPHWKHSLWIWVCLSSMQCQOYHUMTHSSIMEASH   VSPHWKHSLWIWVCLSSMQCCQOYHUMTHSSIMEASH   VSPHWKHSLWIWVCLSSMQCQOYHUMTHSSIMEASH   VSPHWKHSLWIWVCLSSMQCCQOYHUMT	1	1	1	ſ		į.	
KIQGSSTSWKFLGVQWCGDCR	l	1	1	1			
DVPSKVKDKLHLHAPPTTKKE   QHLTGLFGFRRKYIPYLGVLLG   PHYQVTRKAASTQWRPEQEKA   QQVQAAMQAALPLGPYDPAG   MVLEIAVADTEAWGHWHS. SFPSHPCHCPMGP*TKWP*WQ   WRLCMGSATWTSTHEG*PGY   HQ*VPNLPAAETNTEPAI*HHS   SRRSASYLVAG*LYWTSCIME!   AEWHLLWIWVCLSMQCFQOD   YHPWHIGMPYPPLWYSTQLC   *PRRISLYH*RSVAYGSGWSIS   VLPCSPS*SSRVDRITVERPFE!   TTMPTSQESRVQESRGGGGGG   THHHP**STSNIFASCFYGITTC   WSRGLSSRGRNAATRRQNIS!   L*VKIATWTLWAPPTSKL   AEWHLAWWAPPTSKL   QQVQAVQAALPLGPYDPADPP   VLEVSVADRDAVWSLWQAPIE   LQQVQVAVQAALPLGPYDPADPP   VLEVSVADRDAVWSLWQAPIE   SGQRPLGFWSKALPSSTDNY: GFRCAINY*PMGCQ*FGWSKALPSSTDNY: GFRCAINY*PMGCAINY*GFRGAINY*PMGCAINY*GFRGAINY*GFTGAIN*	1	1	1				
QH.T.GL.FGFRRX/IPYLGVLLL   PIYQVTRKAASFQWPPEQEKA   QQVQAMQAALPLGPYDPAC   MVLEIAVADTEAVWGHWHS.   SFPSHPCHCPMGP*TKWP*WQ   WRLCMGSATWTSTHEG*PGYM   HQ*VPNLPAAETNTEPAI*HHS   SRRSASVLVAG*LYWTSCHEE  AEHILLWIWVCLSCMQCFCQD   YHPWHGMB*PPLWYSTQUCL   **PRIBLYH*RSVAVGSCSWNSI   VLPCSPS*SSRVDRTVERPFEI   TTMPTSQESSRVQESRGGGSGG*THHHP**STSNIFASCFYGITFC   WSRGLSRGGRNAATRQNNSI   L*VKLATWTLWAPPTSKL   PIXVKEKLHLAPPTISKL   PIXVKEKLHLAPPTISKL   PIXVKEKLHLAPPTISKL   PIXVKEKLHLAPPTISKL   PIXVKEKLHLAPPTISKL   PIXVKEKLHLAPPTISKL   PIXVEYADROAVWSLWQAPIC   BSQQRPLGFWSKALPSSTDNYS   CFRCAHIY**PRGCQ*FGWINFI   LEEA*LENW*QRNLGKRYDC   PL*VVNNWKDLGPCS*PSTOD   SRGGF**SSG*DDPFCGHNSASI   PSHFCCRPMGP*TKWPWWQFE   RLCMBAATWTSTHGS*PDYSH   C*VPNLPAAETNTETSIWHHS   G*SASYLLAG**LHTSSIMEKAL   VSPHWNKHSLWIWVCLSSMQC   FCQOYHPWTHSMPYPLSWYST   QHCLSLQRERHSLYR**RSAAVC   ACS   A 17409   1 915   17395   47765   A 17501   1 1332   17396   47765   A 17501   1 1332   17397   47765   A 17503   151   674   17599   47767   A 17505   134   447	1	1	1	l			
PIYQVTRKAASFQWRPGGEKA   QQVQAAMQAALPLGPYDPAC   MVLEIAVADTEAVWGHVMIS.   SFPSHPCHCPMGP*TKWP*WQ   WRILCMGSATWTSTHEG*PQY-HQ*VPNLPAAETNTEFA1*HIS   SRRSASYLVAG*LYWTSCIME!   AEMILWIW*CLSCMQCFQQD   YHPWTHGMPYPPLWYSTQLC: *PRRISLYPH*SXVAGSCWSWS!   VLPCSPSS*SSRVDRTVERPE!   TTMPTSQESR VCQSGGSGT   THHPP*STSNIFASCFYGTITC   WSRGLSSRGRNATRRQNNS!   L*VKIATWTLWAPFTSKI.   EVKIATWTLWAPFTSKI.   L*VKIATWTLWAPFTSKI.   AEMILWIW*CLSCMQCFQQD   VQVAVQAALPLGPTQPADPP   VLEVSVADRDAVWSLWQAPE!   LYGQLGFWRQHIPHLGALLW   YQATQKAASFEWGPEQEKALC   QQVQVAVQAALPLGPTQPADPP   VLEVSVADRDAVWSLWQAPE!   ESQQRPLGFWSKALPSSTDNY: CFRCAIN**PMGCQ*FGWYSKALPSSTDNY: CFRCAIN**PMGCQ*FGWYSKAPSTDNY: CFRCAIN**PMGCQ	1	1	1	l		į.	
QQQQAMQAALPLGPYDPAG   MVLEIAVADTEAVWGH/WHS    SPPSHPCHCPMGP*TKWP*WQ    WRLCMGSATWTSTHEG*PGY    HQ*VPNLPAAETNTEF1A*I*HS    SRRSASYLVAG*1,YWTSCIME    AEHILWIWVCLSCMQCFQGD     YHPWTHGMBYPPLWYSTQLC    *PRRISLYH*RSVAVGSCSWSI     VLPCSPS*S*SKVDTVERPE!   TTMPTSQESR VQESRGGSGST     THHIPP**STSNIFASCFYGITC     WSRGLSSRGRNAATRRQNNS    L*VKIATWTLWAPPTISK     WGRGLSSRGRNAATRRQNNS    LVQLGFWRQHIPHLGALLWI     YQATQKAASFEWGFEQEKALC     QQQVAVQAALAPTIKKEAQ     LEEA*LENW*QRNLGKRYDC     PL*VVNIWADLGPCFCSTFOD     SRGGF**SSG*DDFCGHISASI     PSRVVEKLILLAPTIKEAG     PSRVYEMCHLILLAPTIKKEAQ     C*VPNLPAAETNTETSIWHHS     G*SASYLLAG*IHTSIMEAG     G*SASYLLAG*IHTSIMEAG     G*SASYLLAG*IHTSIMEAG     G*SASYLLAG*IHTSIMEAG     C*VPNLPAAETNTETSIWHHS     G*SASYLLAG*IHTSIMEAG     G*SASYLLAG*IHT	1	1	1		1	1	
MVLEIAVADTEAVWGHWHS    SFPSHPCHCPMGP*TKWP*WQ    WRLCMGSATWTSTHEG*PGY,   HQ*VPNLPAAETNTEPAI*HHS    SRRSASVLVAG*I,VMTSCME    AEHILLWWVCI.SCMQCFCOD    YHPWTHGMPYPPLWYSTQLCI    **PRHSLYH*RSVAVCSCSWNSI    VLPCSPS\$*SSRVDRTVERPFEI    TTMPTFOGESR VCGSGSG   THHHP**STSNIRASCFYGTFC    WSRGLSSRGRNAATRRQNNSI    L*VKLATWTLWAPPTSKL    WSRGLSSRGRNAATRRQNNSI    L*VKLATWTLWAPPTSKL    WSRGLSSRGRNAATRRQNNSI    L*VKLATWTLWAPPTSKL    WSRGLSSRGRNAATRRQNNSI    L*VKLATWTLWAPPTSKL    PSKVKEKLHLAPPTIKKEAQR    UVGQLGFWRQHFHLGALLW    YQATQKAASFEWGPEQEKALQ    QVQVAVQAALPLGPYDPADPA    VLEVSVADRDAVWSLWQAPIE    ESQQRPLGFWSKALPSSTDNY;   CFRCAINY*PROCQ*FGWINT    LEEA*LENW*QRNLGKRYVDC    PL*VVNNWKDICPECS*TGOD    PL*VVNNWKDICPECS*TGOD    SRGGF**SSG*DDPFCGHHSASI    PSHPCCRPMGP*TKWPWWQFE    RLCMDSATWTSTHGS*PDYSH    C*VPNLPAAETNTETSIWHHS    G*SASYLLAG*I-H*TSSIMEKAI    VSPHWNKHISLWWVCLSSMQC    CQODYHPWTHSMPYPLSWYST    QHCLSLQRERHSLYR*RSAAVC    ACS    AT766   A 17499   1 915     17395   47765   A 17501   1 1332     17396   47766   A 17505   134   4475     WILLIAMS   WILLIAMS   1 1332     TTSSM   47766   A 17505   134   4475     WRLCMGSATWTSTHEG*PDYSH    WRLCMGSATWTSTHGS*PDYSH    AF766   A 17505   134   4475     WRLCMGSATWTSTHGS*PDYSH    WRLCMGSATWTSTHGS*PDYSH    WSRGLSSTHGSTHGSTHGSTHGSTHGSTHGSTHGS*PDYSH    WSRGLSSTHGSTHGSTHGSTHGSTHGSTHGSTHGSTHGSTHGSTH	1	1	1		1	l	
SPPSHPCHCPMGP*TKWP*WQ WRLCMGSATWTSTHEG*PGYM HQ*VPNLPAAETNTEPAI*HHS SRRSASYLVAG*LYWTSCIMEI AEWILL.WIWVCLSMQCFCQO YHPWTHGMPYPDLWYSTQLC *PRRISLYH*RSVAVGSGWNSI VLPCSPSS*SSRVDRTVERPFEI TTMPTSGESR VQESRGGSGSG THHHP**STSNIFASCFYGITEC WSRGLSSRGRNAATRRQNNSI L*VKLATWTLWAPFTSKL   VKLATWTLWAPFTSKL   VKLATWTLWAPFTSKL   VQVAVQAALPLGPYDPADPP VLEVSVADRDAVWSLWQAPIE   SSQQRPLGFWSKALPSSTDNY CFRCAIN**PRGCQ*FGWNKI   LEEA*LENW*QRNLGKRYVVOC   PL*VVKNWKDICIPCECSPTGD   SRGGF*SGS*GDPFCGHHASI   SSGGF*SGS*GDPFCGHHASI   SFBHCCRPMGP*TK WPWWQF   LEEA*LENW*QRNLGKRYVVOC   PL*VVKNWKDICIPCECSPTGD   SRGGF*SGS*GDPFCGHHASI   SFBHCCRPMGP*TK WPWWQF   RLCMBSATWTSTHQS*PDYSH   C*VPNLPAAETNTETSIWHHS   G*SASYLLAG*LH*TSSIMEKAI VSPHWNKHSLWVCLSSMQ   FCQOYHPWTHSMPYPLSWYST   QHCLSLQRERHSLYR*RSAAVC   ACS   17393 47761 A 17301 I 1908   17395 47765 A 17501 I 1932   17396 47765 A 17503 I 11 1832   17397 47765 A 17503 I 11 1832   17399 47767 A 17505 I 134 447	1		1		1		
WRI.CMGSATWTSTHECPOYM   HQ*VPNLPAAETNTEPAI*HHS   SRRSASVLVAG*L*YWTSCHME  AEHILL.WIWCI.SCMQCFCQD   YHPWHTIGMPYPLWYSTQCLG*	1	1		1	1		
HQ*VPNLPAAETNTEPAI*HIS   SRRSASVLVAG*LYMTSCIME    AEHILLWIWVCI.SCMQCPCQD   YHPWTHGMPYPPLWYSTQLC    *PRRISLYH*RSVAVGSCWMS    VLPCSPSS*SSRVDRTVERPEI*   TTMPITGOESR VCQSGG*   THHHP**STSNIFASCFYGITFC WSRGLSSRGRNAATRRQNISI.   L*VKIATWIL WAPPTSKL   L*VKIATWIL WAPPTSKL   L*VKIATWIL WAPPTSKL   L*VKIATWIL WAPPTSKL   VQATQKAASFEWGPEQEKALC    QVQVAVQAALPLGPTVPADPN VLEVSVADRDAVWSLWQAPIE    ESQQRPLGFWSKALPSSTDNY    CFRCAIN**PMGCQ*FGWINT    LEEA*LENW*QRNLGKRYVDC    PL*VVKNWKDICIPCECSPTGD    SRGG**SSG*ODPFCGHBASS.   PSHPCCRPMGP*TK WPWWQF    RICMBSATWISTHGS*PDYSH    G*SASYLLAG*LH*TSSIMEKAI VSPHWNKHSL.WIW*CLSSMGC FCQDYHPWTHSMPYELSWYST    QHCI.SLQRERHSLYR*RSAAVC ACS    17393   47761   A 17498   1 9968     17395   47765   A 17501   1 1332     17396   47765   A 17503   151   674     17399   47765   A 17505   134   4477     14767   A 17505   134   4477     CRACHINE OF THE STREET OF THE STRE	ļ	1		ì	ì	1	
SRRSASYLVAG**LYWT*SIME    AEHILWIWCLSCMQCFQD    YHPWTHGMPYPPLWYSTQLC    *PRRISLYH*RSVAVGSCSWSI   VLPCSPS**SRVDRTVERPET    TTMPTSQESR VQESRGSGSGT   THHP**STSNIFASCFYGITC   WSRGLSSRGRNAATRQNNSI   L*VKIATWTLWAPPTISKL   L*VKIATWTLWAPPTISKL   VGQLGFWRQHIPHLGALLWI   YQATQKAASFEWGFEQEKALC   QVQVAVQAALAPTISKEAQE   LEEA*LENN*QRNICHRAYDOC   PL*VVNNWKDICPCESSTGTOD   SRGGF**SSG**DDFFCGHISASI   PSHPCCRPMGP*TKWPWWQE**   LEEA*LENN*QRNICHRAYDOC   PL*VVNNWKDICPCESSTGTOD   SRGGF**SSG**DDFFCGHISASI   PSHPCCRPMGP*TKWPWWQE**   C*VPNLPAAETNTETSIWHHS   G*SASYLLAG**ITSTHIQ**PDYSH   C*VPNLPAAETNTETSIWHHS   G*SASYLLAG**ITSTHIQ**PDYSH   C*VPNLPAAETNTETSIWHHS   G*SASYLLAG**ITSTHIQ**PDYSH   C*VPNLPAAETNTETSIWHHS   G*SASYLLAG**ITSTHIQ**PDYSH   C*VPNLPAAETNTETSIWHHS   G*SASYLLAG**ITSTHIQ**PDYSH   C*VPNLPAAETNTETSIWHHS   G*SASYLLAG**ITSTHIGA**PDYSH   C*VPNLPAAETNTETSIWHHS   G*SASYLLAG**ITSTHIGA**PDYSH   C*VPNLPAAETNTETSIWHHS   G*SASYLLAG**ITSTHIGA**PDYSH   C*VPNLPAAETNTETSIWHHS   G*SASYLLAG**ITSTHIGA**PDYSH   C*VPNLPAAETNTETSIWHHS   G*SASYLLAG**ITSTHIGA**PDYSH   C*VPNLPAAETNTETSIWHHS   G*SASYLLAG**ITSTHIGA**PDYSH   C*VPNLPAAETNTETSIWHHS   G*SASYLLAG**ITSTHIGA**PDYSH   C*VPNLPAAETNTETSIWHHS   G*SASYLLAG**ITSTHIGA**PDYSH   C*VPNLPAAETNTETSIWHHS   G*SASYLLAG**ITSTHIGA**PDYSH   C*VPNLPAAETNTETSIWHHS   G*SASYLLAG**ITSTHIGA**PDYSH   C*VPNLPAAETNTETSIWHHS   G*SASYLLAG**ITSTHIGA**PDYSH   C*VPNLPAAETNTETSIWHS   C*VPNLPAAETNTETSIWHS   C*VPNLPAAETNTETSIWHS   G*SASYLLAG**ITSTHIGA**PDYSH   C*VPNLPAAETNTETSIWHS   C*VPNLPAAETNTETSIWHS   C*VPNLPAAETNTETSIWHS   C*VPNLPAAETNTETSIWHS   C*VPNLPAAETNTETSIWHS   C*VPNLPAAETNTETSIWHS   C*VPNLPAAETNTETSIWHS   C*VPNLPAAETNTETSIWHS   C*VPNLPAAETNTETSIWHS   C*VPNLPAAETNTETSIWHS   C*VPNLPAAETNTETSIWHS   C*VPNLPAAETNTETSIWHS   C*VPNLPAAETNTETSIWHS   C*VPNLPAAETNTETSIWHS   C*VPNLPAAETNTETSIWETSIMETSIMETSIMETSIMETSIMETSIMETSIMETSIM	1	1			1		
AEHILLWIWCI.SCMOCFCOD   YPPWTHGMPYPPL WYSTQLCI	1	1			1		
YHPWTHGMPYPPLWYSTQLC		1	1		1		
*PRRISLYH*RSVAVGSCSWASI   VLPCSPS*SSRVAVTVERPEI   TTMPTSQESS VQESRGGGGGG   THHHPF*STSNIFASCFYGTTC   WSRGLSSRGRNATRQNNSI   L*VKIATWTL WAPPTSKL   TTMPTSQESS VQESRGGSGGG   THHHPF*STSNIFASCFYGTTC   WSRGLSSRGRNATRQNNSI   L*VKIATWTL WAPPTSKL   PSKVKEKILHLAPPTSKL   PSKVKEKILHLAPPTSKL   PSKVKEKILHLAPPTSKL   PSKVKEKILHLAPPTSKL   PSKVKEKILHLAPPTSKL   PSKVKEKILHLAPPTSKL   PSKVASSFEWGFEGEKAL   QVQVAVQAALELGPYDPADP   VLEVSVADRDAVWSLWOAPIC   ESQRPLGFWSKALPSTSTDYS   CFRCAIIY*FMGCCQ*FGWINT   LEEA*LENN*QRNLGKRYVDC   PL*VVNNWKDICPECSSTOD   SRGGF**SSG*DDPFCGHISASI   PSHPCCRPMGP*TKWPWWQE   RLCMDSATWTSTTHGS*PDYSH   C*VPNLPAAETNTETSIWHHS   G*SASYLLAG**LHTSSIMEKAL   VSPHWNKHSLWIWVCLSSMQFCQDYHWTHSMPYPLSWYST   QHCI.SLQRERHSLYR*RSAAVC   ACS   A 17409   1 915   17395   47765   A 17505   2 670   17395   47765   A 17505   1 1 1332   17396   47765   A 17505   1 1 1332   17399   47765   A 17505   134   447	1	1	}	1	1		
VPCSPS\$*SSRVDRTVERPEIT   TTMPTSQES\$*SSRVDRTVERPEIT   TTMPTSQESRVQESRGGSGSGT   THHIP**STSNIFASCFYGTTC   WSRGLSSRGRNATRRQNNSI   L*VKIATWILWAPPTSKL     17392   47760   A   17497   2   1120   PSKVKEKLIHLAPPTIKKEAQR   UGQLGFWRQHIPHLGALLWI   YQATQKASSFEWGPEQEKALL   QQVQVAVQAALPLGPYDPADPR   VLEVSVADRDAVWSLWQAPIE   ESQQRPLGFWSKALPSSTDNY; GFRCAINY**PROXVSLWQAPIE   ESQQRPLGFWSKALPSSTDNY; GFRCAINY**PROXVSLWQAPIE   ESQQRPLGFWSKALPSSTDNY; GFRCAINY**PROXCQ*FGWINGH   LEEA*LENW*QRNLGKRYVDC   PL*VVKNWKDICIPCECSPTGD   SRGGF**SSG*DDPFCGHHASSI   PSHFCCFPMGP*TK WPWWQF* RLCMBSATWISTHQS**PDYSH   C*VPNLPAAETNTETSIWHHES   Q*ASXTLAG**LH**TSSIMEKAI   VSPHIWNKHSLWIVCLSSMQC   FCQDYHPWTHSMPYPLSWYST   QHCLSLQRERHSLV***RSAAVC   A   17498   1   1908   17394   47762   A   17499   1   915   17395   47763   A   17501   1   1332   17396   47764   A   17501   1   1332   17397   47765   A   17505   134   4477   1477		1	1	ĺ	1	1	
TTMPTSGESR VQESRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	l	ı	1	1	1		
THHHP**STSNIRASCFYGITC   WSRGLSRGRNAATRRQNNSI   L*VKIATWIL WAPPTSKL   PSKVKEKLHILAPPTIKKEAGR   UVGQLGFWRQHIPHLGALLW    YQATQKAASFEWGPEGEKAL   QVQVAVQAALPLGPYDPADPM   YUEVSVADRDAVWSLWQAFIL   ESQQRPLGFWSKALPSSTDNYS   CFRCAIN**PROECO*FGWINT   LEEA**LENW**QRNLGKRYVDC   PL**VVKNWKDICIPECSPTGD   SRGGF**SSG**OIDPFCGHFASSI   PSHPCCRPMGP**TKWPWWQF*   RLCMBSATWISTHGS**PDYSH   C*VPNLPAAETNITETSIWHIPS   G*SASYLLAG**LH**TSSIMEKAI   VSPHWNKIBLWWVCLSSMQ   FCQDYHPWTHSMPYPLSWYST   QHCLSLQRERHSLYR**RSAAVC   ACS   A	1	1			1		
WSRGLSSRGRNATRQNNSI    17392   47760		1	1		1		
		1	1				
17392   47760   A   17497   2   1120   PSKVKEKLHILAPPTIKKEAQR UGQLGFWRQHIPHLGALLWI YQATQKASFEWGPEGEKALG QVQVAVQALPLGFYDPADPR YVEWSVADRDAVWSLWQAPIE ESQRPLGFWSKALPSSTDNY; GFRCAINY*PROECQ*FGWINK LEEA*LENW*QRNLGKRYVDC PI-*VVKNWKDICIPCECSPTGD SRGGF**SGS*DDPFCGHHASSI PSHFCCFPMGP*TK WPWWQF RLCMBSATWTSTHG\$*PDYSH C*VPNLPAAETNTETSIWHHFS G*ASRYLAG*LH*TSSIMEKAI VSPHWNKHSLWIVCLSSMQC FCQDYHPWTHSMPYPLSWYST QHCLSLQRERHSLYR*RSAAVC ACS   17394   47762   A   17498   1   1908   1915   1915   1915   1915   1915   1915   1916   1916   1916   1917	1	1	1		1		
LVGQLGFWRQHIPHLGALLWI	ļ	1	_				
YQATQKAASFEWGPEGEKALC   QVQVAVQAALPLGPYDPADPN   VIEVSVADRDAVWSLWQAFFE   ESQQRPLGFWSKALPSSTDNYS   CFRCAINY*FMGCO*PGWINT   EEGA*ILENW*QRNLGKRYDG   PL*VVKNWKDICIPCECSPTGD   SRGGF**SSG*ODPFCGHFMSSI   PSHFCCRPMGP*TKWPWWQF* RLCMBSATWTSTTHQS*PDYSH   C*VPNLPAAETNTETSIWHFIS   G*SASYLLAG*LH*TSSIMEKAI VSPHWNKHSLWIWVCLSSMQ   FCQOYHWTHSMPYPLSWYST   QHCLSLQRERHSLYR*RSAAVC   ACS   A 17499   1 915   173954   47762   A 17505   2 670   173954   47765   A 17501   1 1332   17397   47765   A 17501   1 1332   17397   47765   A 17503   151   674   17398   47766   A 17505   134   4475	17392	47760	A	17497	2	1	
QVQVAVQAALPLGPYDPADPR   VLEVSVADRDAVVSLWQAPIC   ESQQRPLGFWSKALPSSTDNYS    CFRCAINY*FMGCCQ*FGWIVR    LEEA*LENW*QRNLGKRYVDG    SRGGF**SSG*DDPFCGHISASI   PSHPCCRPMGP*TK WPWWGE    RL.CMDSATWTSTHQS*PDYSH    C*VPNLPAAETNTETSIWHHFS    G*SASYLLAG*LH*TSSIMEKAI   VSPHWNKHSL.WIWVCLSSMQC    FCQDYHPWTHSMPYPLSWYST    QHCLSLQRERHSLYR*RSAAVC    ACS    ACS    ACS    ACS    ACS    AT766    A 17499   1 915     A 17395   A7764   A 17501   1 1332     AT765   A 17501   1 1332     AT766   A 17501   1 1332     AT766   A 17501   1 1332     AT766   A 17501   1 1332     AT766   A 17505   134     AT767   A 17505   134     AT767   A 17505   134     AT767   A 17505   134     AT776   A 17505   134     AT776   A 17505   134     AT776   A 17505   134     AT776   A 17505   134     AT776   A 17505   134     AT776   A 17505   134     AT776   A 17505     A 17505   134     AT776   A 17505     A 17505   134     AT776     A 17505   A 17505     A 17505	1				1		
VLEVSVADRDAVWSLWQAPRE	1	1	ı		1		
BSQQRPLGFWSKALPSSTDNY:   CFRCAIIY*FMGCCQ*FGWINRI   LLEA*LENN*QRNLGKRYVOC   PL*VVKNWKDICIPCECSPTGD    SRGGF**SSG* DDPFCGHHASI   SPHCCRPMGP*TKWPWWQE   RLCMBSATWISTHQS*PDYSH   C*VPNLPAAETNIETSIWHHFS   G*SASYLLAG*LH*TSSIMEKAI   VSPHWNKHSLWIVCLSSMQ   FCQOYHPWTHSMPYPLSWYST   QHCLSLQRERHSLYR*RSAAVC   ACS   ACS   ACS   ACS   ACS     ACS   ACS   ACS   ACS   ACS     ACS   ACS   ACS   ACS     AT760   A   17501   1   1332     AT761   A   17501   1   1332     AT765   A   17503   151   674     AT766   A   17504   1   825     AT767   A   17505   134   447     ACS   ACS   ACS   ACS     ACS   ACS   ACS   ACS     ACS   ACS   ACS   ACS     ACS   ACS   ACS   ACS     ACS   ACS   ACS     ACS   ACS   ACS     ACS   ACS   ACS     ACS   ACS   ACS     ACS   ACS   ACS     ACS   ACS     ACS   ACS     ACS   ACS     ACS   ACS     ACS   ACS     ACS   ACS     ACS   ACS     ACS   ACS     ACS   ACS     ACS   ACS     ACS     ACS   ACS     ACS	1	1	1		1	1	
CFRCAIN*PMGCCQ*PGWIVRI   LEEA*LENW*QRNLGKRYVDG   PL*VVKNWKDICIPCECSP*TGD   SRGGF**SSG*DDPFCGHHSASI   PSHPCCRPMGP*TK WPWWGPS   RLCMDSATWTSTHQS*PDYSH   C*VPNLPAAETNTETSIWHHIS   G*SASYLLAG**LH*TSSIMEKAI   VSPHWNKHSL.WIWVCLSSMQG   FCQDYHPWTHSMPYPLSWYST   QHCLSLQRERHSLYR*RSAAVC   ACS	1	1	1	1	ł		VLEVSVADRDAVWSLWQAPIG
LEEA*LENW*QRNLGKRYVDG   PL*VVKNWKDICIPCECSPTGD   SRGGF**SSG**DDPFCGHHASSI   PSHPCCRPMGP*TKWPWWQF*   RLCMBSATWTSTHQS**PDYSH   C*VPNLPAAETNTETSIWHHFS   G*SASYLLAG**LH**TSSIMEKAI   VSPHWNKHSLWIW*CLSSMQ   FCQDYHPWTHSMPYELSWYST   QHCLSLQRERHSLYR*RSAAVC   ACS   ACS   ACS   ACS     ACS   ACS   ACS   ACS     ACS   ACS   ACS     ACS   ACS   ACS   ACS     ACS   ACS   ACS     ACS   ACS   ACS     ACS   ACS   ACS     ACS   ACS   ACS     ACS   ACS   ACS     ACS   ACS     ACS   ACS   ACS     ACS   ACS     ACS   ACS     ACS   ACS     ACS   ACS     ACS   ACS     ACS   ACS     ACS     ACS   ACS     ACS   ACS     AC		1	1		ł		ESQQRPLGFWSKALPSSTDNYS/
PL*VVKNWKDICIPCECSPTGD   SRGGF**SSG*DDPFCGHHSASI   PSHPCCRPMGP*TK WPWWQF   RLCMDSATWTSTHQS*PDYSH   C*VPNLPAAETNTETSIWHEN   C*VPNLPAAETNTETSIWHEN   VSPHWNKHSL WIWVCLSSMQ   FCQDYHPWTHSMFYPLSWYST   QHCLSLQRERHSLYR*RSAAVC   ACS   ACS   A   17499   1   915   17395   47762   A   17500   2   670   17395   47763   A   17501   1   1332   1332   1337   47765   A   17501   1   1332   1332   1337   47765   A   17501   1   1332   1339   47766   A   17501   1   1332   1339   47766   A   17501   1   1332   1339   47766   A   17501   1   1332   1339   47767   A   17505   134   447		1	1	1			CFRCAHY*FMGCCQ*FGWIVRD
SRGGF**SSG*DDPFCGHHSASI		1			1		
PSHPCCRPMGP*TK:WPWWQE   RLCMDSATWTSTHQS*PDYSH   C*VPNLPAAETNTETSIWHHS   G*SASYLLAG*LH*TSSIMEKAI   VSPHWNKHSL.WIWVCLSSMQC   FCQDYIPW*THSMPYPLSWYST   QHCLSLQRERHSLYR*RSAAVC   ACS			1		l	1	PL*VVKNWKDICIPCECSPTGDL
RI.CMBS.ATWTSTHQS*PDYSH   C*VPNIPAAETNTETSIWHHFS   G*SASYLL.AG*LH*TSSIMEKAL   VSPHWNKHSL.WIWYCLSSMQ   FCQDYHPWTHSMPYPLSWYST   QHCI.SI.QRERHSLYR*RSAAVC   ACS   A		1	1		1	l i	SRGGF**SSG*DDPFCGHHSASF
C*YPNLPAAETNTETSIWHHES   C*SASYLLAG*LH*TSSIMEKAI VSPHWNKHSLWIWVCLSSMQC FCQDYHBWTKHSLWIWVCLSSMQC FCQDYHBWTKHSLWIWVCLSSMQC FCQDYHBWTKHSMPYELSWYST QHCLSLQRERHSLYR*RSAAVC ACS		1	1	l	Į.	į į	PSHPCCRPMGP*TKWPWWQE*
G*SASYLLAG*LH*TSSIMEKAI VSPHWNKISLWIWVCLSSMQG FCQDYHPWTHSMPYPLSWYST QHCLSLQRERHSLYR*RSAAVC ACS   17393   47761		1	1		ł		RLCMDSATWTSTHQS*PDYSH
VSPHWNKHSLWIWVCLSSMQC   FCQVIHWTHSMPYRLSWYST QHCLSLQRERHSLVR*RSAAVC   ACS   A 17498   1   1908   17394   47762   A 17499   1   915   17395   47763   A 17500   2   670   17396   47764   A 17501   1   1332   17397   47765   A 17503   151   674   17398   47766   A 17503   151   674   17399   47767   A 17505   134   447		1					C*VPNLPAAETNTETSIWHHFS
CQDYHPWTHSMPYPLSWYST QHCLSLQRERHSLYR*RSAAVC ACS	1	1	1		I		G*SASYLLAG*LH*TSSIMEKAE
QHCLSLQRERHSLYR*RSAAVC   17393   47761   A 17498   1   1908   1   1908   1   17394   47762   A 17499   1   915   17395   47763   A 17500   2   670   17396   47764   A 17501   1   1332   17397   47765   A 17503   151   674   17398   47766   A 17504   1   825   17399   47767   A 17505   134   447	1	1	1	1	I		VSPHWNKHSLWIWVCLSSMQC
QHCLSLQRERHSLYR*RSAAVC   17393   47761   A 17498   1   1908   1   1908   1   17394   47762   A 17499   1   915   17395   47763   A 17500   2   670   17396   47764   A 17501   1   1332   17397   47765   A 17503   151   674   17398   47766   A 17504   1   825   17399   47767   A 17505   134   447	1	1	1	1	1		FCQDYHPWTHSMPYPLSWYST
17393   47761			1	1			QHCLSLQRERHSLYR*RSAAVG
17394     47762     A     17499     1     915       17395     47763     A     17800     2     670       17396     47764     A     17501     1     1332       17397     47765     A     17503     151     674       17398     47766     A     17504     1     825       17399     47767     A     17505     134     447	1	1	1				ACS
17395     47763     A     17500     2     670       17396     47764     A     17501     1     1332       17397     47765     A     17503     151     674       17398     47766     A     17504     1     825       17399     47767     A     17505     134     447	17393	47761	A		I		
17396     47764     A     17501     I     1332       17397     47765     A     17501     I51     674       17398     47765     A     17504     I     825       17399     47767     A     17505     I34     447							
17397     47765     A     17503     151     674       17398     47766     A     17504     I     825       17399     47767     A     17305     134     447					2		
17398 47766 A 17504 I 825 17399 47767 A 17505 134 447					1		
17399 47767 A 17505 134 447			-		151		
11595 11101					1		
17400   47768   A   17506   98   778			-				
	17400	47768	A	17506	198	778	

SEQ ID	SEQ ID NO:	Mar	SEQ ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop endon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
17401	47769	I <sub>A</sub>	17507	11	830	I MHCFFIFSAAWFCLWSISLHLV
17401	47709	^	17307	1'	850	ERPDMAVLLFPFGLRLGLMLQ
					\	CPRGYWPVLLGAEWLLIYWL
		l				QAVGLTHFPLLMIGSLLTLLPV
						ALISRYRHORDWRTLLLOGAA
						LTAAALLQSLPWLRHGKESWY
		1				ALLLTLTG/EPDAGPDMSGVL/
		1				LSRQ*HLAAARSVTGFSANQL
		l				
		1				RATSGLVLAAVCYQSLAPVGL
		l				GRTVALYAILSGAADYRAGLA
		1				LWLARGADCDVDERHRADRH
		l				QSWRDLPWTYCSGDCDSRHG
		ļ.				QGQKARAPPKHDQFPHAIFRG
17402	47770	Α	17508	2252	2772	RSKTTAFTPLRVRTSAHARPAC
		l				PAPIIATFLPVCFTPDISGRQPISI
						ALSLI*RSMLPMVTAPNSSFRV
	1	1				QEPS/SQTVLRADSSANFRQGV
			İ			GLVRQFRRFKNTPLVGELQPVI
						DVVVYRAFPLAVWVAARQAA
						VSLRFGLAFGKRLVNFNKLNF/
_						DLQRFLWRINALQVDKLITF
17403	47771	Α	17509	539	1077	
17404	47772	С	17510	192	396	
17405	47773	С	17511	10	294	
17406	47774	A	17512	2	379	KRPGSGITEATSSRRQRPTRRL
		l			1	GQLPGQEKRVLKATEGIANPS
		l			1	WGWGGAVSPLRASLTSLRHKI
		l				NNHYNTENWKLPIKDS\HLIPSI
		l				QAPSMPFPLANPPW\APHPREK
		L_				MWNPQIQGTNCIWVCGP
17407	47775	Α	17513	291	590	
17408	47776	Α	17514	187	589	VLSFLIHRWEGDKDSLLGPNFS
	1	l			1	QTPQPSRRFICAFPWENPS*EPS
		ı				YPSISDPGFLILLPSKGDVWIHL
		İ				GPIFSKKPLYS*SSFLVIFYPVTF
						SFLFLGYKFPLAHAVFRVEPTL
						LLIQNSHCHGCYTYPDGPE
17409	47777	A	17515	1509	1748	IGVVREGIPVLCLFSKGMLPVF
						AHSV*YWLWVCHR*LLLF*DT:
		1				HQYLIY*EFLA*SVVDFCQRPFI
		1				
						HLVLDFFWLVSY
17410	47778	A	17516	152	568	
17410	47778	A	17516	152	568	CQLELSCMKCPSTPVGRSLPVC
17410	47778	A	17516	152	568	CQLELSCMKCPSTPVGRSLPVC CTRSGTQLRWHSVPWQSWCTV
17410	47778	A	17516	152	568	CQLELSCMKCPSTPVGRSLPVC CTRSGTQLRWHSVPWQSWCTV LGESLLSGLVVLFRASRPE**NI
17410	47778	A	17516	152	568	HLVLDFFWLVSY  CQLELSCMKCPSTPVGRSLPVC  CTRSGTQLRWHSVPWQSWCTY LGESLLSGLVVLFRASRPE**NI  LKLLPQLPLPPDALSQGDGSFV  CKHPTGAVTFPSGMPLGSMTIF

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
17411	47779	A	17517	152	1568	COLELSCMKCPSTPVGRSLPVG
17411	4///9	<u>۱</u> ^	17317	132	1500	CTRSGTOLRWHSVPWOSWCTV
			ŀ			LGESLLSGLVVLFRASRPE**NP
						LKLLPOLPLPPDALSOGDGSFV
		1				CKHPTGAVTFPSGMPLGSMTIF
		1				KILILPIHEHGMFFSLSVSSFVSL
10410	45500	١.	10010	150	479	
17412	47780	Α	17518	152	4/9	CQLELSCMKCPSTPVGRSLPVG
						CTRSGTQLRWHSVPWQSWCTV
						LGESLLSGLVVLFRASRPE**NP
1						LKLLPQLPLPPDALSQGDGSFV
		L				CKHPTGAVTFPSGCPTHTLQA
17413	47781	A	17519	1	474	
17414	47782	Α	17520	1326	1712	FLYVIKALGKKQLQFGQQILIPS
		l				IELLDYLINPGSGCVSLWKLNK
		1	l			PQYCYLIHFSGLTELSWKVHTIL
		l				LEGHYEFLEYAADR*PICLFSW
						KERQLVSFLDYSLHHLLGSFYV
						VFFFFLYLLVRLCWDL
17415	47783	Α	17521	18	236	
17416	47784	A	17522	281	1005	TGWSPLQLSKATVARLPLWIPP
						LWAGHLGELWLASGEYPSGLK
		ł				LPEEGTGSNLRCSAASAGDTQA
					ĺ	NRVWSGPAANFSRPAAEGPAF
						HALRGPSVHCSPLCVHEFSSFSS
		l				LISENMQYLVFCSGVRFLRIMVI
						SSIHILCLVPKRTRVLGRLSLTC
						FRFLRGPKEPRITIPHSSAPPLGH
	ľ	l			l	VIAIPLP*SFMKPSPEADAPMTG
					ŀ	SFLKSPSEADTGATLPVQSVVPI
		1				PLSILPILEVGGVLFT
17417	47785	Α	17523	1	1524	
17418	47786	Α	17524	881	1108	SRKMGAPNA**SAWSWSREGL
		l				AAP*SMFSSLSADSSADCKLPE
						GKVQPASSTGLTARASKDLYFC
						CCFSISARAS
17419	47787	С	17525	l	867	
17420	47788	Α	17526	203	514	SSSTARPSQTSSAEESPTSWYRG
			l			DNPSKPMDPLVAGVFGAIVGA
						ASVLGNAPLDGIETGCGAWSST
			1		1	NAEHTGLWLQILRKEGLKDL*N
			l		1	GTVPRLGRWTASPWM

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
17421	47789	Α	17527	1	1578	MAKKEOLLSAAPSKTNAEGOE
						PSGVYTTRALGFKHKTGOPFGO
						TPSYPQEFILYTNDTWNASKTE
						PFTPLERGLKPGSQESSGWHLV
						GTPLGRSFQRKEQAAIFAVLQP
						PLVIPROTGSGVDLOOTPTDLO
						KRVLTVRRKTNSININKKDDH
						KTTSKGHQQQRPKVDKSTKMF
						KNOCKKATNSKNONVSSPPKD
						HNSSTAKEONWMENEFDKLTE
					ŀ	VGFRSSQFDQVEERISDIEDKLN
					1	EIKHEDKIREKRMKKKEQSLQE
						IWEYVKRPNLRLIGVPESDGEN
			Ì			GTKLENTLQDTIQENFPNLARQ
						ANIQIQEIQRTPORYSSRRATPR
	İ	i				HII/E*IHQG*NEGKTVKGSQRE
						K*GQEIPSGVYTTRALGFKHKT
						GQPFGQTPSYPQEFILYTNDTW
					1	NASKTEPFTPLERGLKPGSQESS
						GWHLVGTPLGRSFQRKEQAAII
						AVLQPPLVIPRQTGSGVDLQQT
					1	PTDLQKRVLTVRRKTNSININK
						KDDHAKTTSKGHQQQRPKVDI
						STKMRKNQCKKATNSKNQNV
						SPPKDHNSSTAKEQNWMENEF
						DKLTEVGFRSSQFDQVEERISD
		i				EDKLNEIKHEDKIREKRMKKKI
						QSLQEIWEYVKRPNLRLIGVPE
						SDGENGTKLENTLQDTIQENFP
						NLARQANIQIQEIQRTPQRYSSF
					İ	RATPRHIIGRFTKVEMKEKRLR
						AVREKSRVTHKGKLIRLTADLS
17422	47790	Α	17528	738	1323	ATGGHSNQRQRS*KLSKKFRR
						MYN*NNQYREVLKGADGAEN
						QGSRTTETLCM*RMRQSLQF\D
						SDLVRHQRKHSGEKPYECCEC
						GKAFRGSSELIRHRRIHTGEKPY
						ECGEYKSYECIACGKAFGRSST
						LIENQRIHTGEKPYECNECGKSI
						NQSSALTQHQRIHTGEKPYECS
						ECRKTFRHRSGLMQHQRTHTR
17423	47791	Α	17529	I	656	MAGKPEYDKTISTSIVLNALNA
						LGVSAEASGRNDLVVKTVEGD
						RKVSGSAYRETKDRGFHHGTL
		1				LLNADLSRLANYLNPDKKKLA
		1	1			AKGITSVRSRVTNLTELLPGITH
		1	1			EQVCEAITEAFFAHYGERVEAE
				1		IISPNKTPDLPNFAETFARQSSW
						EWNFGQAPAFSHLLDERFTWG
						GVELHFDV/GKRPYHPRPGVYR
	1	1	l			QPQPRAAGSPRRTTARLPFLSL

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	eodon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence	1	07/340,217	sequence	or peptide sequence	decedon, (~possible naciconae insertion)
l			ľ	-		
17424	47792	Α	17530	1046	1401	LLDIRMLCHGKGVIIHVLRLQF
						LLGRPAPHRLHAALQLPGLSLH
						GTLALGLWLQLRQLLLLGQPF
						GISGCGSGCDPEQDCV/DCGRG
			1			CWPRKCPQGSHSAPRSRGAPHR
						PRPQQRAAGRQ
17425	47793	Α	17531	I12	1170	YPFFHLIDSTIDTCVCFTKFLCC
				ļ		VFQLHQVIYVLL*TGYSLIFDAD
l				ì		DLWMGFLRGHPFC*CYCFLFVS
i		1		ļ		FPSNSQAPLLQVCWSLLEVHSR
İ			l	1		PCSPGYHQRRLQNSKDCCLLLP
						LEALSQSGTHQMPAGALLYEM
1						SVNPCWEEHQTDQLFTHESTFI
1						RSKTQKKVPDKLLDSSTVTPLF
1		1				KITENIGCVMTGMTADSRSQVQ
						RARYEAANWKYKYGYEIPVD
						MLCKRIADISQVYTRNAEMRPL
						GCCMILIGIDEEQGPQVCKCDP
				l		AGYYCGCKATAVGVKQTESTS
i						FLEKKVKKKFDWTFEQTLETAI
ļ						TCLSTVLSIDFKPSEIEVGVVTV
		l				ENPKFRILTEAEIDAHLVALAER
17426	47794	Α	17532	2244	2432	DGQQLIALHRLALRELQQAVH
Ì		l				AGIAPAGENPV*WWFRNRQNP
						LIALRSLPAFQSGNLSCQLH
17427	47795	Α	17533	251	546	SSISDILSSA*SIRLLILVYAS*SS
ĺ						RAVFFSTIRSFIFFSKLVILVSPSC
ĺ	ļ					NLLSRFLASFHWVRTCSFSSKEF
						VIITHLLPTSVNSSYSSLFSFVHF
						G
17428	47796	A	17534	597	1092	FTNQKESRTRWIHSRILPEVQG
ł						GTGTIPSETIPINRKRGNPP*LIL*
						GQRHSDTKAG\RDTTKKENFRP
				1		ISLMNIDAKILNKILANRIQQHI
1	l					KKLIHHDQVGFIPGMQGWFNIR
İ						K/CNKCNPAYKQSQRQK/HT*L
1				Į.		SQ*MQKKPLTKFNNPSC*KLSIN
						*VLVGRISK
17429	47797	Α	17535	1	2153	
17430	47798	A	17536	2164	2427	
17431	47799	A	17537	1	322	GPRWGPRVHRAPDPVRIPSSGP
		l				LLPPRFYPRYVLP\PPSASTSRPC
						QRTSASGRCPCPMH/DTVKATM
1		l	1			PIWV/DPPVPDHYEGEAEHQGIL
						VTHPHHQRCPAGHRHRVVF
17432	47800	Α	17538	1	627	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		l		sequence		
17433	47801	A	17539	583	1145	GNGRTVDTQVCQAPITSQSLER
						PADPNP\GEODAEAGPASRRDT
		l				EAERLRFROFOYHVASGPHLA
				l		VGQLWTLCRQWLRPEARSKEQ
		l				MLEVLVLEOFLGALPSKMRTW
		l				VQSQGPRSCREAASLVEDLTQ
	1	l				MCQOEGLAAHPSHDTAIRGIPR
		l				LAASWETASAMEATADAROKR
		l				THTEKEAWLLEAPHELA
17434	47802	A	17540	1	1301	THEREA WEEDAI HEDA
17435	47803	Ā	17541	1	1232	
17436	47804	A	17542	1	549	MNTANVEKPYVOKYOTAFVLV
17450	47304	<u> </u> ^	17342	ľ	347	MKHROCOLASHLVONYRS/IOL
		1			i	WAWE\KIODPGTTCPSFNTITOG
						SKKPYPDFVARLRDAAONSITD
		ĺ				ENARKVIVELMAYGNANPECO
		1				SATKPLKGKVPTGSDVISDOKA
						VGVOAAKRRNRTDTGLGRSAR
	ĺ	1				KSGKGVTRMLPKHASMILDGG
	1	i				GPATSPSCCRFL
17437	47805	A	17543	146	510	SPYWNKGKSPGWLAES\FKRPV
1/43/	4/805	l <sup>A</sup>	17543	146	310	
						FRQGAK\EPYPDFAASLQDAAQ
					i	KSITNENARKVIVELMAYENAN
	i					PECQSAIKPLKGKVPVGSDVISR
						GFQGQQPPLSQVLQGMGQLPQ
17100	1000				200	YSNCPRPQAAVQQ
17438	47806	A	17544	2	828	
17439	47807	A	17545	1	420	
17440	47808	A	17546	1	1947	
17441	47809	Α	17547	1	399	PLKVNIYPDSKYAFHILHHHER
		l				GFLTTQGSSIINASLIKTLLKAA
						LLPKEARVIHCKGHQRASDPIA
	1					QDNAHTDKIAKKAASIPTYTPH
		1				FQFFSFSS\ATPTYSPAETSTYQS
		<u></u>				LPTQGKWFLDKETYFLPASQ
17442	47810	A_	17548	1	2382	

2206

SEQ ID	SEQ ID NO:					Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/340,21/	sequence	or pepulae sequence	detention, (-possible adelectide insertion)
17443	47811	Λ	17549	1	2194	MAPEQGRVSILQTLFIEYHGYSI
						FVVKGDLPDCEADQLLQMIRV
		l				QQMHRPKLIGEELAQLKEQRV
	ŀ	l		ŀ		HKTDLERVLEANDGSGMLDED
	ŀ	l				EEDLQRALALSRQEIDMEDEEA
		l				DLRRAIQLSMQGSSRNISQDMT
						QTSGTNLTSEELRKRREAYFEK
		i				QQQKQQQQQQQQQGDLSGQ
	ļ	1				SSHPCERPATSSGALGSDLALLL
		1				TQSLFGSLFTWTRVTFGAEDPG
	ł				İ	QEDSFRRRVPCPCPHSVRRSTY
						DLGSSDQPAQGTSHEFQIGLLL
		1		1		TRLSQVPILPQPPVPHPIILLSPPP
						HTVSGLOFLSVTSPPLPAOOFLL
	ł	ĺ				KEVAGAEGIAKVIPTCPVPLLG
	ŀ					QDILTKLSASLIIPGLQPHLIATL
	<b> </b>				-	LPNPKPPSPLPLVSPNLNPOVW
					i	DTSTPSLATDOTPITIPLKPNHP
	ŀ					YLAQCHYSIPQLALRGLKPVIT
		l				RLLOHGLLKPINSSYNSPILPVO
	i					KPDKSYRLPODLDLINOIVLPIH
	ĺ	ŀ				PVASPHIIPDTTPDPHDCISLIHL
1						AFTPFPHTSFFPIPHPDHTWFID
	ł					GSSTWPNRHSPAKVGYAIVVSS
		İ				TSILEATALPPSTTSQQAELIALT
						RALALAKGLHVNIYTDSKYAF
	İ					HILHHNAVIWAERGFLSTORSSI
		i		1		IIASLIKTLLKAALLPKEAGVIH
						CKGHQKASDPIAQGNAYADKS
						DNGLAFTSQI/I/HKQFLRLLVFS
	1	l			İ	GTFIPLTVLNLQERTGQYFYLLP
						FTELEPVLEKLOGTVHLNFYMD
17444	47812	Α	17550	1	355	
17445	47813	С	17551	99	335	
17446	47814	A	17552	21	447	LGPLPFSLSPCCLHCQGKRLCG
		l				HHEEARRKNVSIPRKEAGIIHC
						KGHQK/A/SDPIAQGNAYADKT
						KFLDLAFPPLRLSFTCQITQAVS
						QALGIQWNLHTLTILNLQKRIR
						ACPQDATGYSPFELLYGCSFLL
						GPSLIPDTSPT
17447	47815	A	17553	119	239	TOKGORAALFLICILSPSPLPTL
	•					GKNFKN*IPALKPHNRI
17448	47816	A	17554	1	798	
17449	47817	В	17555	460	1059	
		_	<b></b>			

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	cudon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
17450	47818	Α	17556	3	1476	IPTCPVPLLGQDILTKLSASLIIP
						GLQPHLIATLLPNPKPPSPLPLV
		l				SPNLNPQVWDTSTPSLATDQTP
						ITIPLKPNHPYLAQCHYSIPQLA
						LRGLKPVITRLLQHGLLKPINSS
						YNSPILPVQKPDKSYRLPQDLD
						LINQIVLPIHPVASPHIIPDTTPDP
			l .			HDCISLIHLAFTPFPHTSFFPIPHP
						DHTWFIDGSSTWPNRHSPAKV
						GYAIVVSSTSILEATALPPSTTS
		1				QQAELIALTRALALAKGLHVNI
						YTDSKYAFHILHHNAVIWAER
			İ			GFLSTQRSSIIIASLIKTLLKAAL
						LPKEAGVIHCKGHQK\ASDPIA
						QDNAYADKLAKKAASVPTSVP
						HGISQAPPPLPTHQARYWQIDF
						THMPRVRKLKYLLVWVDTFTG
						WVEAFPTGSKKATAVISSLLSDI
						IPQFSLPTSIHSDSRLAFISQITQA
1	1					VSQALGIQWNLHISYRPQSSGK
	}					VEQTNGLLKTHLTKLSLQLKK
						DWTVLLPLALLRIRACP
17451	47819	Α	17557	24	594	VGSGDLPWEGNPLSSCSLLHEK
		1				DPPTTSGPQTDQPKEHLTNFKS
			l			GCSSPGPARSQFFLSLRSSTL*SF
						YHLPSSHLVCLTVSFRD*PSPTC
						PAIDS*KGG/CELKA/RVKEHFC
	İ					HDLPASSMQSNYPVHDSGHLT
						TGPSLFKPTLNIEYSTGHAPYHV
			İ			RSACFPFAFCHDCQFPEASPEAE
						AAAILSVQPAEP
17452	47820	Α	17558	1	1152	
17453	47821	С	17559	301	462	
17454	47822	A	17560	1	423	
17455	47823	Α	17561	421	856	KLINLFSNFCSYSRQFLSFSSTL
						YFVWVFCYNRCCFSK*RMIVHI
	1	1		l		TNRDINCQIAYARIEGDMIVCA
1			ĺ			AYAHELPKYGVKVGLTNYAAT
1						YCTGLLLAHRLLNRFGMDKIC
1	1	1				YLDAGLARTTTGNKVFGDLDG
	L			l	l	GLSIPQSTK*FPGYD

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17456	47824	A	17562	3	1082	GPLCIALALQEFGTRRRWACRS LSSSGRRSLFRRRWGSYKAVINK AYFKRYQWKFRRREGKTIDYY ARKRILVIQDKNKYNTPKYMMI VRVTNRDINCQMLYA/RRIEGD MIVCAAYCTPNLPKIWY-RVGL THYYAAAYCTGLLLARRLLP*/ REGMDKIYEQOVELTGDEYNY ESIDGQPGCLPPAYLIDAGPCSE PTHWPLKFFGAPEGKLWMGGL SIPSQYPNRFPGYDSEKORNIN AEIVHRKAHSWGQNCCRFTWR YFIMEEDIEDAYKKIQPSQVIIK NSVTPDMMEEMYKKAHAAI RENPYL WKRRPKIKEVIKKRW NRPKMSLAQIKKDRVAQKKAS FLQSSRSGLLESLTPAIFP
17457	47825	Α	17563	2	4967	
17458	47826	A	17564	56	284	RQTRRAAGIVRGDCPASSPTNC DLGQC/NSTS/LEPRFVQTVHLL CPWT/GGSSPLLAARGSLPVSLL GPLKPMVSCAGR
17459	47827	Α	17565	1	3525	
17460	47828	В	17566	35	3691	
17461	47829	В	17567	80	3787	
17462	47830	Α	17568	225	507	
17463	47831	A	17569	2	2621	
17464	47832	A	17570	14	1658	
17465	47833	Α	17571	1	3654	
17466	47834	В	17572	1	3570	
17467	47835	Α	17573	1	3663	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
17468	47836	A	17574	485	2347	TEPKTKTT*LSQ*MOKRPLTKF
						NNTSC*KLSIN/IVLEVLARAIRO
						EKEIKGIOLGKEEVKVSLFADD
i						MIVYLENPTVSAONLLKLIGNF
						SKVSGYKINVOKSOAFLYTNNR
						QTERQIMSELPFTIASKRIKYLGI
		1				QLTRDVKDLFKENNKPLLKEV
		1				KEDTNEWKNIPCSWVGRINIVK
ļ		1				MAILPKVIYRFNAIPIKLPMTFF
	l	1				TELEKTTLKFIWNQKRACIAKSI
		1				FSQKNKAGGITLPDFKLYYKAT
1	l	l				VTKTAWYWYQNRDIAQWNRT
	l					EPSEIMLHIYNYLIFDKPEKNKQ
		1				WGKDSLFNKWCWENWLAICR
						KVKLDPFLTPYTKMNSRWIKD
	1					LNVRPKTIKTLEENLGITIQDIG
	1					VGKDFMSKTPKAMATKAKIDK
	ı	1				WDLIKLKSFCTAKETTIRVNRQ
		1				PTTWEKIFATYSSDKGLISRIYN
		ļ				ELKQIYKKKTNNPIKKWAKDV
	i	1				NRHFSKEDIYAAKKHMKKCSS
	ļ	l		1		SLAIREMQIKT,TMRYHLTPVRM
		ļ			1	AIIKKSGNNRKIQ/GGIWCDRIL*
1						R*TTCRVAKEIQSL*RRI/WKRL
		1				QRTLSIPVLDAV*PPMF*ASVID
						TMTI*CFEARDTCFTLTLESFWD
1					1	MHRCLAASKGIGLLLC*PLIWH
						MSLMGVKSPPFVFSCLWTSAV
17469	47837	В	17575	I	3354	
17470	47838	Α	17576	1	3297	

SEQ ID NO:	SEQ ID NO: of peptide		SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
17471	47839	A	17577	I	2563	MKAEIKMFFETNENKDTTNQN
1		l' -		ľ		LWDAFKAEEVESLNRPITGAEI
		l				GAIINSLPTKKSPGPDGFTAEFY
		1				QRYKEELVPFLLKLFQSIEKEEI
						LPNSFYEASIILIPKPGRDTTKKE
1						NFRPISLMNIDAKILNKILANRI
	l		i			QQHIKKLIHHDQVGFFPGMQG
						WFNIRKSINVIOHINRAKDKNH
						MIISIDAEKAFDKIQQPFMLKTL
						NKLGIDGTYFKIIRAIYDKPTAN
						IILNGQKLEAFPLKTGTRQGCPL
						SPLLFNILLEVLARAIROEKEIK
						GIOLGKEEVKLSLFADDMIVYL
		ŀ				ENPIVSAQNLLKLISNFSKVSGY
						KINVOKSQAFLYTSNROTESQI
1						MSELPFTIASKRIKYLGIQLTRD
	}					VKDLFKENYKPLLKEIKEDTNK
1	İ					WKNIPCSWVGRINIVKMAILPK
		ŀ				VIYRFNAIPIKLPMTFFTELEKTT
		ľ				LKFIWNQKRAHITKSILSQKNK
						AGGITLPDFKLYYKATVTKTA
	ŀ					WYCYONRDIDOWNRTEPSEITP
						HTYNYLIFDKPEKNKOWGKDS
						LFNKWCWENWLAIWRKLKLD
		Į.				PFLTPYTKINSRWIKDLNVRPKT
						IKTLEENLGITIODIGMGKDFMS
		l l				RTPKAMATKAKIDKWDLIKLK
						SFCTAKETTIRVNRQPTTWEKIF
						ATYSSDKGLISRIYNELKOIYKK
						KTNNPIKKWEKDMNRHFSKED
		ĺ				IYAAKKHMKKCSSSLAIREMQI
		l				KTTMRYHLTPVRMAIIKKSGNN
17472	47840	A	17578	1	3514	MELKTKARELREECRSLRSRCD
17472	7,040	ľ	17370	ľ	5514	QLEERVSAMEDEMNEMKREG
						KFREKRIKRNEOSLOEIWDYVK
						RPNLRLIGVPESDVENGTKLEN
		ļ.				TLODIIOENFPNLAROANIOIOEI
						ORTPORYSLRRATPRHIIVRFTK
		1				VEMKEKMLRAAREKDRSTROK
						VNKDTQELNSALHQADLIDIYR
	1	l				TLHPKSTEYTFFSAPHHTYSKT
1	1	1				DHIVGSKALLSKCKRTEIITNYL
						SDHSAIKLELRIKNLTKSRSTTW
1						KLNNLLLNDYW
17473	47841	A	17579	1	3693	KLINILLENDI W
1/4/3	147041	<u>۱</u> ۸	1/3/9	1	3023	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hed	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
17474	47842	A	17580	1577	3354	TEPKTKTT*LSQ*MQKRPLTKF
17474	47042	l^	17380	1377	3334	NNLSC*KLSIN/IVLEVLARAIRO
		1				EKEIKGIQLGKEEVKLSLFADD
		l				MIVYLENPIVSAONLLKLISNFS
		1				KVSGYKINVQKSQAFLYTNNR
1				l		QTESQIMSELPFTIASKRIKYLGI
1		l			l	OLTROVKOLFKENYKPLLKEIK
						EDTNKWKNIPCSWVGRINIVK
				l	ļ	MAILPKVIYRFNAIPIKLPMTFF
						TELGKTALKFIWNQKRARITKS
						LSQKNKAGGITLPDFQLYCKAT
		1		l	1	VTKTAWFPSGDVGLEADFSPSH
		1			i e	TLKTOFFSCLAEFAAASCFFOR
1		1				
		1	l		I	MNGFGMAMTTTYSTGAAESPL PSCSIDQGDDTKLHRARSPGRT
		ŀ				FPAAAGIPAAAAPDGPPLSLLH
		l		1		KLWFPVELGGRALPRAEESHGE
		ŀ				VAALGVMVVAQGGKNQGEEA
				]	İ	RSTPWLRPTSHLPPCSSSSAWW
				1		TEQTDAHPLLFLLCLGIYLLNA
						LSNLSMVALVRSDGALRSPMY
						YFLGHLSLVDVCFTTVTVPRLL
		1			1	AGLLHPGQAISFQACFAEMYFF
		1				VALGITESYLPAAMSYDRATAA
		1				CRPLRYGALVTPWALRLAARY
		l				DRLASVVYAVITPTLNPFINSLR
						NKEVKGALKRGLRWRAAPOE
17475	47843	A	17581	1	3042	
17476	47844	В	17582	1	3384	-
17477	47845	В	17583	1	3264	
17478	47846	Α	17584	1	3780	
17479	47847	Α	17585	1	3165	
17480	47848	Α	17586	1	3894	
17481	47849	A_	17587	1	3345	
17482	47850	Α	17588	523	3981	
17483	47851	Α	17589	1	3429	
17484	47852	A	17590	1	3921	
17485	47853	В	17591	1	4797	
17486	47854	Α	17592	1	6499	MVKGSIQQEELTILNIYAPNTG
	1	l				APRFIKQVLSDLQRDLDSHTLI
	1	l				MEDFNTPLSTLDRSTRQKVNK
		1	1		I	NTQELNSALHQADLIDIYRTLH
		I			1	PKSTEYTFFSAPHHTYSKIDHIV
	1	1	1		1	GSKALLSKCKRTEITNYLSDHS
		I	1		I	AIKLELRIKNLTQSRSTTWKLN
		I	1		I	NLLLNDYWVHNEMKAEIKMFF
		1				ETNENKDTTYQNLWDAFKAVC
	1	1			1	RGKFIALNAYKRKQERSKIDTL
	1	1	1		1	TSQLKELEKQEQTHSKASRRQE
	L					ITKIRAELKEIETQ

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
17487	47855	Ā	17593	1359	2520	IOCHPHOATNYFLHRIGKNYFK
						LHMEPNKSLHSQDNPKQKGTK
					1	LEV/CTLPDFKLYYKATVTKTA
						LYLYO/NORCRSMEONRALRN
						NATYIYNYLIFDKPEKNKOWG
						KDTLFNKWCWENWLAICRKLK
						LDPFLTPYTKINSRWIKDLNVRP
						KTIKTLEENLGNTIODIGMGKD
						FMSKTPKATATKAKIDKWDLIQ
						LKSFCTAKETTIRVNROPTEWE
1						KIFGIYSSDKGLISRIYNELQQIY
						KKKTNNPIKKWVKDMNRYFSK
						EDIYAAKRHMKKCSSSLAIREM
		ł				QIKTTMRYYLTPLRMAIIKKFG
						NNRQETVREMACLLSGTMDFR
						HRACFVLSKPDFSTRWPGADA
		ı				QRPPVLVVVALDSSLPFPQASG
ĺ		ı				QRPPSLEDVDGGAGALVAPC
17488	47856	Α	17594	1	1227	
17489	47857	Α	17595	2	2774	NLCSLIIPLREVTIVEKADSSSVL
		l				PSPLSISTRNRMTFLFANLKDRD
		l				FLVQRISDFLQQTTSKIYSDKEF
		l			!	AGSYNSSDDEVYSRPSSLVSSSP
	İ	l				QRSTSSDADGERQFNLNGNSVP
	1	1				TATQTLMTMYRRRSPEEFNPKL
		1				AKEFLKEQAWKIHFAEYGQGIC
		1				MYRTEKTRELVLKGIPESMRGE
		1				LWLLLSGAINEKATHPGYYEDL
		1			İ	VEKSMGKYNLATEEIERDLHRS
						LPEHPAFQNEMGIAALRRVLTA
17490	47858	<u>_</u>	17596	i	3472	YAFRNPNI
17491	47859	A	17597	1	900	
17492	47860	A	17598	<del> </del>	1290	
17493	47861	Ä	17599	153	3834	
17494	47862	A	17600	299	1184	
17495	47863	Α	17601	I	729	
17496	47864	Α	17602	I	2232	
17497	47865	A	17603	36	224	TQWGPSVCWCLIPWPSFPDQ*P
						GF*AVLLPWRCQGFWPLLLAC
		1				APAGPATAAEPAVSSPAEP
17498	47866	Α	17604	1	624	
17499	47867	Α	17605	I	578	RDLDLFSLPQDITL\VHYVDGIM
			l			LIGSSEQEVASTLDLLVRHLHA
			l			RGWEINLTKIQGLATSVKFLGV
		1				QWYGACRDIPSKVKDKLLHLA
		1	l			PPTTKKEAQHLAASFEWGPEQ
					I	KGLQQVQVAVQAALPLGLYDP
		1			I	ADPMVLEVSVADRDAVWSLW
			1			QAPIGESQWRPLGFQNKALPSA
l		1			L	DNYSPFERQLLACYWALVETE

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleutide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	cudun for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
17500	47868	Α	17606	I	282	PIYRVSRKAANFEWSPEQEKAL
		1				QQVQAAVQAAWPLGPYDPAD
		1				PMVLEVSVADRDADWSCWQA
		l				SI/GHKVGHAQQHSIIKWKWYI
	1	1				RDWARADPEGT
17501	47869	A	17607	1	338	SIYLVTQKAA/SSEWGPEQEKA
117301	47,007	l^	1,00,	ľ	330	LQEVQAAVQAALILEPYDPAGP
						VVLEVSLADRDAVWSLWQAPI
						GESQQRPLGFWSKALPSSA/DH
		1				KACHAQQHSIIKWKWYIHDRA
		_				RAGPEGT
17502	47870	A	17608	1	757	
17503	47871	A	17609	1	1317	
17504	47872	A	17610	2	24	LCQRLLLAEPNEKPGSLGNVM
		1				AVARIEIGICEYYHEKTTEKALD
		1				SHGVLAGSTIKGVRSFQRNLEL
				ŀ	l l	KLPATERATANAIELLTVLDQA
		1				YENFAPOILPSTGSPTSQETAOF
		1				KANQNKPLVRGKGSPHEAIRYI
1		1				SAAHREWKPAILTSAIRSFCST
1		ļ				WLVFTSKNFPKLVTOHGSTIAG
						NGOSSDETOVOGAAWKSDSRG
1						TKRQIPTWILAEGNNAGAQLDI
						PGPTIPAPNCSLKVPQSWSTTPS
1						
						MPSSLGKAYWLLACYWALVET
						E/RLAMGHQVTM\KPELPVMN
						WVLSDPSSHKVGGAQQHSINK
1						WKWYIRNRARAGPEGTS*LPAP
						LIG
17505	47873	Α	17611	ł	1815	
17506	47874	Α	17612	875	1916	PGKQGLEWTPRKLQQTCKRGA
						GQLEEKLANRKQ*HQH*QKG*P
1		1				/PQKLNAKDHNSSPTREQNWTE
1						NEFDELTEVGFRRWVITNSSEL
	l					KEHVLTOCKEAKNFDKRLEEL
1	1	1				LIQITSLEKNISDLMELKNTARE/
1	1	1		l		LLEAYTSINSOIDQAEMDR*PD*
1	1	1		l		*RRKERRIK*HNKK**RGYHN*S
1	1	l		l		OEIOTTIREYYKHLYANKLENL
1		l				EEMDKFLDTYTLPRLNQEEVEP
1		l		1		LNRPITSSEIEAVINSLPNOKSPG
		1				
1	1	1		1		QTNSQLTSTRDAEKAFNKIQHP
						FMLKTLNKLDIDGTYLKITRAI/
				l		S*QTHSQCHTEWAKAGSIPFEN
				l		RHKTRMPSLTTPIQYSIGNSGQ
						GNQEFWKLHLVEREW
17507	47875	В	17613	1	1158	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide locatinn of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17508	47876	A	17614	851	I344	IILKPSPSPLYPWKNCLPRNPSL VPKRQTGSGVDIWQTAADLQQ RGLLEGKLTNRKE*YQHQQKR CPHQNPI*RSPTSNTKARE(QNW TENEFDELTEVGFRRWIITNSSQ LKEHLLTQCKEAKNLEKRLEEL LTRITISLEKNINDPMELKNTAEE PHEAYTSINS
17509	47877	В	17615	99	716	
17510	47878	Α	17616	1	588	
17511	47879	Α	17617	1	1140	
17512	47880	Α	17618	1	774	
17513	47881	А	17619	3	527	AENSKKQNASSPPND/RNSS/EA QNWTENEFDELTEVGFRRWIV TNSSKLKEHVLTQCKEAKNLD KRLQELLTRITSLEKNINDLMEL KNTARELREAFTSFCVNCEAVS LITSLREDSHWLEDSKGHRM/R RHQE*KCEYFHPPHPGLQFYQL PESDSHSDPLWPHGGSFLSSVV
17514	47882	A	17620	1	1383	
17515	47883	A	17621	1	990	
17516	47884	В	17622	337	1515	
17517	47885	Α	17623	153	474	QTKSNNVNIKKQDVHTKTPSEC HQHQRPK\DHNSLPAREQNWIE NEFDELTEVGFRRWVITNSSEL KEHVLTQCKEAKNLEKRLQEL LTRITSLEKNINDLMELKNTA
17518	47886	A	17624	1	771	MPFSDTERVITGPSTKVHSYPG GLQALLCJGLHSLMWRWSAA VAIGVHVRCDLLAVHPVLWAV PGWQEPIEKMLTLIPGPRITATI GLYQHEGIRAYCDSRVYYIKPS SGIESVLTRPSTQDHNSSPAREO WYTENEFOBLTEVGFKK.WVIT NSFELKEHVLTQWKEAKNLEK RLANLLTRITSLENINDLMELK NTAQELHEAYASINSRINGSEER ISEIEDQLTEIEGVDKIREKRIK/R RNEOSL*FEIWDYV

NO:	SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
17519   47887   A   17625   53   S14   PGKQGLEWTPRKLQQTCKRGA GQLEKLANRKQ*HQH**OKG** PQKLAKAHNNSPTREQNWTE NEFDELTEVGERRWITNSSEL LEAYTSINSQIDQAEMDR**PDFREQNWTENSEKLEL LIQITSLEKNISDLMELKNTAKE LLEAYTSINSQIDQAEMDR**PDFREQNWTENSEKLEKHVLTQCKEAKNFDKRLEEL LIQITSLEKNISDLMELKNTAKE RAVLQPPLVITRQTGSGVDPQK TPADLQKRGRTVRRKTSQQKA VASTLTKRITTQKLANKAHNNSPTREQNATE PDFREQNCTENEFDELTEVGFRR WVITNSSELKEHVLTQCKEAKNFDKRLANKAHNNSPTREQNATE PREQNATE PREQNATE PREQNATE PREQNATE PREQNATE PREQNATE PREQNATE PREQNATE PREQNATE PREQNATE PREQNATE PREQNATE PREQNATE PREQNATE PREQNATE PREGNAT							
17519   47887   A   17625   53   814   PGKQGLEWTPRKLQQTCKRGA GQLEEKLANRKQ*HQH*QKG* PQKLAKADHNSSPTREQNWTT NFFDELTE*VGFREWVITNSSELL KFHVLTQCKEAKNFDKRLEEL LIQHTSLEKINSDLMELKNTARE LLEAYTSINSQIDQAEMDR*PD* **RRKERRIK*HINKK**RKEQAA FAVLQPELVTRQTGSGVDPDG* TPADLQRRCRTVRRKTSQKA VASTLTKRHTQKLNAKDHNSS PTREQNCTENEPDELTE*VGFRE* WVITNSSELKEHVLTQCKEAKN FDKRLEELLIQTSLEKINSDLM ELKNTARERWKHTQVSIAKSIK QKWTASQTNKEEKREENSTIK NDKGDITTDFTEDLTE*VGFRE* NOKGDITTDFTEQTTLET*VYFK* LYANKLENLEEMDKFLDTYTL PRLIADGE*VPELNEFTISSELAVI* NSLPNQKSPGQTNSQLTSTR   17520   47888   A   17626   I   1566   SINGLORE STANDARD S				09/540,217	codon for peptide	of peptide sequence	
GQLEKLANKKQ*HOH**OKG*    PQKLNAKDHNSSPTREQNWTE   NEFDELTEVGRRWVITNSSELE   KEHVLTQCKEAKNFDKRLEEL   LIQITSLEKNISDLMELKNTAKE   LILEAYTSINSQIDQAEMDR**PDD** RRKERIK**HNKK**RKEQAA   FAVLQPPLVITRQTGSGVDPQK   TPADLQKRCRTVRRKTSQQKA   VASTLTKRITTQKLANAKDINSS   PTREQNCTENEFDELTEVGFRR   WVITNSSELKEHVLTQCKEAK*   FDKRLEELLIQITSLEKNISDLM   ELKNTARERWKHTQVSIAKSIK   QKWTASQTNLEEKREESNSTIK   NDKGDITTDFTEQITTREYYK- LYANKLENLEMBKFLDTYTL   PELNQEEVEPLNRPITSSEIEAVI   NSLPNQKSPQQTNSQLTSTR     17520   47888   A   17626   I   1566     1552   47890   A   17628   I   2172     17522   47890   A   17628   I   2172     17523   47891   A   17629   I   504     17524   47892   A   17630   2   1601     17525   47893   C   17631   132   278     17526   47894   A   17632   380   \$28				l	sequence		
GQLEKLANKKQ*HOH**OKG*    PQKLNAKDHNSSPTREQNWTE   NEFDELTEVGRRWVITNSSELE   KEHVLTQCKEAKNFDKRLEEL   LIQITSLEKNISDLMELKNTAKE   LILEAYTSINSQIDQAEMDR**PDD** RRKERIK**HNKK**RKEQAA   FAVLQPPLVITRQTGSGVDPQK   TPADLQKRCRTVRRKTSQQKA   VASTLTKRITTQKLANAKDINSS   PTREQNCTENEFDELTEVGFRR   WVITNSSELKEHVLTQCKEAK*   FDKRLEELLIQITSLEKNISDLM   ELKNTARERWKHTQVSIAKSIK   QKWTASQTNLEEKREESNSTIK   NDKGDITTDFTEQITTREYYK- LYANKLENLEMBKFLDTYTL   PELNQEEVEPLNRPITSSEIEAVI   NSLPNQKSPQQTNSQLTSTR     17520   47888   A   17626   I   1566     1552   47890   A   17628   I   2172     17522   47890   A   17628   I   2172     17523   47891   A   17629   I   504     17524   47892   A   17630   2   1601     17525   47893   C   17631   132   278     17526   47894   A   17632   380   \$28							
POCKLAKDHINSSPITECONWTENSPIT	17519	47887	Α	17625	53	814	PGKQGLEWTPRKLQQTCKRGA
NFFDELTEVGFRRWVITNSSEL   KEHVLTQCKEAKNFDKRLEEL   LIQITSLEKNISDLMELKNTARE   LLEAYTSINSQIDQAEMDR*PD**   REKRERIKI*HINK***NEQAA   FAVLOPPLVITRQTGSGVDPQK   TPADLQKRCRTVRRKTSQKA   VASTLTKRITTQKLNAKDHNSS   PTREQNCTENEFDELTEVGFRR   WVITNSSELKEHVLTQCKEAK*   FOKRLEELLIQITSLEKNISDLM   ELKNTARERWEHVLTQCKEAK*   EVANAKENLEEMDR*CLDYTL   PFOKRLEELLIQITSLEKNISDLM   ELKNTARERWEHVTQSIAKSKI   QKWTASQTNKEEKREESNSTIK   NDKGDITTDPTEQITTREVYK: LYANKLENLEEMDKFLDYTL   PRIANQEEVPELNRPITSSEIEAVI   NSLPNQKSPQOTNSQLTSTR   17520   47889   A 17626   I 1566   I 1566   I 15752   47890   A 17628   I 2172   I 1005   I 17524   47892   A 17630   Z 1601   I 17524   47893   C 17631   I 17524   47893   C 17631   I 17526   47893   C 17631   I 17526   47894   A 17632   380   S28   EVLRVMIELNAVIYPYPKDTGC   QRL*PLARASINSPEYMGATQ   LKPLRFCKKCPKALEGGH*EW   MEARIRNLGTHALPCSTHFF*   TTTAQGEWLCCLCHCGEHPQG   GRHPCIC*HCYSCHTLAPPVQW   TPNVAEPDINKAGAQVKSPRV   TTTAQGEWLCCLCHCGEHPQG   GRHPCIC*HCYSCHTLAPPVQW   TPNVAEPDINKAGAQVKSPRV   TTTAQGEWLCCLCHCGEHPQG   GRHPCIC*HCYSCHTLAPPVQW   TPNVAEPDINKAGAQVKSPRV   TTTAQGEWLCCLCHCGEHPQG   GRHPCIC*HCYSCHTLAPPVQW   TPNVAEPDINKAGAQVKSPRV   TTTAQGEWLCCLCHCGEHPQG   GRHPCIC*HCYSCHTLAPPVQW   TPNVAEPDINKAGAQVKSPRV   TTTAQGEWLCCLCHCGEHPQG   GRHPCIC*HCYSCHTLAPPVQW   TPNVAEPDINKAGAQVKSPRV   TTTAQGEWLCCLCHCGEHPQG   GRHPCIC*HCYSCHTLAPPVQW   TPNVAEPDINKAGAQVKSPRV   TTTAQGEWLCCLCHCGEHPQG   GRHPCIC*HCYSCHTLAPPVQW   TPNVAEPDINKAGAQVKSPRV   TTTAQGEWLCCLCHCGEHPQG   GRHPCIC*HCYSCHTLAPPVQW   TPNVAEPDINKAGAQVKSPRV   TTTAQGEWLCCLCHCGEHPQG   GRHPCIC*HCYSCHTLAPPVQW   TPNVAEPDINKAGAQVKSPRV   TTTAQGEWLCCLCHCGEHPQG   GRHPCIC*HCYSCHTLAPPVQW   TTTAQGEWLCCLCHCGEHPQG   GRHPCIC*HCYSCHTLAPPVQW   TTTAQGEWLCCLCHCGEHPQG   GRHPCIC*HCYSCHTLAPPVQW   TTTAQGEWLCCLCHCGEHPQG   GRHPCIC*HCYSCHTLAPPVQW   TTTAQGEWLCCLCHCGEHPQG   GRHPCIC*HCYSCHTLAPPVQW   TTTAQGEWLCCLCHCGEHPQG   GRHPCIC*HCYSCHTLAPPVQW   TTTAQGEWLCCLCHCGEHPQG   GRHPCIC*HCYSCHTLAPPVQW   TTTAQGEWLCCLCHCGEHPQG   GRHPCYSCHTLAPPVQW   TTTAQGEWLCCLCHCGEHPQG   GRHPCYSCHTLAPPVQW   TTTAQGEWLCCLCHCGEHPQG   GRHPCYSCHTLA				l	l		GQLEEKLANRKQ*HQH*QKG*F
				İ	l		/PQKLNAKDHNSSPTREQNWTE
LIQITSLEKNISDLMELKNTARE   LLEAYTSINSQIDQAEMDR*PD' *RRKERKIK*HINKK**RKEQA							NEFDELTEVGFRRWVITNSSEL
LLEATTSINSQIDQAEMDR-PD- *RRKERIK*HNKK**RKEQAA FAVLQPPLVITRQTGSGVPPQK TPADLQKRCRTVRRKTSQQKA VASTLTKRITTQKLNAKDINNS PTREQNCTENEFDELTEVGFRR WVITNSSELKEHVLTQCKEAKT FDKRLEFLLQITSLEKNISDLM ELKNTARERWKHTQVSIAKSIK QKWTASQTNKEEKREENSTIR NDKGDITTDPTEQTTIREVYKE LYANKLENLEEMDKFLDTYTL PRLNQFEVPELNFRITSSEIEAVI NSLPPQKSPQQTNSQLTSTR    17520   47889   B   17627   1   1005     17521   47889   B   17627   1   1005     17522   47890   A   17628   1   2172     17523   47891   A   17629   1   504     17524   47892   A   17630   2   1601     17525   47893   C   17631   132   278     17526   47894   A   17632   380   828   EVLRVMIELNAVIYPYPKDTGC QPLV*HAAASLNSPEVMGATQ LKPKPREKGENGHEW MEARHNLGTLHGLPCSRTHF* TITTAQGEWLCCLCHCGEHPQG GRHPCIC*HCYSCHTLAPPQVW TRNVAEPDNKAGAQYKSPRV    17527   47895   A   17634   2   368     17528   47896   A   17634   2   368     17529   47897   A   17635   1   1881     17530   47898   A   17636   755   939   ARKNTRIIYSYGVCKNVETWR MFCTLLGRQQGCATVGKGDCC GPLRYYASWRKGDVLQCD				1			KEHVLTQCKEAKNFDKRLEEL
PRREERIK*HINK***REQAA							LIQITSLEKNISDLMELKNTARE/
FAVLOPPLVITROTGSGVDPQK TPADLQKRCRTVRRKTSQKA							LLEAYTSINSOIDOAEMDR*PD*
FAVLOPPLVITROTGSGVDPQK TPADLQKRCRTVRRKTSQKA					l		*RRKERRIK*HNKK**RKEOAAI
TPADLQRCRITVRRKTSQQKA				1			
VASTLTRRITTOKLNAKDINSS   PTREQNCTENEFDELTEVGFRR   WYSTNSSELKEHVLTQCKEAK   FPKRLEELLQITSLEKNISOLM   ELKNTAKERWKHTQSIASKI   QKWTASQTNKEEKREESNSTIK   NDKGDITTIDPTEIQTTIREYYKE   LYANKLENLEEMDKFLDTYLT   PTRAQGEVEPLNRFITSSELEAVI   NSLPPQKSPGQTNSQLTSTR   17521   47889   B   17627   1   1005   1   17522   47890   A   17628   1   2172   1   17524   47892   A   17630   2   1601   17525   47893   C   17631   132   278   1   17526   47894   A   17632   380   528   EVLRVMIELNAVIYPYKDTGC   QPLV*HAAASLNSPEVMGATQ   LKPLRFCKKCPKLLEGGH*EW   MEARHRNLGTLAGCSTHEFT   TTTTAGGEWLCCL.CHGGEHPQG   GRHPCIC*HCYSCHTLAPPVQW   TPNVAEPDNKAGAQYKSPRV   17528   47896   A   17634   2   368   EFSDPIHHTFDHMWRTKEHNE   AGWLLLSSVDKVMKENDELGI   SISQLQKQILSLSKAKIALSESLI   SCRERTEIVEK*T*ALIMLVADL   Q*KYIJAQPHHAQPRQVSTVKV   RALVVQEVTDP   17529   47897   A   17635   1   1881   17530   47898   A   17637   367   423   423   428							
PITREQNCTENEEDELITEVGFER   WVITNSSELKEHVLTQCKEAKN   FPKRLEELLIQITSLEKNISDLM   ELKNTARERWKHTQVSIAKSIK   QKWTASQTNKEKEREENSITSLM   GKWTASQTNKEKREESNESTH   NDKGDITTDPTEIQTTIREYYKE   LYANKLENLEEMDKFLDTYTL   PRLNQEEVPEN, PREVENTENSEIREAVIN   NSLPPNQKSPQQTNSQLTSTR   17521   47889   B   17627   1   1005   1   17521   47899   A   17628   1   2172   17523   47891   A   17629   1   504   1   17525   47891   A   17629   1   504   1   17525   47892   A   17630   2   1601   17525   47893   A   17631   132   278   1   17526   47894   A   17632   380   828   EVLRVMIELNAVIYPYPKDTGC   QPLV*HAAASLNSPEVMGATQ   LKPLPREKKEPRLEGGH*EW   MEARHRNLGTLHGLPCSRTHF*   TITTAQGEWLCCLCHCGEHPQG   GRHPCIC*HCYSCHTLAPPVQW   TRNVAEPDNKAGAQYKSPRV   17528   47896   A   17634   2   368   EFSDPIHHTFDHMWRTKEHNE   AGWILLISSVDKVMKENDELGG   SISQLOKQUISLKSKAKIALSESLI   SCRERTFIVEK*T*ALIMLVADL   Q*KVHAQPHHAQPRQVSTVKV   RALIVLQEVTDP   17529   47897   A   17635   1   1881   17530   47898   A   17636   755   939   ARKNTRIIYSYGVCKNVETWR   MFCTLLGRQQGCATYGKGGRC   GFLRYYASWRKGDVLQGD   17531   47899   A   17637   367   423						1	
WYITNSSELKEHVLTQCKEAKS							
FORKLEFLLIQITSLEKNISDLM   ELKNTARERWKHTQVSIAKSIK   QKWTASQTNKEEKREESNSTIK   NOKGDITTDPTEIQTTIREYYK-   LYANKLENLEMDKFLDYTYL   PRLNQEEVEPLNRPITSSEIEAVI   NSLPPNQKSPQTNSQLTSTR   17520   47888   A 17626   I   1566     17521   47889   B 17627   I   1005     17522   47890   A 17628   I   2172     17523   47891   A 17629   I   504     17524   47892   A 17630   2   1601     17525   47893   C   17631   132   278     17526   47893   C   17631   132   278     17526   47894   A 17632   380   828   EVLRVMIELNAVIYPYPKDTGC   QPL*HAAASLISPEVMGATQ   LKPLRPCKKCPKALEGGHEW   MEARIRNLGTLADECSTHEF   TTTTAGGEWLCCLCHCGEHPOG   GRHPCIC*HCYSCHTLAPPVQW   TPNVAEPDIKAGAQYKSPRV   17528   47896   A 17633   I   963   963     17528   47896   A 17634   2   368   EFSDPIHHTEDHWRTKEHNE   AGWILLISSVDKVMKENDELGI   SISQLOKQIGISLKSAKILASESLI   SCRERTEIVEK*T*ALIMLVADL   Q*KVIJAQPHHAQPRQVSTVKV   RALIVQEVTDP   17529   47897   A 17635   I   1881   17530   47898   A 17636   755   939   ARKNTRIIYSVGVCKNVETWR-MFCTLLGRQQCATVGKGDRC   17531   47899   A 17637   367   423							
ELKNTARERWKHTQVSIAKSIK QKWTASQTNKEEKREESNSTIK NDKGDITTDPTEQTTTREYYK							
QKWTASQTNKEEKREESNSTIK   NDKGDITTIDPTEIQTTIREYYKE   LYANKLENLEEMDKFLDTYTI.							
NDKGDITTPTEIQTTIREYYK-    LYANKLENLEEMDKFLDTYTL   PRLNQEEVEPLNRPITSSEIRAVI    NSLPPQKSPGQTNSQLTSTR     17521 47889	1				ŀ	•	
LYANKLENLEEMÖKELDIYTL			1	1			
PRIANGEVEPLARPITSSEIEAVI   NSLPNQKSPGQTNSQLTSTR     17520   47888							
NSLPNQKSPGQTNSQLTSTR     17520		ł					
17520   47888   A   17626   I   1.566					1		
17521   47889   B   17627   1   1005	10500	10000		1000		1000	NSLPNQKSPGQTNSQLTSTK
17522   47890					-		
17522   47891   A   17629   1   504     17524   47892   A   17630   2   1601     17525   47893   C   17631   132   278     17526   47894   A   17632   380   \$28			Ε				
17522   47892   A   17630   2   1601							
17525   47893   C   17631   132   278			_				
17526   47894   A   17632   380   828   EVLRYMIELNAVITYPYRDTGG QPL*HAAASINSPEVMGATQ   LKPLRPCKKEPKLEGGH=W   MEARIRNLGTLHGLPCSRTHF* TTTAQGEWLCL.CHGCEHPQG GRHPCIC*HCVSCHTLAPPVQW TPNVACEPDNKAGAQYKSPRV   17527   47895   A   17633   1   963     PSDIHHTFOHMWRTKEINE AGWLLLSVDKVMKENDELGT   SISQLQKQILSLKSAKIALSESLL   SCRERTEIVEK*T*ALIMLVADL Q*KVHAQPHIAQPRQVSTVKV   RALIVLQEVTDP   17529   47897   A   17635   1   1881   ARKNTRIIYSYGVCKNVETWR*MFCTLLGRQQGCATVGKGDRC GPLRYYASWRKGDVLQD   17531   47899   A   17637   367   423							
QPLV*HAAASLNSPEVMGATQ   LKPLRPCKKCPKILEGGH*EW   MEARIRNLGTILHGLECSRITHF     TITTAQGEWLCCL.CHCGEHPQG   GRHPCIC**HCVSCHTLAPPVQW   TPNVAEPDNKAGAQYKSPRV     17527   47895   A   17633   1   963       17528   47896   A   17634   2   368   EFSDPIHHTFDHMWRTKEHNE   AGWLLLSSVDKVMKENDELGI   SISQLQKQILSKAKIALSESLI   SCRERTEIVEK*T*ALIMLVADL   Q*KVIJAQPHHAQPRQVSTVKV   RALIVLQEVTDP   (17529   47897   A   17635   1   1881       17530   47898   A   17636   755   939   ARKNTRIIYSVGVCKNVETWR   MFCTLLGRQQGCATVGKGDRC   GFLRYYASWRKGDVLQGD   (17531   47899   A   17637   367   423   423			_				DUI DUI (IEINIA III III III III III III III III III
LKPLRPCKKCPKNLEGGH*EW    MEARHRNLGTLHGLPCSRTHF*   TTTAQGEWLCLCLPGGEHPQG    GRHPCIC**HCYSCHTLAPPVQW TPNVAEPDNKAGAQYKSPRV    17527 47895   A 17633   1 963     17528 47896   A 17634   2 368   EFSDPIHHTFDHMWRTKEHNE AGWLLLSSVDKYMKENDELGI SISQLQKQILSLKSAKIALSESLI SCRERTEIVEK*T**ALIMLVADL Q**KVHAQPHIAQPRQVSTVKV RALIVLQEVTDP    17529 47897   A 17635   1 1881     17530 47898   A 17636 755 939   ARKNTRIIYSYGVCKNVETWR*   MFCTLLGRQQGCATVGKGDRCG    17531 47899   A 17637 367 423   423	17526	47894	Α	17632	380	828	
MEARHRUGTLHGLPCSRTHFTTTTAQGEWLCCLCHCGEHPQGGRHPQGGRHPQGGRHPQTTTTAQGEWLCCLCHCGEHPQGGRHPQGGGRHPQGGGRHPQGGGRHPQGGGRHPQGGGGGGGGGG							
TTTAGGEWLCCL.CHGGEHPQG   GRHPCIC*HCYSCHTLAPPVQW   TPNVAEPDNKAGAQYKSPRV     17527							
GRHPCIC*HCYSCHTLAPPVQW   TPNVAEPPVQW   TPN							
TPNVAEPDNKAGAQYKSPRV				ľ			
17527   47895   A   17633   I   963							
17528   47896   A   17634   2   368   EFSDPIHITFOHMWRTKEINE AGWILLSVILKVAKEINE AGWILLSVILKVAKEINE SISQLQKQILSLKSAKIALSESLI. SCRERTEIVEK*T*ALIMLVADL Q*KVHAQPHIHAQPRQVSTVKV RALIVLQEVTDP   17529   47897   A   17635   1   1881							TPNVAEPDNKAGAQYKSPRV
AGWLLLSVDKVMKENDELGI   SISQLQKQILSLKSAKIALSESLI   SCRERTEIVEK** 74.LIMLVADL   Q*KVHAQPHHAQPRQVSTVKV   RALIVLQEVTDP   17529   47897   A   17635   I   1881     17530   47898   A   17636   755   939   ARKNTRIIYSYGVCKNVETWR*   MFCTLLGRQQGCATVGKGDRC   GPLRYYASWRKGDVLQGD   17531   47899   A   17637   367   423							
SISQLQKQILSLKSAKIALSESLI   SCRERTEIVEK*T*ALIMLVADL   Q*KVİIAQPİHİAQPRQVSTVKV   RALIVLQEVTDP	17528	47896	Α	17634	<sup>2</sup>	368	
SCRERTEIVEK*T*ALIMILVADI. Q*KVIIAQPHHAQPRQVSTVKV RALIVLQEVTDP   17529   47897   A   17635   1   1881     17530   47898   A   17636   755   939   ARKNTRIIYSYGVCKNVETWR* MFCTLLGRQQGCATVGKGDRC GPLRYYASWRKGDVLQGD   17531   47899   A   17637   367   423					l		
Q*KVHAQPHHAQPRQVSTVKV RALIVLQEVTDP   17529   47897   A   17635   I   1881     1881     17530   47898   A   17636   755   939   ARKNTRIIYSYGVCKNVETWR* MFCTLLGRQQGCATVGKGDRC GPLRYYASWRKGDVLQGD   17531   47899   A   17637   367   423							SISQLQKQILSLKSAKIALSESLI
RALIVLQEVTDP			1				
17529   47897   A   17635   I   1881							Q*KVHAQPHHAQPRQVSTVKV
17530   47898   A   17636   755   939   ARKNTRIIYSYGVCKNVETWR*   MFCTLLGRQQGCATYGKGDRC   GPLRYYASWRKGDVLQGD   17531   47899   A   17637   367   423							RALIVLQEVTDP
MFCTLLGRQQGCATVGKGDRC GPLRYYASWRKGDVLQGD							
GPLRYYASWRKGDVLQGD   17531   47899   A   17637   367   423	17530	47898	Α	17636	755	939	ARKNTRIIYSYGVCKNVETWR*
17531 47899 A 17637 367 423							MFCTLLGRQQGCATVGKGDRC
							GPLRYYASWRKGDVLQGD
17532 47900 A 17638 3 1925	17531	47899	Α	17637	367	423	
	17532	47900	Α	17638	3	1925	
17533 47901 A 17639 1 1137	17533	47901	A	17639	1	1137	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17534	47902	Α	17640	153	474	QTKSNNVNIKKQDVHTKTPSE HQHQRPK\DHNSLPAREQNWI
		l				NEFDELTEVGFRRWVITNSSEL
		1				KEHVLTQCKEAKNLEKRLQEI
		_				LTRITSLEKNINDLMELKNTA
17535	47903	A	17641	1	1068	
17536	47904	В	17642	1	717	LUI OL LIN OPPRI PL PL PL PRI OPPRI PL
17537	47905	Α	17643	585	2302	VLQLLRQERLELFVPPGELVV
	l	1				LASGVKLQTFAGGKAWLLQT
		ŀ				SDLGEQKLTTFIPISLSLKVIFW
	1	l				NWPEAKTAAYDGEQATCEPV
	İ	1				KAMFLADTHLLREFLGHWLD
						LRREWQVERAFQTALWLLQP
		l				VVFILEDVFDEGKWSTSEAWV
		l				DDVEQFRKMFRHPSHVQLKV
		l				AGNHDTGFHYETNTYEVERW
		l				NRNNPSFIMGSITPTDYALSKO
	1	1				LPPEDVVLIIYCGVKLPDRIVD
		1			1	KAGLLKLPVLKNVISTQLQFP
		1		l		MDQLLVYNLFNETSPLVMCL
	l					VMAMSNRGNHHLAATRLRK
		ł				LDHNSLPAREQNWTENEFDE
		l				EVVFRRWVITSSSELKEC/DVI
				i		QWKEAKNLEKRLDELLTRITS
		l				QKNINDLIELKNTAQELHEAY
		1				SINSQIDQVEERISEIEDQLNEI
		1				CEDKIREKRMKRNKQTLQET
	1	1				DYVKRPNPCWIGVPESDGEN
		1				TKLENTLQDII\QENFPNLARQ
	1	l			ŀ	NIQIQEIQRTPQRYSSRRATPR
		l				IVRFTKVEMKEKMLRAAGEK
		1			1	DETDNNEFFLWSQKGKRAGT
						NDHVEESCPPTKNACLGTPIH
17538	47906	Α	17644	1	282	PIYRVSRKAANFEWSPEQEKA
	l					QQVQAAVQAAWPLGPYDPA
		l				PMVLEVSVADRDADWSCWQ
		l				SI/GHKVGHAQQHSIIKWKWY
						RDWARADPEGT
17539	47907	Α	17645	3	903	
17540	47908	Α	17646	1	349	
17541	47909	Α	17647	1	489	
17542	47910	Α	17648	1	352	
17543	47911	A	17649	]1	505	KTDGSWRMTVDYHKLNQVA
	1	l		l		PVAAAVPDVVSLLEQINTSLD
	1	l		l		WYAAIDLGNVFFSIPVHKVHO
	1	ı	1	l		KFAFSWQGQQYTFTVLPQGY
		l		1		SPALCRHFVRRHLD/RFSLPQE
	1	1		i		TVVHYIDDIMLVG\PLIYRMTI
				1		KAAIFEWGPEQKALQQVQAA
	1	l	1			QAALPLGPYDPADPMRLR

SEO ID	SEO ID NO:	Mar	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of pentide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide inscrtion)
				sequence		
17544	47912	_	17650	1	1557	MASPEAVASODNDGFSOKPPPT
1/544	4/912	Λ	1/650	ļ,	1337	PLFASRSVNRLKSORTPRGEVE
						SVTDGEKTDGSWRMTVDYCKL
			l		i	NOVVTPIAAAVPDVVSLLEQIN
						TSPDITLVHYIDDIMLNGSSEQE
						VTNTLDLLVRHLCATGWEINPT
i		l				KIQGSSTSVKFLGVQWCGDCR
				ŀ		DVPSKVKDKLLHLAPPTTKKEA
						OHLTGLFGFRRKYIPYLGVLLC
		ŀ				PIYQVTRKAASFQWRPEQEKAL
		l				QQVQAAMQAALPLGPYDPAGP
1						MVLEIAVADTEAVWGH/WHSA
		l				SFPSHPCHCPMGP*TKWP*WQG
						WRLCMGSATWTSTHEG*PGYG
		l				HQ*VPNLPAAETNTEPAI*HHS/
1						SRRSASYLVAG*LYWTSCIMER
		i			i	AE\HLLWIWVCLSCMQCFCQD
		l			İ	YHPWTHGMPYPPLWYSTQLCL
						*PRHSLYH*RSVAVGSCSWNSL
			l		İ	VLPCSPSS*SSRVDRTVERPFEIT
			1		i	TTMPTSQESRVQESRGGSGSGT
1						THHHP**STSNIFASCFYGITFC
						WSRGLSSRGRNAATRRQNNSIK
						L*VKIATWTLWAPPTSKL
17545	47913 47914	В	17651	47	838 1566	
17546	47914	A	17652	1	981	MVAIAKVLIAYKEDSDSHNQPN
1/34/	4/913	l <sup>A</sup>	1 /655	l l	961	TRMTVSKGPVSAVEGGRRGOD
		1	:			SDDCVEENDAVRTWPPSRILRT
						ESHPSPHTCSWRRHLLSSCPYT
						GMSFPIPSSGNISSTHAVISFPPL
İ						SEEMNPMLPKATVMTSLEAAA
						RONLKSROAPRCEVESVTHEEV
ŀ		1				YYTRKELFEFSNLYRKKSGEQI
ŀ		1				REWILRKTDGSWRITVDYRKL
		l				NOMVTPIAAAVPDV/VVSLLEO
		l	1			INTSPGTWLCHNLIWRDLDCFL
						LPONITLVHYTDDIMOIGSSEOE
l		l	l			VANTLDLLPALMASW/ENSP*SI
		l				DRGRED*SLVHKWFCTICRHHP
l						KVDsCsTTAPF*DIPEGQQL
17548	47916	В	17654	179	1219	
17549	47917	Ā	17655	1	2655	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
ĺ				sequence		
17550	47918	Α	17656	11	942	MVGKAKWKPLELPLPRKIVNO
111000	11710			ľ	· -	KOHHIPEGIAEIAATIKDLKDAG
						VVIPTTSPFNSPIWPVOKTDGS
						WRMTVDYCKLNQVVTPIAAAV
						PDVVSFLEEINTSLGTWYAAID
						LANAFFSIPVHKVHOKPFAFSW
		1				OG/OOYTFTVLPODYINSLAL*H
i	1	İ				NLIWRDLDYF\LLLODITLVHYI
		l				DDIMLIGSNDHKVGGAQQHSII
		Ī				KWKLYIHDQAQTGPEGTTTSVI
						AQWAHEQSGPGSRDGGYAWA
		ļ.				OOHGLPLTKADLATTTAECPVC
1		l				QQQRPTLSPRYGTIPSLPLTKAL
						TLOLKKCSSGPMLMEFTGLAM
İ	l					FPIILKQLD
17551	47919	A	17657	1	868	FFIILKQLD
17552	47920	Â	17658	83	346	
17553	47921	A	17659	1	643	MVGKAKWKPLELPLPRKIVNO
111000			17007	ľ		KOHHIPEGIAEIAATIKDLKDAG
	1	1				VVIPTTSPFNSPIWPVQKTDGS
						WRMTVDYCKLNOVVTPIAAAV
1						PDVVSFLEEINTSLGTWYAAID
		1				LANAFFSIPVHKVHQKPFAFSW
1						QG/QQYTFTVLPQDYINSLAL*H
						NLIWRDLDYF\LLLODITLVHYI
	1	1				DDIMLIGSNDHKVGGAQQHSII
	1	1				KWKLYIHDQAQTGPEGT
17554	47922	c	17660	38	202	
17555	47923	Α	17661	3	410	LKSRQAPRCEVESVTHEEVYYT
						RKELFEFSNLYRKKSGEQIREWI
	1	ĺ				LRKTDGSWRITVDYRKLNQMV
	l					TPIAAAVPDV/VVSLLEQINTSP
	1					GTWLCHNLIWRDLDCFLLPQN
						ITLVHYTDDIMQIGSSEQEVAN
	1					TLDLL
17556	47924	Α	17662	2	526	
17557	47925	Α	17663	2	431	
17558	47926	В	17664	55	1506	
17559	47927	A	17665	73	753	OL A PROPERTY OF STREET
17560	47928	Α	17666	73	310	QLAEPPHWLPD*KGAGFEWGP
						EQKKALQ*VQAAVQAALPLGP
1	1	1			1	YDPADPMVLVVSVADKDAVWI FHLSGSDRWRRTYRCL
17561	47929	١.	17667	323	687	
17561	4/929	Α	17667	323	100/	KTDGSWR/TVDYRKLNQVVTPI
1	1	1			1	AAAVPDVVSLLEHINISPGIW/H
	1				1	HQKQFAFS*QGQQFT/FTVL/PH
1	1	1			I	GYINSLALCHNLIRRDLDHFSLP
1					1	QDITLVHYIDDIVLTGSSEQEVA GS\LESTCRHTKV
17562	47930	L.	17668	3	1363	OSILES ICKHIKV
17562	47931	A	17669	1	1203	
11/303	4/931	ΙΛ .	1,003	μ	11203	

17564   47932   B   17670   130   1374   17565   47933   A   17671   1   1063   17566   47934   A   17672   3   239   17567   47935   A   17673   231   368   NKHQEDSLKPPIPGPS: RPTLGQKGTCCTEKK GRI   17569   47937   A   17674   10   10   10   10   10   10   10   1	known,	Amino acid sequence ( X=Unkno	Nucleotide location of last	Nuclcotide	SEQ ID NO:	Met	SEQ ID NO:	SEQ ID
17564   47932   B   17670   130   1374		*=Stop codon, /=possible nucleoti				hod		NO:
17565   47933   A   17671   1   1063	e insertion)	deletion, \-possible nucleotide ins	of peptide sequence		09/540,217		sequence	
17566   47934			1374	130	17670	В	47932	17564
17567   47935			1063	1	17671	Α	47933	17565
RPTLGQKGTCCTEKK GRI			239	3	17672	A	47934	17566
17570		NKHQEDSLKPPIPGPSSW KPTLGQKGTCCTEKKKK GRI	368	231	17673	A	47935	17567
17570   47938			1270	1	17674	Α	47936	17568
17571   47939   A   17677   35   347			270	100	17675	C	47937	17569
DQQEALGRVRGSKVT			1978	459	17676	Α	47938	17570
PASPGAPFSNEILSEPG	rgewegr BILEVGGT BHPHHLLF PPS*PPSP					A		
KNA/GQEGRPGASRGS   TTGPQGVMROYH*CS   TTGPQGVMROYH*CS   VGLW*MLPEGIGITLQ   GPRQVQNYCPGAKAL   PA*CKASNQRSVYLE   EQIIVTEKTNILLEYLH   RTLPRKTRSKQRKL1   YRSTGSNARLPLMFIK   RLVVDAAWFOTHPSG   WPKAGPELLSRSQGFE   RLMFYPTMAAPVPK   17574   47942   A   17680   618   755	GPTLAPM GDPGWPS ARVQMG IPGGA	PASPGAPFSNE\ILSEPGPT PT/GAPCRSHGAGHSGDP SSPTGEDTNSAGPGAAR\ CGHCVSLVPR*/CCWTPG				А		
	SSPMATA LRPKGSS QDSGLPS LNQGPQE PTREYPS HQQWTK TYGYCH CTQGFFS GQWAPF	TDHRDRADKHPPALPAS. KNA/GQEGRPGASRGSSP TTGPQGVMPGYH*CSLRI VGLW*MLPGLGLTLQDS GPRQVQNYCPGAKALNC PA*CKASNQRSVYLPTR EQILVTEKTNILLRYLHQC RTLPRKKTRSKQFKLTYC YRSTGSNARLPLMFIKTQ RLVVDAAWPGTHPSGQW WPKAGPELLSSQGESC RLMFYPTMAAPVPK						
17575 47943 A 17681 796 1092			755	618	17680	A	47942	17574
1 1 1 1 1			1092	796	17681	A	47943	17575
17576 47944 A 17682 1 391			391	1	17682	Α	47944	17576
17577 47945 A 17683 1 697			697	1	17683	Α	47945	17577
17578 47946 A 17684 I 888			888	1	17684	Α	47946	17578
17579 47947 A 17685 749 1667			1667	749				
17580 47948 A 17686 1 2088								
17581 47949 A 17687 189 438								
17582 47950 A 17688 387 497								

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
l	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
		<u> </u>				
17583	47951	Α	17689	1	728	MAQEIEGDRLFRARLTRRVQG
						KGPCGPLKAPLGMVPECHSVK
	ŀ	1				PSRDTFDSTKSFKALLLSFLKIP
						AIDVHKPIDHPINFTFPDPGHRA
	l	1				PARHRHSTAAAVTMSPSGP/PA
	1					AAPSPCSPIPRHG*GPLRATSYC
l	1	ŀ				PVSWKQKQNSVSNKQTNEQTK
	1	1			ŀ	TAKAEGARSRGPRNKIPGLPPG
l		1				PRSGLRIWLPPPREGSGFQTPAR
						GHPQPPCSGKGTECQSIAQNLA
		1				SRISPVGTSCGRTSRQTIRVRK
17584	47952	A	17690	1	819	
17585	47953	A	17691	i	2115	MSGSYSSVWAEDDIOFDSRFLE
	1	ľ.		-	1	LKGDTKIDLKRFSSQGYVEPGK
		ı		ł	l	YNLQVQLNKQPLAEEYDIYWY
	i	1			ŀ	AGEDDVSKSYACLTPELVAQF
		1	1	1		GLKEDVAKNLOWSHDGKCLKF
1	l	1				GQLEGVEIKADLSQSALVISLPQ
	l	1			ľ	AYLEYTWPDWDPPSRWDDGIS
	Į	1				GIIADYSITAOTRHEENGGDDS
1	ł	1	1			
-		1				NEISGNGTVGVNLGPWRMRAD
		1			i	WQTNYQHTRTQLALGEDYLNS
1						DIFDGLNYVGGSVSTDDQMLPP
10006	47954	١.	17692		1000	HLRGYAPDISGVAHTTAK
17586 17587	47954	A	17692	1	1080 253	
17588	47956	B	17694	1	1069	
17589	47957	A	17694	1	764	
17590	47958	C	17696	136	990	
17591	47959	A	17697	130	1422	
17592	47960	A	17698	547	1017	
17593	47961	A	17699	176	431	
17594	47962	A	17700	1	846	
17595	47963	A	17701	1	1815	
17596	47964	A	17702	1	1578	
17597	47965	A	17703	1	1149	
17598	47966	A	17704	22	441	
17599	47967	A	17705	828	920	
17600	47968	A	17706	1	231	MESKRLDNA/CAGGGD*PQLH
1,000	77500	^	1,700	l.	l=-'	OCPR*TAVD*RRNQTAFA*RDA
1		1	1	1	1	
1		1		1		STYRHESGGNASPECHGLYQR
17601	17000	١.	12202	,	563	QKNADGGGGQRRI
17601	47969	A	17707	19	372	
17602	47970	A	17708	134	491	
17603	47971	A	17709			
17604	47972	A	17710	1	969	
17605	47973	A	17711	59	839	
17606	47974	A	17712	186	725	
17607	47975	A	17713	1	251	
17608	47976	A	17714	1381	2217	
17609	47977	Α	17715	357	804	

NO:	leotide insertion)  NESRSWFFEKI
17610   47978   B   17716   I   2361	NESRSWFFEKI KREKNQIDTI
17610   47978   B   17716   I   2361	KREKNQIDTI
17612   47980	KREKNQIDTI
17612   47980	KREKNQIDTI
17613   47981   B   17719   143   3122     17614   47982   A   17720   I   3018     17615   47983   A   17721   I   4371     17616   47984   B   17722   I   2010     17617   47985   A   17723   I   2168     17618   47986   A   17724   I   2067   MKEIEIQKSLPKIN     HKIDRLLARLIKK KNDKGDITANPT, KHLYANKLENLE     TLPRLNOEEAESL   AIINSLPTKKSPGP     RYKEELKKEGILL     PKPGETTKKENI     AKILNKILANRIQK     AKILNKILANR	KREKNQIDTI
17615   47982   A   17720   I   3018	KREKNQIDTI
17615   47983   A   17721   I   4371     2010     17617   47985   A   17723   I   2010     17617   47985   A   17723   I   2168     17618   47986   A   17724   I   2067   MKEIEIQKSLPKIN HKIDRLARLIKK KNDKGDITANPTL KHLYANKLENLE TLPRLNQEEAESL AINSLPTKKSPGP RYKEELKKEGILL PKPGRDTTKKENL AKUNKILANRIQK AKUNKILANRIQ	KREKNQIDTI
17616   47984   B   17722   I   2010	KREKNQIDTI
17617   47985   A   17723   I   2168	KREKNQIDTI
17618 47986 A 17724 I 2067 MKEIEIQKSLPKIN HKIDRLLARLIKK KNDKGDITANFT KHLYANKLENLE TLPRLNQEAESL AIINSLPTKKSPGP RYKEELKKEGILL PKPGRDTTKKENI AKILNKILANRIQ	KREKNQIDTI
HKIDELLARLIKK KNDKGDITANPT, KHLYANKLENLE TLPRLNGEAEL AIINSLPTKESPGP RYKEELKKEGILL PPPGROTTKLENI AKUNKILANRIQK	KREKNQIDTI
KNDKGDITANPT/ KHLYANKLENLE TLPRLNQEAESL AIINSLPTKKSPGP RYKEELKKEGILL PKPGRDTTKKENI AKILNKILANRIQ	
KHLYANKLENLE TLPRLNGEAGSI AINSLPTKKSPGP RYKEELKKEGILL PKPGRDTTKKENI AKILNKILANRIQ	AIOTTIREYY
TLPRLNQEEAESL AIINSLPTKKSPGP RYKEELKKEGILL PKPGRDTTKKENI AKILNKILANRIQ	
AIINSLPTKKSPGP RYKEELKKEGILL PKPGRDTTKKENI AKILNKILANRIQ	EMDKFLDTY
RYKEBLKKEĞILL PKPGRDİTKLENI AKILNKILANRIQ	NTPITGSDIE
PKPGRDTTKKENI AKILNKILANRIQO	DGLTAEFYQ
AKILNKILANRIQO	SSFYEASILLI
	FRPISLMNID
	OHIKKLIHHD
QVGFIPGMQGWF	
HINRTKDKNHTIIS	
IQQPFMLKTLNKL	
RAIYDKPTANIIL	
KTGTRQGCPVSPV	
AREIROEKEIKGIO	
LFADDMIVYLENI	
LISNFSKVSGYKIN	
YTNNRQTESQIMS	
IKYLRIQLTRDVK	
LLNEIKEDTNKWI	
INIVKMAILPKGIF	
MTFFTELEKTTLK	
IAKSILSRKYKAG	
CYKATVTKKAWY	
QWNRTEPSEIMPF	
EKNKQWGKDSLF	
LTICRKLKLDPFL	
IKDLNVRPKTIKT	
DIGMGKDFMSKT	
IDEWDLLKLK\SFG	
VNRQPTEWETIFA	JYSS
17619 47987 A 17725 I 3457	
17620 47988 A 17726 1 3630	
17621 47989 B 17727 1 3384	
17622 47990 B 17728 I 2199	
17623 47991 A 17729 I 3924	
17624 47992 A 17730 I 3345	
17625 47993 A 17731 I 2382	
17626 47994 A 17732 I 3720	
17627 47995 A 17733 I 3894	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17628	47996	A	17734		2427	MGCVRQIIPLGTHPVVHQLTSII QNCQSPQKTRKDREIGOPRGA' GOMBSKCNVMLMMESWNRK TLEIQTTIREYYKHLYTKLEN EEMDKFLDTYTLPRLNOEEVE: LNRPITHSDIVTIINSLPTKKISPC PDRFTAKFYQRYKEELVPFLLL LCGSIEKZEILDYNSFYEASIILIPL LGRDTTKKENFRPISLMYTDAP LIKKILANRIQOHIKKLIQHDQV GFIPGMQGWFNIRKSINIQHIN RIKDKNHMIISIDAEKAFDKIQG FPRIMKTLNKLGIDGTYLKIIRAI YDKPTANIILNGQKLEAFPLKT GTRQGCPLSPLLFIVLEALAR AIRQEKEIKGIGLGKEEVKLSLI ADDMIYYLENPIVSAQNLLKLI NFSKVSGYKINVQKSQAFLY NRQTESQIMSELPFTIASKRIKY LGIQLTRDVKDLFKENYFPLLA EIKEDTNIK WKNIPCSWIGRINI KMAILHKALYRPNAIPIKLPMT FFTELEKTLKFIWNQKRACIA KSILSQKNKAGGITLPDFKLHY KATVIKTAWYWYQNRDIDOX KKWGKDCLPNKWQNWLA CRIKLDLLTHYTKNSWIK KWGKDCLPNKWGNOWWLA CRKLKLDPLLTPYNSTRIFKLDTN KWGKDCLFNKWGNOWWLA CRKLKLDPLLTPYNSTRIFKLDTN KKWGKDCLFNKWGNOWWLA CRKLKLDPLLTPYNSTRIFKLDTN DLNVFRKTIKTLEENLGITIQDI GMGKDFMSKTPKAMATKDRII KDWLIKLISSCTAKETTIRVYR
		L				QPTKWEKIFVTYSSDKGLISRIY
17629	47997	A	17735	1	3780	
17630	47998	A	17736	I	2808	
1763 I	47999	A_	17737	I	4842	
17632	48000	В	17738	331	3282	
17633	48001	Α	17739	1	2880	
17634	48002	Α	17740	I	3213	

SEQ ID NO:	of peptide	Met hod	SEQ ID NO: in USSN	location of first	codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \"possible nucleotide insertion)
17635	48003	A	17741	I	2561	MKAEIKTFFETNKNKDTTYQN
				1		WDTFKAVCRGKFIALNAHKRE
						QERSKIDTLTSQLKELEKQEQT
						YSKASRRQEITKIRAELKEIETQ
					,	KTLQKINESRSWFFEKINKIDRI
		1				LTRLIKKKREKNQIDSIKNDKG
						DITTDPTEIQTTIREYYKHLYAN
		1		l.		KLENLEEMDKFLDTYTLPRLN
		1		İ		EEVESLNRPITGSEIEAIINSLPT
		1		.		KKSPGPDGFTAEFYQRYKEEL
		1				PFLLKLFQSIEKEGILPNSFYEA
		1		1		IILITKPGRHTTKKNFRPISLMN
		1		l		GAKILNKILANRIQQHIKKLIHF
						DQVGFIPGMQGWFNIRKSINVI
						QHINITNDKNHMIISIDAENAFI
						KIQQRFMLKTLNKLGIDGMYL
		1				KIIRAIYDKPTATQNLLKLIGNF
		1				SKVSGYKINVQKSQAFLYTNN
				1		QTESQIMTELPFTIASKRIKYLG
				ł		QLTRDVKDLFKENYKPLLSEIK
				1		EDTKKGKNIPCSWVGRINIMK MDILPKVIYTFNAIPIKLPMTFF
				1		EVEKTTLKFICNOKRARIAKSF
		1				SQKNKAGGITPPDFKLYYKAT
		1				TKTACYWYQNRDIDQWNRTEI
						SEIMQHIYNYLIFDKPDKNKQV
		1				GKDSLFNKWCWENWLAICRK
						KLDSFLTPYTKINSRWIKDLNIF
			1			PKTIKTLEENLGSIIQDIGMGKE
		1	l			FMSKTPKAMATKAIIDEWDLIK
		1	İ			LKSFCTAKETTMRVNRQPTEW
		1			ĺ	EKIFATYSSDIGLISRIYNELKQI
17636	48004	A	17742	1	5042	MTGSNSHITILTLNINGLNSAIK
		1				RHRLASWIKSQDPSVCCIQETH
		1				LMCRDTHRLKIKGWRKIYQAN
		1	ŀ			GKQKKAGVAILVSDKTDFKPT
		1				KIKRDKEGHYIMVKGSIQQEEL
	ļ	1				TILNIYAPNTGAPRFIKQVLSDL
		1	1			ORDLDSHTLIMGDFNTPLSILDI
		1				STRQKVNKDTQELNSALHQAD
		1				LIDIYRTLHPKSTEYTFFSAPHH
		1				TYSKIDHIVGSKALLSKCKRTE
		1				ITNYLSDHSAIKLELRIKNLTQS
		1				RSTTWKLNNL
17637	48005	Α	17743	101	471	MLSRILASRNRMRFAVEVVRA
		I				VRE/RVGNDFIIIYRLSMLDLVE
		I				DGGTFAETVELAQAVEAAGAT
		I				INTGIGWHEARIPTIATPVPRGA
		1				FSWVTRKLKGHVSLPLVTTNRI
		L				NDPQVADDILSSTH
17638	48006	Α	17744	161	311	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Aminu acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletiun, \=possible nucleotide insertion)
17639	48007	Α	17745	221	799	
17640	48008	Α	17746	20	346	
17641	48009	Α	17747	431	1578	
17642	48010	Α	17748	1	771	
17643	48011	A	17749	3	863	AVLRREMRQMEGAWLGSDLV
		l				DQGKERLNRLGFFETVDTDTQ
1						RV/PGSPDQVDVVYK\IVSLGGR
1						LFYNDFQADDADLSDYTNKKIE
						IIDSHADYFHIDIMDGHFVPNLT
						LSPFFVSQVKKLATKPLDCHLM
			ľ			VTRPQDYIAQLARAGADFITLH
						PETINGQAFRLIDEIRRHDMKV
						GLILNPETPVEAMKYYIHKADK
						ITVMTVDPGFAGQPFIPEMLDK
						LAELKAWREREGLEYEIEVDGS
						CNQATYEKLMAAGADVFIVGT
						SGLFNHAENIDEAWRVMTAQIL
						AAKSE
17644	48012	Α	17750	2	893	
17645	48013	Α	17751	139	2057	
17646	48014	Α	17752	2	361	
17647	48015	Α	17753	497	897	PRSASFSAWLAFCST/TKDSHPL
					•	LAQLLDGVENLDHRQHLLFTA
						GHGARPLIRAHADVEENCDHPF
			ĺ			ILIVHPSIHPIIYLSIHPSTIRGERL
						MTQIPLIKHFLAGVTGLKLTQQ
						MRFCENVCLPLIATAGNRQTH
17648	48016	A	17754	83	1038	PSRAGHLPPKIKSSMAGTTPCLS
						IMVRQRK/PLVPAPLYQGMRDG
						KIVRFEEITRTPLEVQDCLLASA
						LALGLALMGNAQAVTTIPFWH
			ł			SMEGELGKEVDSLAQRFNAEN
						PDYKIVPTYKGNYEQNLSAGIA
						AFRTGNAPTYFAGHIMQACGV
						ALSATIYFIRRKVVSLSDQKLNI
						AMTFVGSMSGALLVQYVQAD
						VLRQILPILVICIGLYFLLMPKLG
				l		EEDRQRRMYGLPFALIAGGCV
						GFYDGFFGPAAGSFYALAFVTL
			1	l		CGFNLAKATAHAKLLNATSNIG
			1			GLLLFILGGKVIWATGFVMLVG
10010	10017	_	10000		1500	QFLGAPHGVPTCV
17649	48017	A	17755	571	1728	,
17650	48018	A	17756	332 581	511 637	DAL DAGLODGGA MAGAGIZO
17651	48019	A	17757			RALR*SLQDGSAKRGASVS
17652	48020	A	17758	1	1098	
17653	48021	Α	17759	1	366 '	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, /=possible nucleotide insertion)
17654	48022		17760	321	611	GEGENYCDSVVMTWVAI*QN WQCHCCSLRCASLRQG*RQDV TDTRGETIKREMARNWV/WRA RVINAGFSRGSLLRGPISDHRRK RLSASIRQFYPRP
17655	48023	В	17761	95	645	
17656	48024	В	17762	1	3978	
17657	48025	Α	17763		328	MLIABGLMTAKNITVITNSLPA AFALSENKDITUT VVGGTVERIK TRSMHGSIAERSLQDINADLMF VGADGIDAVNGITTFNEGYSIS GAMYTAANSVIAVLDSSKFNR RGFNQVLPIEKIDIIITDDAVSEL FRTASTIGERDGTQVEMILFAGF VYLVISLASSLLVLTDCSTEVK KGEVVVVCOPSGSGKSTLIKTV NGLEPVQQGEITVDGIVVNDKK TDLAKLRSRVGMVFQHFELFPH LSIIENLTI.AQVKVLKRDKAPA REKALKLLERVGLSAHANKFP HYSGGQQGVAIARALCMP HYSGGQQGVAIARALCMP IAMLFOFFTSALDPEMINEVLD VMVELANEGMTIMMVVTHEM GTAVKWRIGSTQQGAQLHCNR WLHVRKHLLVAYYNLVGIKFG KESYMKLISEKALDDFPCSLU YLSAGHFSIYERILHKLEGNGQ LARGAKIWPQLEANTOQIMDY VJSSLETAIDHDNYLEFQQVLS DIGGEALEAAFVLEDKLILLVLD DIGGEALEAAFVLEDKLILTVLD DIGGEALEAAFVLEDKLILTVLD DIGGEALEAAFVLEDKLITTPATATATATATATATATATATATATATATATATATAT
17658	48026	A	17764	216	473	DALRVASGNGCYSALLPLFCRL L*AESA*VPVQRPCGETLMRSS VVCLGGTAPECSSLGCAEKSGR SWPRKVAHTLGSWTVPRES
17659	48027	В	17765	1	1570	
17660	48028	A	17766	1580	1764	PASSLVMR*CLNRIA\SRAHQPA VRAY*SASAPGIA*KENA*G*RL HHR*NPAGKPDPGLL
17661	48029	A	17767	1	1827	
17662	48030	В	17768	1	1281	
17663	48031	В	17769	72	1169	

SEQ ID	SEQ ID NO:	Me	SEQ ID NO:	Nucleotide	Nucleotide location of lace	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon,/=possible nucleotide
	sequence		09/540,217	eodon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
17664	48032	A	17770	120	552	SAGDA*DWFWHGGVAGGNG*
1700.	1.0032	l.,		120		RSP*A/VTSSALKCIHRALVRAW
		l				LLRMKKV*ATCA*CVTMRLKC
		l				CIK*/CPDNSLRMVOLFFPDPWH
			l			KARHNKRRIVQVPFAELVKSKL
ļ					1	OLGGVFHMATDWEPYAEHML
		1				EVMSSIDGYKNLSESNDYVPRP
		i				ASRPVTKFEQRGHRLGHGVWD
		ļ		L		LMFERVK
17665	48033	Α	17771	3287	3568	CAFQRNIWHAKLNASPTPVFVP
1		l				**LLASLTIPMKPAAMPGGKMD
						WWRVCRASASRPCQK*SLCQT
		1				PASVNTLLTVTAVCCASMASTT
				1		TRLWKI
17666	48034	Α	17772	1	3126	
17667	48035	Α	17773	249	3943	
17668	48036	В	17774	1	2178	
17669	48037	Α	17775	263	434	
17670	48038	Α	17776	619	1184	MRTSCGSFIKRRVMRRIASGMV
				1		AENRAV**PSGICAIMVSTSSMK
ŀ						PMRSISSASSRTRPLSL/AEVQSA
1						TFQVVQQTARSTDNDLRPLTQ
				ł		GA*LHVITLAAVQS/IPHLRRAC
						V*RNPSLLOOPVPPVRGSVPAP
						ESVVLSAQDQDSATEVKRMLQ
		1				FFRSPSGPYPERRGHSADVEYT
	ł	ŀ				LPELEMVFRNPDR
17671	48039	Α	17777	1	1485	
17672	48040	A	17778	497	1838	
17673	48041	A	17779	534	922	
17674	48042	A	17780	1	458	MOOLEEALKOLAOGSGSSOAL
1.707-	100.2	١.		ľ	1	TOVRRWDSACOKLPDANLALI
						SVAGEYAAELANQALDRNLNV
				1		MMFSDNVTLEDEIQLKTRARE
				i		KGLLVMGPDC/WYVDDCRHTA
				i		GFC*RDAGRQYWRHWRFRYR
		1		1		DSGAVFADCAGRGGNYSRDWP
						WRARPOP
17675	48043	A	17781	2	270	OAGKYYGGAVFAPVFGAIMGG
1,1013	40043	l <sup>A</sup>	1'''81	-	1210	VLRTMNIEPDALTSVDKNEFVI
	1	1		1	I	
		l			1	NHGEGTGGRS*FARPSCSVGAR
		1	I	1	I	RTFASTARDDTRQPCGCGGRSL
		_				CS
17676	48044	A	17782	1	1437	
17677	48045	В	17783	63	201	
17678	48046	A	17784	1016	1263	
17679	48047	A	17785	1	933	
17680	48048	В	17786	1	1888	
17681	48049	A	17787	845	2220	
17682	48050	Α	17788	110	581	
17683	48051	Α	17789	696	989	I

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17684	48052	Α	17790	199	573	
17685	48053	A	17791	1	3270	
17686	48054	Α	17792	1	3018	
17687	48055	В	17793	1	708	
17688	48056	A	17794	264	512	FLAQWLPELPLSRHLRQCTWCR RHRNRW*VRSLHRCWLADCRC PELRIRSHDL*SLAQRSLYDRTR TPDRRQLRTVLHWLLC
17689	48057	A	17795	1	2109	
17690	48058	A	17796	1239	1854	YHDDRNQPDAGNPSNADSGPQ I*QATGSPRRLVRRRWKRVNR LLAGKLAIVIDDFGYRPHINENQ VLAMPSAISVAVLPDSPHAREM ATKAHNSGHEVLIHLPMAHLSK QYTAGEKYATFOBGRRN*AHY S*WVNNVPYAVGINNHMGSK MTSNLFGMGKVMQALERVNL YFLDSVTIGNTQAMRAAQGTG VKVITRKVFLDGFAK
17691	48059	В	17797	1	2243	
17692	48060	A	17798	74	295	TISVLWLMLSLNTSKKRLA*TG SIGFFGLHSFTPRNGLRGASGTA FFGGVEVSTCGSFSKLLAFTSV MSGGRL
17693	48061	A	17799	1	1872	MLRIICMOHWYNLSDGAMED ALYEIASMRLFARLSLDSALPD RTTIMNFRHLLEOHQLARQLFK TINRWLAEAGVMMTOGTLVD ATIIEAPSSTKNKEQQRDPEMH QTKKGNQWHFGMKAHIGVDA KSGLTHSLVTTAANEHDLNQL GNLLHGEEQFVSADAGYQGAP QREELAEVDVDWLIAERPGKV RTLKQHPRKNRTGISIAYMTGSI RARVEHPFRIIKRQFGFVTARYR GCLNTITNGDVFPLATWFGG
17694	48062	Α	17800	1	1269	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17695	48063	Α	17801	1	1988	MNDSEFHRLADQLWLTIEERLI
		l				DWDGDSDIDCEINGGVLTITFE
		ŀ				NGSKIIINRQEPLHQVWLATKQ
						GGYHFDLKGDEWICDRSGETF
						WDLLEQAATQQAGETITGFRV
						YTLQLNAQLRLGFLRLPYSVNI
						ATEYKSLTHYTKVPEATNPSLE
						SSVDVKLSANRLKYPMMRKRI
						MKMWREAKALHSDPVEAWAS
						IIEDADKAKSFKQARGRGGFVF
	l	l	1			SSWQEVNELIAASNVYTIKNYO
						PDRVAGFSPIPAMSMVSYASG/
		1	1	1		RYLSLIGGTCLSFYDWYCDLPF
					ł	ASPQTWGEQTDVPESADWYNS
				1		SYIIAWGSNVPQTRTPDAHFFT
		l				VRYKGTKTVAVTPDYAEIAKL
						CDLWLAPKQGTDAAMALAMO
	1	ŀ			İ	HVMLREFHLDNPSQYFTDYVR
	ĺ	l			ŀ	RYTDMPMLVMLEERDGYYAA
					1	GRMLRAADLVDALGQENNPE
		1				WKTVAFNTNGEMVAPNGSIGF
		1				RWGEKGKWNLESIA\RIENPHF
		1				RSVKHNPVLVRQLPVKNLTLV
		1			1	DGNTCPVVSVYDLVLANYGLI
	ŀ	Į.				RGLEDENSAKDYAEIKPYTPA
		ı				WGEQITRVPRQYIETIAREFAD
		1				AHKTHGRSMILGAGVNHWYF
		l				MDMNYRGMINMLIFCGCVGQ
		l				GGGWAHYVGQEKLRPQTGWL
						PLAFALDWNRPPRQMNSTSFF
17696	48064	١.	17802	3854	5726	NHSSQWRYEKVSAQELLSPLA
17696	48064	A B	17802	3854	1869	
17698	48066	A	17804	391	1246	
17699	48067	A	17804	58	1353	
17700	48068	A	17806	872	2123	
17701	48069	A	17807	1	1422	
17702	48070	A	17808	217	509	
17703	48070	A	17809	76	422	
17704	48072	A	17810	2	288	-
17705	48072	A	17811	1	1626	
17706	48074	A	17812	779	832	
17707	48075	A	17813	1	1818	
17708	48076	A	17814	1	645	
17709	48077	A	17815	157	293	ALVCSSPWPSEKCKSKPQ*DTI
.770)	-30//	ſ	. 7013	["		HQLEWQSLKSQETTGAGEDVE K
17710	48078	A	17816	1	1446	
17711	48079	A	17817	1	306	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
17712	48080	A	17818	71	513	TIRSGLGWSQMEMRNMLGTGA
17712	140000	, .	17070	ľ.	1.5	KKYKLPSENTINTSTOIN*KI*K
		1				KRINSSTHTLSOD*TRKKLNL*I
						DQ*QELKLWQ*SIAYQPKRVQD
		1				QMDSQ/REFYORYKEELHINRA
						KDKNHMIISIDAEKAFDKIOORF
		1				MLKTLNEVLMGRISK
17713	48081	Α	17819	ī	828	
17714	48082	В	17820	I	567	
17715	48083	Α	17821	I	1224	
17716	48084	Α	17822	I	897	
17717	48085	A	17823	207	547	NHFLQGLGPLLQFPTSSSSPSET
				ŀ		TSAWTLCPHHYQAFGQSHSTSL
		1				*EV/HKLSHIFMSSSEPSKLFQPL
		1		l		PVTQFQSRFHIFRYLFSSIPLYW
		_				CQFTVLVHFPAADKDISVTTIP
17718	48086	В	17824	I	1128 765	
177I9 17720	48087	A	17825 17826	I	952	
17721	48089	A	17827	1570	2176	FLQSTHLTKG*YPESTMNSNKF
17721	40009	<u>۱</u> ^	1/02/	1370	2170	TRKKOPNORAKDMKRPFSKED
		1				IDAANKHMKKCSSSLAIREMOI
		1		ł		KTIMRYHFTPVRMAIIKKSGNN
		l				RCWRGCGEIGTLLHCWWDCKL
		l			ł	IOPLWKSMWRFLKDLELEIPFD
						PAIPLLGIYPKDYKSCCYKDTCT
				ł		HMFIAALFTIAKTWNOPKCPTM
						IDWIKKMWHIYTMEYYGAIKR
						MSSCPL
17722	48090	Α	17828.	I	53 I	
17723	48091	Α	17829	I	462	
17724	48092	Α	17830	876	1111	
17725	48093	Α	17831	2	276	LLPGFFCSNLAPVPPSGGHQHD
		l				LPYPSSA*NPGASGTGQARMGQ
		1				SHQWAFLWRKDAHVRKESGY
1		1				MYSLYDRAYGERTTGRRGRGR
		_				GPIPRP
17726	48094	A	17832	I	1290	DOWNER WE OF A TEAL PROPERTY.
17727	48095	A	17833	1293	1863	RSTPSMKE/QLATALPRHMTAE
				l	1	RMIRIANTEFRKVPALGNCDTM
	1			l		SFVSAIVQCPQLGLEPGSASGH
	1			I		AYLLPFGNKNEKSGKKNVQLII GYRGMIDLARRSGOIASLSARV
				l	1	GYRGMIDLARRSGQIASLSARV VREGDEFSFEFGLDEKLIHRPGE
		1		l		NEDAPVTHVYAVARLKDGGTO
				ĺ		FEVMTRKOIELVRSLSKADTD\*
						PWMCPCPMKRKSAT
17728	48096	c	17834	1	786	I WIVICI CENTRICATI
17720	140070	<u></u>	17034	l	1,00	

17729   48097   A   17835   2   654   FCRQ  GTHR	, \=possible nucleotide insertion)
GTHR	
	RQCQVYRRGRFTHAAFT
	DNVLQVQSKLRADGCAL
I I I I I I I I I I I I I I I I I I I	SQSEQVLPSELAFDEAPQ
	KVFNITLRTIMEGOSIVN
	TRAARFFYQARQRDLYG
	NAICADVQHKFLRIGVRC
	DAHIMMMSASLLQEGDV
	THSGRTSDVKAAVELAK
KNGA	KIICITHSYHSPIAKLADY
IICSP/	APETPLLGRNASARILOLT
LLDA	FFVSVAQLNIEQANINMQ
	M*KRP*NWOKRTGORLF
	TIHR*RNWPIILFAHOPRK
RRY*	VVMPRQEYYN
17730 48098 A 17836 I 4806	
17731 48099 A 17837 I 466	
17732 48100 B 17838 193 1045	
17733  48101   A  17839   1196   2732	
17734 48102 B 17840 1 732	
17735 48103 A 17841 290 664	
17736 48104 A 17842 302 1716	
17737 48105 A 17843 249 909	
17738 48106 A 17844 36 340	
	LRP/GLDIMRNRLNIRQQ
	QAAYEMTALRAATIELGP
	LPHLRTIHRQLYQDIFDW RITLINHGFVPKSTTVVET
	DOSIAMRRPGOTISRIHOV
	GIELTNCYEHSGLPDIKN
	JCROTHARPARLARLIFT
	NTINALVDIEVDDFFTDA
	CCFETGSHSVLARLGGAS
	QLDATSASHGSK
17740 48108 A 17846 1 1668	QUENTIONOMO
17741 48109 A 17847 1 1080	
	GFTSNVLTFLTCTSHFLNT
	DVANVQTATSNFRQIQVF
	OYNGKYILAVEGNPPLGE
	CISSGRPFIEKLKRAAAG
ASAIL	AWGTCASWGCVQAARP
	ATPIDKVITDKPIIKVPGCP
	MSAIITYMVTFDRLPDVD
	RPLMFYGQRIHDKCYRRA
HFDA	GEFVOSWDDDAA\PKVT
ACTK	WAAKGLPPITPVPHTLE*
	SRLLAGGNGLDRGRFSGV
DSSW	ISYLSSAISVTMAPATTLN
QTSK/	AALAACAISTLCNGWPA
VILAC	QHRWMKWSGLAS
17743 48111 A 17849 239 899	

SEQ ID NO:	SEQ ID NO: of peptide	Met	SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
NO:	of peptide sequence	hod	09/540,217	codon for peptide sequence	of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17744	48112	A	17850	155	249	CMRRKTALTGGEPDR*TAMR* HNKSPALTGS
17745	48113	Α	17851	1	1326	
17746	48114	A	17852	1	1394	
17747	48115	Α	17853	46	705	
17748	48116	Α	17854	2	488	
17749	48117	A	17855	563	687	LLARTSRQ*KTSLNCVNKL*MP SGQWAVLLLPVCRCWWLRT
17750	48118	Α	17856	1	1429	
17751	48119	Α	17857	1	1037	
17752	48120	A	17858	2	276	LLPGFFCSNLAPVPPSGGHQHD LPYPSSA*NPGASGTGQARMGQ SHQWAFI.WRKDAHVRKESGY MYSLYDRAYGERTTGRRGRGR GPIPRP
17753	48121	A	17859	1	1290	or in te
17754	48122	Α	17860	1293	1863	RSTPSMKE/QLATALPRHMTAE RMIRIANTEFREVALGNCDTM SEVSAIVQCP(GLEPPGSASGH AYLLPFGNKNEKSGKKNVQLII GYRGMIDLARRSGGIASLSARV VREGDEPSFEFGLDEKLIHRPGE NEDAPVTHVYAVARLKDGGTQ FEVMTRKQIELVRSSKADTDI* PWMCPCPMEVRKSAT
17755	48123	A	17861	207	210	QLSLLLNLPLDSIHHRLASSALK RVNDQVGAAPPRHQSPPPRNA VSLAPRPVPVEWSCAKLLCLSC RVNCQD*GNKALTSIHFVWGE GIVGKMWLFYCTEAHFVRDPS GYSN
17756	48124	A	17862	2	654	FCROROCOVYRRGRFTHAAFT GTHRDNVLQVQSKLRADGCAL EDYFSQSEQVLPSELAFDEAPQ DVVNKVFNITLRTIMEGGSIVN VDEHRAARFFYQARORDLYG AGGSNAICADVQHKFLRIGVRC QAYPDAHIMMMSASLLQEGDV VLVTHSGRTSDWKAAVELAK KNGAKIICITIISYHSPIAKLADY IICSPAPETPLLGRNASARILQLT LLDAFFYSVAQLNIEQANINMQ KTGAM*KR*NWQRKTGQRLF V*PIATIHR*RNWPILFAHQPRK RRY*VVMPRQEYYN
17757	48125	Α	17863	1	4806	
17758	48126	Α	17864	1	466	
17759	48127	Α	17865	214	907	
17760	48128	A	17866	1288	2757	
17761	48129	A	17867	705	839	AGRSRENRRYRAKQPRCGKR*F *CVYRFYPSGRYAEPSSAPNYT

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown.
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
17762	48130	A	17868	199	1628	
17763	48131	Α	17869	746	1013	TRARREITALRESSLVSASPCC
l						NWAAAFSS\YFCQQIVR*PHFDF
						OEKRSVONOPDGCSSSASOSVR
		1				QRPKSPQQPVQSANPSLLLCR
17764	48132	A	17870	2	331	
17765	48133	Α	17871	1	591	
17766	48134	Α	17872	1	1197	
17767	48135	Α	17873	45	3402	NRFSHISVTSACGWYHIPVEE/Q
						PEY/PGNLELERRIRSAIRWNAI
1		ł				MTVLRASKKDLELGGHMASFO
İ		1				SSATIYDVCFNHFFRARNEODG
						GDLVYFOGHISPGVYARAFLEG
		1				RLTQEQLDNFRQEVHGNGLSS
		1		l		YPHPKLMPEFWQFPTVSMGLG
					1	PIGAIYOAKFLKYLEHRGLKDT
		1				SKOTVYAFLGDGEMDEPESKG
		1				AITIATREKLD/NLVFVINCNLO
		1				RLDSP\RWDELLRKDTSGKLIOL
		1				MNETVDGDYQTFK
17768	48136	Α	17874	452	1395	LAGATGTAIRLILHAPLLLPIKM
	1	ĺ				RLP/TVSEGKPDSIPAAEKFAAE
1						NKNTYGALASLELAQQFVDKN
	İ					ELEKAAAQLQQGLADTSDENL
		l				KAVINLRLARVQVQLKQADAA
						LKTLDTIKGEGWAAIVADLRGE
						ALLSKGDKQGKHQRAENCEIQ
					ŀ	GYIDMIKHLVAPLVFTSLILTGC
						QSPQGKFTPEQVAAMQSYGFT
		l				ESAGDWSLGLSDAILFAKNDY
		l			1	KLLPESQQQIQTMAAKLASTGL
						THARMDGHTDNYGEDSYNEGL
		l				SLKRANVVADAWAMGGQIPRS
1		1	1			NLTTQGLGKKYPIASNKTAQGR
						AENRRVAVVITTP
17769	48137	В	17875	1	1579	
17770	48138	Α	17876	182	2069	

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
				<u> </u>	ļ	
17771	48139	Α	17877	1	2017	MESGVATRPIADFDVYIDKLTE
				l		FVYKTNLFMKPIFSQARKAPKR
						VVLPEGEEARVLHATQELVTLG
						LAKPILIGRPNVIEMRIQKLGLQI
				l		KAGVDFEIVNNESDPRFKEYWI
				l		EYFQIMKRRGVTQEQAQRALIS
-						NPTVIGAIMVQRGEADAMICGT
						VGDYHEHFSVVKNVFGYRDGV
						HTAGAMNALLLPSGNTFIADTY
1						VNDEPDAEELAEITLMAAETVR
1		l				RFGIEPRVALLSHSNFGSSDCPS
		l				SSKMRQALELVRERAPELMIDG
						EMHGDAALVEAIRNDRMPDSS
1						LKGSANILVMPNMEAARISYNL
1						LRVSSSEGVTVGPVLMGVAKP
						VHVLTPIASVRRIVNMVALAVL
1		l				FVNADETTVVNFHACFACVEV
1		l	ļ	l		FTVRHTTNRYQHGVVTLRFSG
1						CFFAFHRHINAVFFRFNIQAVFV
1						ALRPEVIAIMHKLREOGHRVVV
			ŀ			LSNTNRLHTTFWPEEYPEIRDA
1		l				ADHIYLSODLGMRKPEARIYOH
1		l				VLQAEGFSPSDTVFFDDNADNI
1		l		1		EGANOLGITSILVKDKTTIPDYF
				'		AKDKARHRTRPLWAWLKLLW
		1	l			QRIDEDNMTTLAGNLAYVSLLS
		1				LVPLVAVVFALFAAFPMFSDVS
				-		IQLRHFIFANFLPATGDVIQRYIE
				1		QFVANSNKMTAVGA\ASLAISS
						YLLSLIANVLMLMS*SVLRMS
						WNPKWAWSSIWYS
17772	49140		17878	21	212	
11///2	48140	Α	1''8''8	31	312	RGTGHCALYRRAAARCAKITL
	İ					TTFISLFSSYFVIYNILLLIYLIFA
	ŀ					ASFCLLVV*CIITVFITVCSAGD
	1					VSGMSATWCAFVAISVDHFTG
17772	40141	<u>.                                    </u>	17070	,	1000	FNRF
17773	48141	A	17879 17880	1	1098	
	48142	A		1		
17775	48143	В	17881	<u> </u>	1917	
17776	48144	A	17882	931	1773	VVVNA 416 + 114 WDVD GIDD 11601
17777	48145	A	17883	785	956	KKWMHSAV*WRKRSIRRVSSL
1						GY*TQAKDRRFALPELRRIVCS
	10111	<u> </u>				TVRRYVRRWRTNRT
17778	48146	A	17884	221	367	
17779	48147	В	17885	I	1318	

SEQ ID	SEQ ID NO:					Aminu acid sequence ( X≃Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
17780	48148	A	17886	1190	1634	APSQTVSLPEVASSMSGVMAG
						VEAVSSPGPYAVCAGSLLPSGW
					ł	LCVKTSVIAMIASAWSAPGAVS
						IKRSSAVSVRIWALCGA\OPECA
						VRSLPSYPAFRQVLAPVTHAL*
						PRRSSGCP*CDYSLQLLLQ*PAH
						*HLQGLLRKQLSCQR
17781	48149	Α	17887	I	2499	
17782	48150	A	17888	454	1698	
17783	48151	Α	17889	635	1665	KSIFWRAPADCEP/QVRQSAKV
						QFGDYQANGMMAVAKKLGM
						APRQLAEQVLTHLDLNGIASKV
					1	EIAGPGFINIFLDPAFLAEHVQQ
				1	1	ALASDRLGVATPEKQTIVVDYS
	1					APNRGFFGGGAPLGTTLQDLTR
l						PTKEDGLQAKPISFWASFALQF
						VNVKIILYGVTALSTFVLPQTQ
			İ	ł		ALSWVVGVSVLLAMIGTFGNV
ł			l		l	CWALAGHLFQRLFRQYGRQLN
1						IVLALLLVYCAAFSKGTSDNVA
1		1				LLFRSQRVKANCITGYTDGQLR
	1					IFFRMLNCIFQSFATQNVNVQV
						LTTFNANFWFHFYWNFTVFNV
		l				TQFAYCNHFIFCITCFCNDATPF
17784	48152	A	17890	73	212	AFFAVQQPERVHRKTAILL
17785	48153	A	1789I	2049	2445	VFPVFLRIYVFWKKPGMKVTN
1,,,03	40155	n	17071	2049	2443	ARNWOLKPLFTELPVILPDTOL
						HYVAWMELYSPAE*ERIOA*FV
	Į.					VWSWNIWLY*A*RLIOK*IIALT
l						PVVRTGKTKLMSAILFNITIHR
						MKAMNLSSPKRRLPPRNCGKK
17786	48154	A	17892	1	1476	
17787	48155	Α	17893	332	572	RGGA*RQKHRRTSALSLLSLP*
1						NMATAVHLHRFSTRRAVTSSS
						ARKWTNSGAMSGLNRASA\AV
						LRV*QSPEDGCCARIR
17788	48156	Α	17894	80	405	PRNLRKSGPPISDA1SPTSKP*TI
				1		TEPISAPSLLATYKAAGCGGTT
			1		1	QCTAINAVHSGMASFNNEVLV
		l		ĺ	1	FLAIEKARGINSTTPTSTNSVMP
		L				QIRPTSTIMTSTESQRQR
17789	48157	A	17895	1	1392	
17790	48158	A	17896	I	1374	
1779I 17792	48159	A	17897 17898	1971	2306	
17792	48160 4816I	A	17898	209	240	
17794	48162	A	17900	I	456	
17795	48163	В	17901	222	3807	
17796	48164	A	17901	3140	3219	
17797	48165	A	17903	240	298	
	1.5105	r	1	1	1	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid	Amino acid sequence ( X=Unknown, *-Stop codon, /-possible nucleotide deletion, \=possible nucleotide insertion)
17798	48166	Α	17904	1902	2047	NQPVYRSNGD/RIWRTGKLFPT TVFRLIRTLSPRAFPPFTSYRRCS VAY
17799	48167	В	17905	1	1994	
17800	48168	Α	17906	1	2151	
17801	48169	A	17907	3	1127	GTFYASQFVIRPVEGSKPLIKQV LDIGAHGTIDKTIAQKLARVAR MHFARORLANVATFACSAQNA IALMEEIAANFSYEMIRLTECIL GFTWINELYQGINVHINAERVRQ LAHDGHELVYVPCHRSHMDYL LSYVLYNGCLVPPHIAAGINL NFWPAOPIFRRLGAFFIRRTFKG NKLYSTVFREYLGELFSKGYSV EYFVEGGRSRTGRLLDPKTGM LRGGTRPITLIPIYIGVEHYMEV TYYAKELRGATKEKESLPQML RGLSKLRNLGQGYVNTGEPMP LMTYLNQHVPDWRESIDPIEAV RPAWLTPTVNNIAADLMVRIN NAGANAMNICTALLASRQR
17802	48170	А	17908	192	486	PVLVYLWVSFSWLCGRSLVCD AFGCVLCVLCFWCGVCWGWF SRCLVLVRVLDCVAVAWVCPL GVGIGLWV/RVLPTGLVSAVPC CCDVLARFRVDLCWG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USSN 09/540,217	location of first codon for peptide	Nucleotide location of last eodon for last amino acid nf peptide sequence	Amino acid sequence ( X=Unknown, *=Stop eodon, /=possible nucleotide deletinn, \=possible nucleotide insertion)
				sequence		
17803	48171	Α	17909	1	2470	MFQPSDSGKSFIFNMSVGYNLE
		l				GIKQPPMQQFIDNMMDASDHP
		1				KFAQYRDTLNKLLQDDAFLAR
						HGLQEKRESLQALPARIPTSMV
		1				HGVTLSTMHGCPPHEIEAICRY
1						MLEEKGLNTFVKLNPTLLGYA
1						RVREILDVCGFGYIGLKEESFD
1						HDLKLTQALEMLERLMALAKE
1		1				KSLGFGVKLTNTLGTINNKGAL
İ						PGDSTSGVLRTYERLLTAWML
						TCPCADEHQRGESVKLATALT
						WWLRGSQNRDEITKDGFQSNH
		l				AGGILGGISSGQQIIAHMALKPT
1						SSIDVPGRTINRFGEEVEMITKG
1						RHDPCVGIRAVPIAEAMLAIVL
						MDHLLRQRAQNADVKTDIPRC
		l				AQSIGSFSNGCIVGADTLPIQSE
į.						HYQVMRTDQRRYFGHPDLVM
						FIQRLSSQVSNLGMGTVLIGDM
						GMPAGGRFNGGHASHQTGLDV
1						DIFLQLPKTRWTSAQLLRPQAL
1		l				DLVSRDGKHVVSTLWKPEIFSL
	1					IKLAAQDKDVTRIFVNPAIKQQ
		l			ŀ	LCLDAGTIATGCAKCDPGVSIG
1						AYAYLLTLRAQCLAHDLPDPLE
	1					PLEIDGTLLPRYVFIHGGPRVFT
	1					YYTPKEESIKLFHDYLDLHRSN
						PNLDVQMVPVSVMFGRAPGRE
	1					KGEVNPPLRMLNGVQKFFAVL
						WLGRDSFVRFSPSVSLRRMADE
						HGTDKTIAQKL\ARVARM\HFA
		_				RQRLAAVGPRLPARQDLFNKL
17804	48172	Α	17910	1	734	
17805	48173	A	17911	1	962	
17806	48174	A	17912	1630	2633	
17807	48175	A	17913	1360	1600	HSTGRWATTINVPITCGTKARH
						STSSICKTGMILLWANALKQHC
1						LLSRNLP*KGESINVANSLLSYF
		_				NLRPQCNQTRTQD
17808	48176	A	17914	1	816	
17809	48177	A	17915	703	1546	O LUD OTTO DOTTO DE LOS TOURS
17810	48178	A	17916	209	485	QVIRPTFIPSTSSNGAISLPASTR
1			1			RDS*MANAS*RCSLA*RATMFP
						A*SATSIFHARPGVEGT*IVRIV
17011	10170	L.	10010		1160	VIMLRLLSRRKVRGIRLPAAVLI
17811	48179	Α	17917	619	1167	L

SEQ 1D	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop eodon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		ŀ		sequence		
17812	48180	Α	17918	Ti	764	DSGQQLDDVQLARYLLSGQNQ
						PKSDRPYRVR*LTGAMLKLILT
l	1					L/VIEGNVTLGIIRVKIGTGCVIK
	l	l				NSGDWR*LRNOSVYRCGRCES
						GSGLYHWARLPVCVLVLSCWK
						VLTSSLVPPD
17813	48181	Α	17919	3	1462	
17814	48182	Α	17920	122	983	
17815	48183	В	17921	1	1287	
17816	48184	Α	17922	289	958	
17817	48185	Α	17923	1	5079	
17818	48186	Α	17924	1	255	
17819	48187	Α	17925	1892	2448	TESRCADGAGSVDVGTEPVVP
			1			RVELVAKWPGSRAGGTGLGCS
						PWVGAGCVGGLGPQARLSGPT
		1				ASTEASAKAASTLASLMWLRV
						RL*GACPFARTGATAPSSSKGP
						ELGVSGLRKATWMGRGSGCCT
1		l				RGLGAGEWRAVPESCGLDESS
	Į.	l	ŀ			EDSDDRDHAVPFSSSSCRRSML
		_				RPRRVARGLCRRRGV
17820	48188	В	17926 17927	929	888	TVWNGTCGLPFSSLMKCMVIM
17821	48189	A	17927	929	1148	
			l			IMRAIQKKMMSKPDTITLVGW N*RRASVFSGQPRVEKVHSAEE
		l				NOVSRTSSS
17822	48190	A	17928	125	937	RISMVFPWCFCSCSRTLATTPAP
17622	46190	Ι^	17926	123	1937	TVRPPSRIAKRRPSSIAIGWIRVT
						TILMLSPGITISTPSGSSMVPVTS
	i	l			ŀ	VVRK*NCGR*PLKNGV*RPPSS
1						LDRMYTSDSNLHGLRPAVSPVT
1	l			İ		NTPA/SDGYYSHDGSLAOVDLS
1						ANYHEGOYTSAGLSLOGGATL
						TTHGGALHRTQNMGGTRLLID
					l .	ADGVADVPVEGNGAAVYTNM
						FGKAVVSDVNNYYRNQAYIDL
					}	NKLPENAEATQSVVQATLTEG
		1	1	l	1	AIGYRKFAVISGQKAMAVVNF
		1	l		1	AEGKVSLAVV
17823	48191	A	17929	3992	4213	VPAIQOKFPRSWKLGGERPPKA
1,7623	13151	ľ	1.,,2,		1	FRLRLSAA*RKSVP*AQRSLAD/
		1	l			SGMPLRLEKCLDTF*TOIV*SAF
			l			KIQREGS
17824	48192	A	17930	1	1636	
17825	48193	Α	17931	1	900	
17826	48194	Α	17932	1	939	
17827	48195	Α	17933	427	1250	
. 7027	1.3175	<u></u>	1	1.27	1.200	

SEO ID	SEQ ID NO:	Met	SEO ID NO:	Nuclentide	Nuclentide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=pnssible nucleotide inscrtion)
		l		sequence		
17828	48196	A	17934	521	805	LCPSNTSPLSCLLCDLVASTEM
17020	46190	n	17754	321	005	APMRVFQPAPKVNA**LFATIEP
ŀ		l				PYSVNKLLKPY**PAWTKSLCL
		l				LAPSIWLRPAAKSYFDTPGCSIF
						GTAA
17829	48197	A	17935	1	2052	GIAA
17830	48198	В	17936	1	573	
17831	48199	A	17937	1	1278	-
17832	48200	A	17938	161	659	
17833	48201	A	17939	1	588	
17834	48202	A	17940	695	1281	KLKPYSWAFSRQSGRSVILTPPR
17054	10202	ľ`	177.0	0/3	1201	VTVVVVAGFGPIPVFGTVMVRP
	1					GWAAP*FLPVASVYFP*AGLAG
					1	FLKKNRGCCANPAPPPIRRPIMY
	1	1				PP/MORLOEPPADWWACAWFS
		1				GKD*\WKKSPPNCTRCA
17835	48203	A	17941	261	2045	GRD WKKSTINCIKCA
17836	48204	A	17942	1	637	
17837	48205	A	17943	31	280	
17838	48206	A	17944	1	582	
17839	48207	A	17945	1	2496	
17840	48208	A	17945	330	507	
17841	48209	Ā	17947	1087	1875	
17842	48210	A	17947	1	476	
17843	48211	A	17949	1	537	
17844	48212	A	17950	2	492	
17845	48213	A	17951	1	1101	
17846	48214	A	17952	2538	2833	TRRNWRPIQSSEESWRAAGSST
17040	40214	<u> </u> ^	17752	2550	2000	PLTTQNRQQTAGIY*RSR*TAA
l .				l	l	RR*SPALPRRNPRLATAG\WOY
ŀ					i .	ATOTROO\RVPOL*LSAPATRK
						NRLLANAWLTM
17847	48215	Α	17953	125	1831	THE STATE OF THE S
17848	48216	A	17954	2	82.5	
17849	48217	A	17955	1	840	
17850	48218	A	17956	1	1725	
17851	48219	Α	17957	463	1824	
17852	48220	A	17958	2	117	
17853	48221	Α	17959	1	2640	
17854	48222	В	17960	223	1560	
17855	48223	A	17961	638	746	RIP*MT*WS*KPWHKNYMMHA
				1		QASVDNLIKWKKGYQ
17856	48224	Α	17962	385	514	
17857	48225	A	17963	17	225	SSPSKFTVAFFASLVMASAVSL
		1		1		ALSLRSLTTLSI/CGLVLQEERT
	1	1	1	I	1	DDALVEQFSPIRRARGHAPQQE
		1				ATEM
		_				

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
17858	48226	A	17964	1	521	LVFLVLFVGFLSCFKSTYTLTY
	1	1		1		GDSPSLCDGLLII*IISRIDTNKPA
						DNSISGIRDVGWVAKSYOVA/V
						GERLHNRTPGTSHOSDTRFDF*
						LC*PGSACPNLVSEHERPOANM
	1					LVEASGRLAA*YQNALSCSFGY
						GVGLVRRODFSSLGRFLOSAFA
				l	,	SNRY*QVVWVFEFQQVS
17859	48227	A	17965	267	554	LRFRFTRAVGRIFHRLDLLVLL
17000	1022/	l' -	11,505			GCNRYGRRGGDHGLCSVLVPR
						SLRLGRLPGGDSAAADAQSRH
ŀ	1					REKCR*DGVLVCDDQNRQTPV
				l		WKPHOEDVOV
17860	48228	A	17966	1	915	WRI IIQED VQV
17861	48229	A	17967	1226	1399	SDSNISICTCAQIH*KHFRII*NCT
17601	40229	^	17907	1220	1355	L*EVEP*RLS*M*LORKCVOGEP
	1					SKVHSLWGI
17862	48230	A	17968	828	1070	SFFDYQTSALEHARR*LHCRT*
1/802	48230	A	17908	020	1070	NAGWLPHRTDRSSGYHGRTCS
		l		1		
İ		l				AAGRCSSGDHSSYQQQNPAEK
1.000	10001	١.	17969		1198	LPAGHPQRSGSPERTG
17863	48231	A	17969	45	508	
17864	48232	A	17970	348	308	RLFRWCPM*S\WASYFPPESQSL
		1				PDSYWLF*ECNLPTAYNSQNAII
		L.				RESHAIYS
17865	48233	A	17971	251	601	MAKKMSLSIAVFWRRLYAY\Y
		1		l		PHLR*KS*TNW/QWWRSALS*A
	1	l			1	V*PNRS/IDSRWSIIWSVLFGML
		1		l		V/AT/ALAPAFWLRY*KKSFSA
		l		ł		WNPTKSPRCLSNARPCCSLSKK
	L	<u> </u>				ASLPWTIAARSR
17866	48234	A	17972	1	2121	
17867	48235	С	17973	1	1710	
17868	48236	A	17974	1	1335	
17869	48237	A	17975	1	1497	
17870	48238	A	17976	2	824	
17871	48239	A	17977	1	1965	
17872	48240	Α	17978	1	3555	
17873	48241	В_	17979	197	2021	
17874	48242	A	17980	1	348	
17875	48243	Α	17981	1	891	
17876	48244	A	17982	1	679	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1			sequence		
		<u> </u>				
17877	48245	A	17983	3	2502	EAIREVSNPI\PQEEIWTHREAVP
						PVQLLTGWCVTAKAPPDISAIS
			l			ALTAVKHGNCSSLTPLLNPPGS
				·		DVIVCAEMDEQWGYVGAKSR
						QRWLFYAYDSLRKTVVAHVFG
			ĺ			ERTMATLGRLMSLLSPFDVVIW
				1		MTDGWPLYESRLKGKLHAILV
					i	TFEEKFQEEPVKKQIIMVSISVS
						DTGGKKEKPKLINLSSKTNGLQ
						NTTEAQLCETKSDFELSFSGFNP
						ISIDTEDMKTGCCFQEQSVRRA
						YFKATSSPRRGLIITKLTTRVDG
1						YVADDPSRRYSGHGDLLWPNA
			Ì			GNSCVETTVGSLLCEVOAAPTP
						HTLEGKHGCRNKEKKRLTHSG
1				l		ACTYTFSELGLELWAWNCGKT
1						EVNLGAVGKGVGGDRGFKKIH
1				1		AKSQFTCSVLYTFTIKQGISLTL
						WSKVMHILEHLKENSKOLTSIC
ļ						TRYQRVFGPTWLHETIFCKVAL
				ŀ		TATLLAELEKTSTLQTFLDKIWI
ŀ				İ		LGAQQHTGSQEPSQALLTCDPA
				i		WKKALRKVTOKGGAFFGVDN
			ŀ	i	i	
l				i		LGSSLSPTTDLLYEEQRLTSLSG
						SWFPICVMVELTLRAGSSPGGR
						LYVEFDQAVTKEPRFLQYKHY
						WDGAVAGSSILRQDSFVAEAST
				ł		TITRIESPSVPSRSSTFLDDFSITQ
				l	Į.	QHRRHAGLSVMLSLIISPPVRGL
						CQERTLRRDFRERLMYLDLEY
						QSGYCRLRTAGSEMQMVPDVL
						IFAHRSGLAGLFPGLDRRLVNA
17878	48246	Α	17984	10	211	GSQSTIFTFAARW\NLWANENT
						DTSISPLGVGEQRHCSSP*RFPD
				·		SDRCSPWSPRSQGQNQSPQTW
						Q
17879	48247	Α	17985	1	1725	
17880	48248	Α	17986	1	379	
17881	48249	A	17987	3	273	
17882	48250	A	17988	3	1157	
17883	48251	Λ	17989	76	378	
17884	48252	A	17990	1527	2005	
17885	48253	A	17991	578	1312	
17886	48254	A	17992	1	1758	
17887	48255	A	17993	1	2433	
.,,007	1.0200	ı.,	1	ı <del>.</del>	2.33	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17888	48256	A	17994	I	537	SQEELLQQALVAQLA/HSEQLE GVQLPEPDEPSARHALPANEPRI VLNNGVYSYNDRPILINLISWQ HIGYYSSELHDYRVSTTVRNV ILSGYFDSIGIYQAVSDRQQKLV QQWLDILGIDKRTADAPFHSLS WGQQRLALIVRALVKHPTLLIL DEPLOGLDPLNRQUIRRFVDVLI
17889	48257	Α	17995	1	536	
17890	48258	Α	17996	I	1319	
17891	48259	С	17997	74	341	
17892	48260	A	17998	3	103	
17893	48261	Α	17999	1	745	
17894	48262	Α	18000	I	663	· · · · · · · · · · · · · · · · · · ·
17895	48263	Α	18001	2	297	
17896	48264	Α	18002	8	340	VPANSLSAIALFRRESVTPLAAL AASPVCAGREVLLKNHRRDLP* ISVPVNSSSNSARSLVWHSGRQ QIAPDWSSKDDFMRLGKPNRFS VLLLATWIR*STVIRRSPFTS

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
1 7007	100 ( 6	_	10000	<del> </del>	124	Marin Bollin Branch Control
17897	48265	Α	18003	1	1341	MVHRFGIRVRFVALGFYQDVIL
						PVRAHRHEWGHYVHLCASIQR
						QIDVSFARDATSHSSCPVTGVR
			ĺ			FWGYPFAANKVVIAGFELEGET
						MTRPGLICAEGGLLVMIVSLRS
						ELYDSYHEFTRQRVTEIVEKAA
						NHLPAVVEMMTLHRCAINRHN
	1					FVRRVGPAGISTFFASSPDGVN
	ļ					AGFSTFRVVFTCQRSRPLQRHS
						HADVQTATLLLNTVNLEQKQA
				l		NAILSGLSDMIPNSSPESAPEIQL
						LQSRMILGKTIAELNLRDIVEQK
	l					YFPIVGRGWARLTKEKPGELAI
	i	1				SWMHIPQLNGQDQQLTLTVGE
1		ı				NGHYTLEGEEFTVNGMVGQRL
				ĺ		EKDGVALTIADIKAKPGTOFVL
	l					SQRTELEAINALQETFTVSERSK
				l		ESGMLELTMTGDDPOLITRILN
	ļ			l		SIANNYLQQNIARQAAQDSQSL
				1		EFLOROLP*TLSKNRPTPFSAA*/
				l		DDMIPNSSPESAPEIQLLQSRMI
1	i			i		LGKTIAELNLRDIVEQKYFPI/D
						GSRLGEINQRKTR*AGDQLDAY
		1		l		STTEWSGSATDT\QVGENGHYT
						LEGEEFTVNG/NGRPASGKRWR
		1				CADYRGH*GQDQQLTLTVGEN
		l				GHYTLEGEEFTVNGMVGQRLE
						KDGVALTIADIKAKPGTOFVLS
		l				QRTELEAINALQETFTVSERSKE
		1				SGMLELTMTGDDPQLITRILNSI
		l		l		ANNYLQQNIARQAAQDSQSLE
		l				FLQRQLPEVRSELDQRKKNSTFI
17898	48266	A	18004	414	893	
1/898	48200	^	18004	414	893	VFAQHGLTVAAIAAHARDRWF VGRTAHANPPVRCSTDGSGRVP
						VTRYSGFVAAAVILLTASPRGG
		1				ECSREAPLCSVSEYLLLQSAGE
						YAPAPRCVLRCVPSVDEDFVPV
						VPD*APPVEVALFLLRLTPVAR
1						PADGGWLLAAIRPDALTSLAIV
	100 (8	<u> </u>	10005	100		VLAAAR
17899	48267	A	18005	432	1108	
17900	48268	В	18006	1	753	
17901	48269	A	18007	46	282	
17902	48270	A	18008	I	1201	
17903	48271	A	18009	1	618	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
17904	48272	Α	18010	I	1045	MLCTKWDKLGLEKNAGKNKN
						AYKWYGWPANAPDEPHIEOLV
					i .	GECRVMRQLKRLISRIAPSPSSV
					l	MVVGESGTAIPVVSHAEFKGGF
						ADIGVHYLDWTSRTTEKSSTKS
						HKDDFGYLEFEGGANFSWGEM
						YGFFDWENFYNGRHNKPGSEO
						RYTFKNTNRIYLGDTGFNLYLH
						AYGTYGSANRVNFHDDM\FLA
		1				GFGFQF*PAGGW/WGSNPFFAK\
						RYTRSKPYYT\GDNGYV\AGWV
					i .	AGYNFMLGSEKFTLTNWNEYE
					l	FDRDATYAADFLPLYDVDCQD
					l .	NGNLEYDTYSQPEWKHNLFDH
						YLAVLYRFKDESGKEQFSGAV
						VKTREATPGKEIEAITRRMLDFS
						PRLKKLA
17905	48273	Α	18011	228	430	YPROHRORADGSDRHR**/CWS
						A*IWANPTSNLPPCRFALTKRK
						RPILCAPPSRQSYAAWCRWEIRI
		İ				A
17906	48274	Α	18012	296	1178	
17907	48275	Α	18013	1	1395	MPSDISLASCRLRATSRLFTDHR
					l	RQSDCMTAINRIPIVDDEDNVR
						RFETHCANNVRTALHLFADIHP
						DVVLMDIRMPEMDGIKALKEM
						RSHETRTPVILMTAYAEVETAV
						EALRCGAFDYVIKPFDLDELNLI
						VQRALQLQSMKKEIRHLHQAL
					ł	STSWQWGHILTNSPAMMDICK
						DTAKIALSQASVLISGESGTGKE
					l	LIARAIHYNSRRAKGAFIKVNC
						AALRESLLESELFGHEKGLFER
						ANEGTLLLDEIGRM/PLVLQAIL
						RILQEREFERIG/GHQTIK/VDIAS
						LLAPTRLQAMVKEGTFREDLFY
						RLNVIHLILPPLRDRREDISLLA
						NHFLQKFSSENQRDIIDIDPMA
				l		MSLLTAWSWPGNIRELSNVIER
		1		I	i	AVVMNSGPIIFSEDLPPQIRQPV
	1					CNAGEVKTAPVGERNLKEEIKR
				1		VEKRIIMEVLEQQEGNRTRTAL
L		L.	10011	l		MLGISRRALMYKLQEYGIDPAD
17908	48276 48277	Α	18014	I	771	
17909	48277	A	18015 18016	I 859	1014	IKTGETHPGIGPSVM*RHSKAD
1 /910	462/8	<b> ^</b>	18010	039	1014	LTHRHCGGIPEPQSVSFGSSQH
		1				GGGQFPPL
	1	1	l	L	ı	OOOQITEL

SEQ ID NO:	of peptide sequence	hod	SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
17911	48279	A	18017	1224	1520	SPLVNO*GA*KFFSRGNLFPQG ETH*KTKGVPCWTRYPDLKRS DSAEIFKTPANASGRTSGSLGC AAQLEKVADGRDLDEKLAEAG IGGSNKTSVWQG
17912	48280	В	18018	182	2392	
17913	48281	Α	18019	72	266	
17914	48282	Α	18020	600	914	PYRGSPRNGHQLCDHCSHRLSE DPFVRYSNHCQSISNYRCDKPP VRPLSPLHQKTDRKHHQRPDRP FQWSAAPAHGRWRSGDS*ETP LHYAQPAGKLRWLWVNY
17915	48283	A	18021	1102	1171	LLGYGQQPPASNLLSEG*RSVV L*ISALRM*ALPPQKSSDAPNG WLPNRWPISSTHMIR
17916	48284	Α	18022	1	1279	
17917	48285	Α	18023	1329	1403	
17918	48286	Α	18024	442	918	
17919	48287	Α	18025	3	1345	
17920	48288	В	18026	436	988	
17921	48289	Α	18027	637	1086	
17922	48290	Α	18028	1	321	
17923	48291	A	18029	1	845	
17924	48292	Α	18030	298	581	GARAEARAGSGQGAGLGVSSP VRWRGWSDKGAERPGGPLSPL REVSRAGPSG/HAARGQQPGRP RFPPPGPRPPRRRCPCTRARPGG AAGGGPCL
17925	48293	С	18031	450	604	
17926	48294	Α	18032	1279	2253	

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
17927	48295	Α	18033	I	1957	MAQFHVSHPPAEWPRHVLLL
						ADSKNELQNMNTGQTCGTRQ
						LKSKLQGWNKPGIQSDPGSQG
						HPRCLKTFPLVAQSSTQERNH
						MEKAVLKSQNWAIIEEFITKIG
		l				WFPDYSGKVKYLSSPKSSCTT
		l				LQVTHFSLFFHPNPDELVSKIK
		ĺ				WSKHRLYQNNSEAFLEVQIPE
						KCEVYSMRTMGRRQPGTAMD
						LNAGGSICNVPRTLLHLTGEST
		1				RDRQRVGAYLDIRGWYILVLV
	İ	l				VDKEKLGIPGQKQNSSKILFGS
		l				KLKQWVYVKNHAKESITQEAI
		1				GIWVGQQRKRQPLGYEERKL1
		1				NRKDIHIKNPSVCHHHQRPKVI
		1				KTTKMGKKQSRKTGNSKNQS'
		1				SPTLKESSSSPATEQSWTENDF
		l				ELREEGFRRSDYSELQEEVQN
		1		į		GKEVKNFGKKLDEWITRITNA
		1				KSLKDLMELKTKARELCDERT
						LSSQCNQLEERVSVMEDEMNE
		1	i			KQEEKFREKRIKRNEQSLQEIW
		1		i		DYMKRPNLRLIG VPESDGENG
		1				KLENTLQDIIQENFPNLARQAN
		1			i	QIQEIQRTPQRYSLRRATPRHII
						RFTKVEMKEKMLRVAREKGR
		1				THKGKPVRLTADLLAETLQAR
		1				RQDTHRLKIK\DGGRFTKQMEI
		1				RKRQGLQS*SQIKQNLNQQRSI
						ETKKAIT*W*RDQFNKKS
17928	48296	Α	18034	i	2838	
17929	48297	A	18035	1	897	
17930	48298	A	18036	26	308	
17931	48299	A	18037	749	1020	
17932	48300	A	18038	1	1773	
17933	48301	A	18039	1	1890	
17934	48302	A	18040	1	756	
17935	48303	A	18041	399	660	CPPEA VMPRRHEPVWEMTGFF
		1		1		LPDVLLSDSSDTSEGFRLHLET
						WAPFLCRCLSLRLIS*HHHQTT
	L	_		<u> </u>		GNSSPPVSASQHQSVDRDSLN
17936	48304	Α	18042	909	2005	
17937	48305	Α	18043	1	490	
17938	48306	Α	18044	104	775	
17939	48307	Α	18045	170	451	
17940	48308	Α	18046	1	207	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop eodon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nuelcotide insertion)
	Ì			sequence		
17941	48309	A	18047	146	678	LGFLLRLSEMPRKQGDYRTRIW
1.,,,,,,	10507		10011			KFEDGLSNVLVIOLNKLIICVM
					i	CLVRDCDVLKTYFHR*SGLLPI
			ĺ			KDTS/RPFTRVTVQWGKKNDQ
						TFOGLLDTGSELTLIPEDPKRHC
						GPPVKVGAYGGQVLHSKWAPI
				l		YHFLSSHNCNGFCYISIANLPKK
İ						FGONIKECLTNNRIVPFNCVOD
17942	48310	A	18048	270	1444	1 50:111.5021.111.6171.01705
17943	48311	Ā	18049	700	1062	
17944	48312	A	18050	3	1096	
17945	48313	Ā	18051	ī	1500	
17946	48314	A	18052	1	6215	MEDNLISINKIKILLAVSDGEIDE
1	105		10052	ľ		TFSLKOLMFNSVPVONEDGSFN
	l					FEGVKAEFRPGTQTQEYIKGME
		1				DSSSEVTVNREVTTDNPYTISVT
						NKTLSAIRIKMEMPRGVRIESN
		1				GDKNGVRVEYEVQQAVDGGSF
						ETVLTDVIEGKTMSGYDRSRRV
				l		NLPNFNNOVIFRVVRKTPDSND
						SNVVDAIQVRSYAEVIDAKFRY
1						PLTGLLFVEFDSKMFPNOLPTIS
1						IRKRWKIVNVPSNYDPESRTYN
						GNWDGTFKKA
17947	48315	A	18053	1325	1417	
17948	48316	A	18054	1	4971	
17949	48317	A	18055	251	1091	
17950	48318	Α	18056	1	2277	
17951	48319	Α	18057	2	448	KNDKGDIIVTTKSGGRGTSTVS
						FKLLKPEKI/GSKFSQKDLEMLF
	İ					HGMRADFTSENFSAAWYLIEN
I				l		HSNTSFEQLKMAVTNLKRQAN
	1					KKSEGSLAYVKGGLSTFFEAQD
			1			ALSAIHQKLEADGTEKVEGSMT
						QKLENVLNRASNTADTVYE
17952	48320	Α	18058	124	984	

NO:	of peptide sequence		in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	eodon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
17953	48321	A	18059	142	1393	DKKPGMVPPPGEESQTVILPP GWQSYLSPQERTYVNTTLE TTWERPSSSPGIPASPGSHRSSLP PTVNGYHASGTPAHPPETAHM SGRKSTGDSQNLGSSSPSKKQS KENTITINCVTPHPDTMPPGQL KPFEWSYDYPWADKKDPQG NGTVAGFELLLQKLKGKQMQ KEMSEPIRERIKIEEDYAKNLAK LSQNSLASQEGSLGEA WAQV KKSLADEAEVHLKFSAKLHSEV EKPLMNFRENFKKDMKKCDHH IADLRKQLASRYASVEKARKAL TERQRDLEMKTQQLEIKLSNKT TEDIKKARRKSTQAGDBLMRC VDLYNQAQSKWFEEMYTTTLE LERLEVERVEMIRQHLCQYTQL RHETDMFNQSTVEFVDQLLRK VDPAKORELWVREHKTGNIRP VDMEI
17954	48322	A	18060	1	435	VENIE
17955	48323	A	18061	3	926	
17956	48324	Α	18062	3	693	RPPLAYLRDGDARAGLNGLQL AVLAMLSSRKMFCKKSQGSYS PSRVLITENDVKEGLQRSHILYD RAGEEHYNCISALHKSMRGSD ONASLYWLARMLEGGEDPL.VV ARRLYRFA\SEDIGLADPSALTQ AVAAYQGCHFICMPECEELLA CVCVYFRAPKSIEVYSAYNN VKACLRNHGGPLPPVPLHLRN APTRLMKDLGYGKGYKYNPM YSEPVDQEYLPEELRGVD
17957	48325 48326	В	18064	19	404	
17959	48327	A	18065	1	407	FRATITSAKMGAYKYIQELWR KKQADVMRFILRVRCWQYRQ LYALHRAPRPTRADKARRLGY NDKQGYVIYRIRVRRGGRKRPD PKGATYGKPVHHGDNQLKIAR SLQSDAEEPAGRHCGALREQSS Y*VGEHST
17960	48328	A	18066	53	328	AKKGAYNYIQELWRKKRADY MRFLLRVRCWQYRQLSALHRA PRPTRPDKARRLGYKAKQGYVI YKIRVRRGGRKRPVPKGATYG KPYHHGANQLKSAQSLQTGVQ ERPGHP*YAMRVLKAYRARPD

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
17962	48330	A	18068	93	836	AKMGAY\KYIHELWRKKQSDV
						MRFLLRARCWQYPALHRAGTE
		l	İ			WQLSALHRAPRPTRPDKARRL
		l				GYKQ\AKQGYVIYRIRVRRYI*D
1		l				SCSPWWLKTAQFPKGCNFTGK
		ŀ				PVHSWVFNQLKSFASKAFQFR
		1				WQEGGEAWDGTCGGLLEEFLN
1		I				FFNWVWV/GKIST*QNFFEGLIL
		1			i	I/VIPFHKS*SEENPDTQWDQPN
i		l l				QSHKHR\EMRG\LTSARPEKSRG
						L/GKKGHKFHHTIGG/SLRRAT
		1				WRRRNTLQAPPLPLI
17963	48331	Α	18069	1495	2055	
17964	48332	В	18070	125	2530	
17965	48333	Α	18071	345	800	RWRLQNLSFCSSCSGSGSEGAT
				1		CFARGR*RPPGNSLNVSRMGTR
ł	Ì					SSYSCRRHSPAFLSWGKGRCHL
		1				CNKAHLLAGA*HYSFLSGSAPY
i		1				*N*VNGQI**R*TAHRSTPDAPT
			ľ			GH*NCCS*L*CHSY*QRA*PGY
		l			1	RHD*CRMCC*CADCSHAC
17966	48334	A	18072	181	1687	
17967	48335	Α	18074	205	1734	
17968	48336	Α	18075	1	705	
17969	48337	A	18076	590	685	
17970	48338	В	18077	1	881	
17971	48339	Α	18078	1043	1248	ITLGIMAIFTVLILPIHEHGMVFH
		l				LFVSSFISLSSGL*FSLKRSFTSL
						VSWIPKYFILFEAVVNGSSL
17972	48340	В	18079	1	1977	
17973	48341	Α	18080	805	1153	AWKVLPFFVSFCF\LSSGL*FSL
						KRSFTSLVSWIPRYFILFEAIVN
1		1				GSSLMIWLSVCLLLVYKNACDF
1						CTLILYPETLLKLLISLRRFELLF
1		1				LSMFSASFRSSCKAGLVVAESL
17974	48342	Α	1808 I	471	1442	IWSFHIVPYFLEALFV*GVRKGS
1	1	1				SFSFLHMAGQFSQHHLLSRESF
						PHCLFFSGLSKTR
17975	48343	Α	18082	188	355	
17976	48344	В	18083	I	1677	
17977	48345	С	18084	35	1816	
17978	48346	Α	18085	557	724	
17979	48347	Α	18086	179	346	

SEO ID	ISEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
		<u>L</u>		<u> </u>		
17980	48348	A	18087	135	1461	INRIYILLSTTSHLFQN*PHSWK*
	l					STPQQM*KNRNYNKLSLRPQC
		1				NQTRTQDEETHSKSLNYMETE
						QPAPE*LLGT*QNEGRNKDVL*
						NQREQRHNIPESLGHI*SNC*QD
						**RRKERRIK*MQ*KC*RCNKN
		1				AKGVITTDPTEIQTTIREYHKHL
						YANKLENLEDTDKFLDTYTLPR
						LNQEEVESLNRPITGSEIEAIINS
						LPTKKRPGPDGFTAEFYQRYKE
						EQRIKYLGIQLTRDVKDLFKEN
		1				YKPLLNEIKEDTNKWKNIPCSW
		1				IGRINIMKMAILPKVIYGFNAIPI
		1				KLPRTFFTELEKITLKFIRNOKR
						ARIAKTILSKKNIAGGIMLPDFK
		1				LYYKATVTKTAWYWFQNRDID
		ı				QWNRTEASEITPHIYNHLIFDKP
		1				EKNKKWGKDSLFNKWCWENW
						LAICRKLKLDPFLIPYTKINSRW
						IKDLNVRPKTIKSLEENLGIPFR
17981	48349	В	18088	1	2016	The Bitter of th
17982	48350	A	18089	659	826	
17983	48351	A	18090	3531	3878	
17984	48352	С	18091	1	2793	
17985	48353	Α	18092	1607	1774	
17986	48354	В	18093	1	1666	
17987	48355	Α	18094	1	1068	
17988	48356	В	18095	1	1549	
17989	48357	A	18096	557	623	KKWINYWTHTPSQD*TRKKLN
		<u> </u>				P
17990	48358	В	18097	1	1231	
17991	48359	Α	18098	263	1461	GGSSCYPSWEATIRTAKMVTLR
		1				K\RTLKVLTFLVLFIFLTSFFLNY
						SHTM/VATTWFPKQMVLELSEN
		1				LKRLIKHRPCTCTHCIGQRKLS
	1				1	AWFDERFNQTMQPLLTAQNAL
		1			]	LEDDTYRWWLSLESVMFSVTM
1		1				GFCLQRPFGDKQGTTQPVYINQ
	ļ	1			1	TGRDLTQQQRLQREKKPNNLN
		1			i	DTIKELFRVVPGNVDPMLEKRS
		1				VGCRRCAVVGNSGNLRESFYG
		1			i	PEIDSHDFVLRMNKAPTAGFEA
		1				DVGTKTTHHLVYPESFRELGDN
1		1	l			VSMILVPFKTIÐLEWVVSAITTG
1	1	1	l			TISHTYIPVPAKIRVKQDKILIYH
1		1	l			PAFIKYVFDNWLQGHGRYPST
l	1	1	ŀ			GILSVIFSMHVCDEVDLYGFGA
						DSKGNWHHYWENNPSAGAFR
1		1				KTGVHDADFESNVTATLASINK
1	1	1	l			IRIFKGR
17992	48360	В	18099	1	4855	
		_			·	

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
17993	48361	A	18100	571	4189	FSLKRSSTSLVSWIPRYFILFEAL
17775	140301	ľ.	10100	J	11107	VNGSSLMIWLSV*AKILVQRA*
1						VLAFHPS*LRFVKDQVVVDMW
ļ						HYF
17994	48362	A	18101	7449	7626	SFRSRLFSFHVVELF*VSFLILSS
17994	46302	^	10101	/449	17020	SLIALWSEROSVIISVLLYFLRS
		l				AFLPTMWSILE
17995	48363	A	18102	63	329	SGORRKEVPSPTLPAPPFILKKK
1 /995	48303	A	18102	0.3	329	EWPDPPRSFFSGGHWAKSSCPS
		1				
						DCSSQLMAC*/CKNAKHQKDN
		1	l			SCLI/STHMKGNSERK*NSGYQ
		<u> </u>				GLG
17996	48364	Α	18103	2	618	GAFLLEVATAAGLSAGLTRLGS
		l				QVGGAMRRSKADVERYIASVQ
		l				GSTPSTLQKSMKGFYFAKLYYE
i		l				AKEYDLAKKYICTYINVQERDP
1		l				KAHRFLGLLYELEENTEKAVEC
		l				YRRSVELNPTQKDLVLKIAKLL
		ı		İ		CKNDVTDGRAKYWVERAAKL
						FPGSPAIYKLKN/DGWVRGQM
1		1				VPKPDDEGVQVRGRSGRPDAG
		_				WRLNRRSSVGGSAW
17997	48365 48366	A	18104	1	995	
17998	48367	A	18105	62	521	
18000	48368	A	18107	1	375	
18000	48369	A	18107	76	480	LVKVCHCTYHHFLTGVVSLPR
18001	48369	^	10100	1/6	400	DGGKGAPCWGRARSPKSALLP
		1				YLAPGRG*VGTYEVON/PNGTS
					i e	PVQSPATDVGRSPALGNQEP/G
		1		1		T*SPGPQIGRGVTGTARPHTGV
		1				SRDSWRRPPSFILNAVANIPKGN
						APIPKE
18002	48370	A	18109	445	1128	AFIFKE
18002	48371	A	18110	784	1189	IPLGKLLLKPVGAPQIERFPFQIP
10005	40371	^	10110	1,04	1107	VPLCSLSFPSHSPSSSSARS*VRQ
		l				ES*LGTPGSAPTGSP/TSHHPSAS
		1				SPPHPSAKAAFLSFVCFLCS*PPF
		1				SSCHPCGLGPGPDPSQKMMICT
						VAHLNQSLIFTVVKVHLL
18004	48372	A	18111	1	2088	THE TOTAL PROPERTY OF THE PARTY
18005	48373	C	18112	169	213	
18006	48374	A	18113	1145	1229	
18007	48375	A	18114	1	975	
18008	48376	A	18115	1	750	
18009	48377	Α	18116	288	368	
18010	48378	Α	18117	34	168	
18011	48379	Α	18118	479	1579	
18012	48380	A	18119	2279	2398	SDCSCPGL*GPPGRWHKRRKSG
		_				SPHLSTPEGTPALTSQA
18013	48381	Α	18120	21	190	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18014	48382	Α	18121	1	1773 -	
18015	48383	A	18122	18	290	VAGTWPNFLKKVGIVGKYGTR YGASLRKMVKKIEISQHAKYTC SFCGITKMKRRAVGIWHCGSC MKTVAGGAWTYK*V*FLVVFG SVWTT
18016	48384	С	18123	325	486	
18017	48385	Α	18124	1	498	
18018	48386	A	18125	3	306	RQEIDSIHQVGVYCLALVPANT LPKTPLGGIIIISQTKQLFLEGSL HPCNILMCPHTCVTNLPKPRQK QP/WCRPCFRDGWESGCWKTY STSCWKGSGTNRRE
18019	48387	A	18126	1	1197	oroc micoormate
18020	48388	Ā	18127	1	390	NSRVDDFVAPGLSEAGKLEGLE FPERQRLAAAVG/CSPMSGVIS MSAPFFLGKIIDAIYTNPTVDYS DNLTRLCLGLSGVFLCGAAAN AIRVYLMQTSRQRVVKRLRTSL FSSILGQEVAFSDKAGTGELI
18021	48389	A	18128	1	695	SGFMDHLEEKADLSELVEKEEL GFFQYYRERCHQKVYHFHTERG GSAKDAAPGGGHHQAGPGQG GDEGIRMMFCVSPNRATFVVS VPLVSIIDVYGRYLRKLTKVT QDSLAQATQLAEERIGNVKITV RAFGKEMTEIEKYPSKVDHVM KYARKEAFARAEGVILNEKSFQ GALEFKNVHFAYPARREVPIFQ DFSLSIPSGSVTALVGPSGSGKS TVLSLLLRLYDPAS
18022	48390	A	18129	1	2136	
18023	48391	A	18130	1	822	
18024 18025	48392 48393	A	18131 18132	257	388 765	MVNALSLAARIHAEVPADESPE MTEGYEGFYHLASMKGTVERA DMHYIIRDFDRKQFEAKKRKM MELAKK VGKGL HPDCVIELVIE DSYYMMREKVVEHPHILDIAQQ AMBCDCIBFELLYIEGGTOAL LSFMGLPCPNLFTGGYNYHA/P SPKFSAVSAMLLASASSAGRCG ESISPSLAYTSSPIESDSCGPAL* RFLKH*PÆIFLTQPVFSENEALD IWNISPTASVSPLMPSRQNAVRE LFLLTVRRPTGTD

SEQ ID NO:	SEQ ID NO:	Met	SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Aminn acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	09/540,217	codon for peptide sequence	nf peptide sequence	*-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
18026	48394	A	18133	1	1166	LITHWVYHLYGIORILIHIPSTSC PNRVRGDIPPLQRIVVPVTVIVQ PRLLIMLLPWQTVRLVQVMRV LILKLVAPFILPAPRRIAVFADE RQRQAPVVAVVKMNFSRRCVI RLFLSGQLLHRQPALRFRPRAF TAHAVCPDFFLQPVQQPHQFSI EHHAVAVLTPFLLERLCQAAPI YRLDTGGVSLHRRQPVSVPAIS VTWRMMGKNYDAAVLAGH CGFGLGATPTAIANMQATIERF GFSHMAFLVYMVGAFFIDIVA ALVIKLYLMPIFAG*PMKR** KSPPOOROMPTITRLISSVRF*
18027	48395	A	18134	48	314	NSTPQQRQMPD LERESSYPSF SSVLSGLLPVVGNVREYGVPG/ ELPGSSPDRAVNPPL LVPMTWVIEASYSIMRKKVGE HPHFLDIAHQAMRDCDIEPELN PIRGGTDGAQLSFMGLPCPNLF
10000	10006		10105		2011	TGGYN\IMVSMSL*LWKVWKK RCR
18028	48396	В	18135	83	3044	
18029	48397	Α	18136	1	1080	
18030	48398	A	18137	3	979	DA WADA WSKKAD VEVENPIO TEKKPERAKIV DAGGK VKKG NI KAJKEPKKOK PHICSIRNPEP CKKEIGRNSRSGMYSRKI AMYR RKIVSAAKSKIVEKKIKEEVLA TIVTKPYOGIODEN RR*POUVELI GCPRYYPISELDVPRKACHS GKETPL VOHUEKNEEAS INPRE PF*FILTGIRHRGKIR VGFPESSL AKLAYLLC*LGPLVLKSEVPLIR RTHQKFCHLPLSTKIDISNIVKI PKHLITGCILSERKKI KKIPRING EGUEIDTEKEKYERIFORKIDO KAVDSQILPKIKAIPQLQGYLRS VFALTINGIYPHKLVYLNCLKNIE
18031	48399	A	18138	858	1418	
18032	48400	A	18139	97	516	

s	of peptide sequence	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
18034 4			09/540,217	codon for peptide sequence	of peptide sequence	deletion, \-possible nucleotide insertion)
	48402	A	18141	110	768	NLFSGÖVESTFRKQPAHQRRSR ARAETMQRRLVQQWSVAVFLL SYAVPSGGRSVEGLSRRJLLKP MRPKNVHVPTKVTTYKRAVSE HQLLHDKGKSIQDLRRRFFLHH LIAEIHTAEIRATSEVSPNSKPSP
						NTKNHPVRFGSDDEGRYLTQE TNKVETYKEQPLKTPGKKKKG KPGKRKEQEKKKRRTRSAWLD SGVTGSGLEGDHLSDTSTTSLE
18035 4	48403	A	18142	338	661	
18036 4	48404	A	18143	443	661	
18037 4	48405	Ā	18144	474	531	
18038 4	48406	Α	18145	208	317	
18039 4	48407	Α	18146	1	807	
18040 4	48408	A	18147	I	1122	
18041 4	48409	Α	18148	283	2204	ASPMAPTSLCVPTLLPSLNQTSS SSTAPTGKASWGWPMLRLPGL TTPWSLSLTLW*SRPTFPTSSPC SFVVLASPSTSLKCWPLSEGA
18042 4	48410	Α	18149	208	1212	
18043 4	48411	Α	18150	202	1677	
18044 4	48412	Α	18151	1	3285	
18045 4	48413	Α	18152	3	2206	
18046 4	48414	Α	18153	1	1041	
18047 4	48415	Α	18154	2	1460	
18048 4	48416	Α	18155	1	792	
18049 4	48417	A	18156	51	362	AHGAA WPSHRKDRESADLGSD GQNGQDLDWGGGCRRCC*RC DVLCWGAPHTFRHSYAMHML YAGIPLKVLQSLLLGQAPCRCG LGQNVGTALPLVSGGPMLFP
18050 4	48418	A	18157	609	690	
18051 4	48419	A	18158	1	2055	
18052 4	48420	A	18159	3	2236	
	48421	В	18160	406	454	
18054 4	48422	A	18161	1	2151	
	48423	В	18162	1	1215	
	48424	A	18163	1	594	
	48425	В	18164	i	1380	
18057 4					692	

SEOID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop eodon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
ŀ		1		sequence		
18059	48427	Α	18166	2	1311	QHVRSTVTELWTGNFVNSIQTA
10033	10427	ı^	10100	-	1.51.	FAAGIGWLITFCSKGGDCLTSO
		1				TRLRLSGMLFLNSLDAKEIYLE
		1				VIHNLPDFELLSANTLEDRLAH
		1		l		HRWLLFFHFGKNENSNDPELK
		l				KLKTLLKNDHIOVDRFGCSSAP
	ŀ	1				DICSNLYVFOPSLAVFKGOGTK
		1				EYEIHHGKKILYDILAFAKESVN
1	İ	l				SHVTTLGPONFPANDKEPWLV
1		l				DFFAPWCPPCRALLPELRRASN
		1				LLYGOLKFGTLDCTVHEGLCN
	ŀ	1		ŀ		MYNIOAYPTTVVFNOSNIHEYE
	İ	l				GHHSAEQILEFIKDLMNPSGGS
l	ļ	l				
	i	l				LTPTTFIELVTQRKHTEVRI/V*F
l		l		i		HCPGWPPWPRLWPMAKKPRNL
		l				LP*SSRPLNT*SSLFCSSNQPDLR
		l				GPLLHRPLSLPRRYRGAQVPNP
	l	l	ŀ	1		DFGHYSVSPSLIHGLHQCSHLFS
		l		1		HSPPPRVLRPPRILTTSTGLPPSP
18060	48428	A	18167	<del> </del>	924	RRSATDVHTAYPPTAD
18061	48429	A	18168	10	1254	
18062	48430	A	18169	1	618	
18063	48431	A	18170	1	460	MAAPMTPAARPEDYEAALNAA
18003	48431	^	18170	l'	400	LADVPELARLLEIDPYLKPYAV
	1	l				DFQRRMFWMFLPFFTLAFSPSV
l		l				LVRFHAADKDIPETGQFTKGRG
	l	l				LLDLOFOVAEDASOSWOKLYL
		1	i			LPNCSGOPHOKLVPTAOKFYIT
	ł	ı				VEWGTFFSVPGOVVGSEGSOM
	1	l		ł		
	į.			l		SVTVEGSEESEDDKMYMTCSS ALLDSFALC**RHT*DWAIYKR
		1				
	1	1				KRFIGLTVP/MWLRMPRNHGRS
	1	ŀ				CISCLIALANHTKNWFPQRRSFI
		1				SQWNGVLFSQCLAKLWALKEV RCO
18064	48432	A	18171	1	582	nco
18065	48433	A	18172	i	1578	
18066	48434	A	18173	1	1293	
19000	70424	Ι^	101/3	Ľ	1275	

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknuwn,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18067	48435	A	18174	344	1358	EAQSVTNHKRNSDCTFKEDNSL
10007	40433	^	10174	344	1330	PVRKPSFLITNPGSNOGPRFAGS
				l		PLGHEFTSLVLALLWTGGHPSK
	1	1		1	l	EAQSLLEQIRHIDGDFEFETYYS
		l		İ	<b>!</b>	LSCHNCPDVVQALNLMSVLNP
						RIKHTAIDGGTFQNEITDRNVM
						GVPAVFVNGKEFGOGRMTLTEI
				i		VAKIDTGAEKRAAEESARKGIR
		ŀ		1	ŀ	TGLMGERFGGQILDTVDIENYIS
				1	İ	VPKTEGQKLAGALKVHVDEYD
				1		VDVIDSTGTRSS/AISGFFHTYDS
						NSPTARCAPT*QNCAPSPSGEY
						APGEKAMRRTILVWRHCDY/PL
						CNAGNEVSMISRATSNTIATMII
		1				*GVCTDNTRLCLYALNCSGDIL
	1					SRTSCD
18068	48436	A	18175	I	1561	
18069	48437	Α	18176	884	1171	PRRLNNEDHKRLMSWLHCLVP
						HHAKWLQRWQWQSAKVV*FA
						*IRAVNFVTAYRAIIYQQSRKQ
		1				HRYLRSACHGRSIITVITQSPTK
						SSATKMPEN
18070	48438	Α	18177	274	416	QADDDADNQSGDTDAAFGALI
		1				Y/CESDDLC*LPLPALKPLCVM
			10170		509	WYQTM
18071 18072	48439 48440	C	18178	24	1932	
18072	48441	A	18180	1	2583	
18074	48442	A	18181	1	495	
18075	48443	A	18182	36	798	KORHSCFWSCWFSRAG*LGEL
10075	10443	(`	10102	150	1,70	V*NPEIA*RPPRPOOOTVSGNG
		1				AWSGKAPRRRHSWHY/YTISFO
		1		1	1	KLPLVECTNAGPIF*VAKAGRK
1	İ					CSIKPPLTSRSYIT\D*PVSLSRSQ
ŀ		1		1		LTGR/AGNFVTGW/QQLDEEIR
ŀ		1				YTMRTTVNAQTRDRRKGVQPP
		l		1		TTWIFNDTKDQLERRIARLETG
						MAWAEEPPSRTRHLISNCQISET
						DIPNVFAVRVNYLLYRAQKER
				1		DETFYVGTRFDKVRRLEDDTG
						ASWNGNRTGSAGIISIT
18076	48444	A	18183	114	724	ARTRVPHFPGHETAGGAAAHP
						HLSLLGQDPGNQTQLPGGRGGI
1	1	1				PGGRGGGRGGGGDDGRRR
1	1	1				ALRRQQVPVLCVQRAGPAMDA
	1	1				AAPRHSSPDRERPKDQEVLHRL
1		1		1		PGHASHSPHLGRHAGQPAGPA
						GLWQAPGLRHHLHAGIQPPE/V
		1				TNTTLTALT*TRRCPAFSSGTVK
		1		1		PLIFIWNLAAGPPLLRKGAASIW
l		1				ICSCSIFQR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18077	48445	A	18184	1	2130	
18078	48446	A	18185	2	433	EMTLDSRVAAAGDLFVAVVGH QADGRRYIPQAIAQGVAAIIAE AKDEATDGEIREMHGVPVIVLS QLNERLSALAGRFYHEPSDNLR LVGVTGTNGKTTTTQLLAQWS QLL/GRNQRGNGHRW*RPAGES DPDRKYNRFGSRCSA
18079	48447	Α	18186	114	586	SYITALGQFSRSGIQLLDRLGNF GTGWPNFDRKRFGSTMRTTVN GQTR/GPPQRRPAADNLDF**H QRPAGAANRPSGNGHGLGRRA AVTHPSLNQQLPDKRNRHPKRI CCAGKLSALSGTKRSAMKHSM LERVSTKFAVWKMTTGACWN GISSWIKR
18080	48448	В	18187	1	3577	
18081	48449	A	18188	2	861	YHSINAASACSALHPVAFLITLI CRTCSSSLAVATISTMR, PNTLP DLIISPVESILSTSFCAVPAFIREE PVTTSAPTIGVMANSAVVETAL PGLQEIPTVRQSWRAYSSPAL YGVRPLAAMPSHHILCR*INIF GINTAFPAIRAFHRVLNGIFSA SNQTNHQTRFHAVCGRTFGDV GWYAKSYQVAEERGSITEHQV QQHQSDDTEHFHGGEIERQQQ HYHRQRGDPVGEIGFELSISBA RHIVCHTGYNPAEPVSPAGEIS NGTANGNKLNMSVCELAP
18082	48450	Α	18189	560	2021	
18083	48451	A	18190	525	804	GG*CRNWCDHYANGCRDTSGT LYDKLAELGPOGLSPR*NNWQ TARRNQSSGRNSCHLRREVE*R RLDKALRRIRQFSAPDEGAKCP WPGIIDCSNHFARLRCQYGRFL EVTSAGDEKPYPLYDHHVGLV VEOLECIITAKVRTRHFYYVLK SHPAVAGLPALRDCGELFNSV YCRKPATGPELQADVMVVVAY GLILRKQCWRCRVLAVSTFMTT AATLARCCTIPTLTRAGDAET GVTIMQMDVEIPVVRCTTSWQ SLAHKAYHHVETIGRHGETR VODETILVTYAEKLSKEERVLTG HFRQHSLNAALRFOSMANELA
18084	48452	A	18191	1	266	SQYPLVAGHEVIGRVVALGSA AQDKGLQVGQRVGIGWTARSC G/QLRRLY*R*SDQLRARCGAD DYESRWLCREVACGLAMGDST ARKY

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18085	48453	Α	18192	5	385	
18086	48454	Α	18193	330	598	VMRFAIVVTGPAYGTQQASSAF
						QFAQALIADGHELSSVFFYREG
i						VYNANQLTSPASDEFDLVRA/S
					1	ATTECATWCGAEYLRSGSITPW
	L				0.00	RC
18087	48455	A	18194	1	2652	
18088	48456	A	18195	1171	2091	
18089	48457 48458	A	18196	486	837 2943	MARKACOUNTENAND ON THE
18090	48458	Ι^	18197	['	2943	MAIYKQSQHMTEVVRRCPHHE RCSDSDGLAPPOHLIRVEGNLR
						VEYLDDRNTFRHSVVVPYEPPE
	1				1	VGSDCTTIHYNYMCNSSCMGG
1	İ	1				MNRRPILTIITLEDSSGNLLGRN
		1			1	SFEVRVCACPGRDRRTEEENLR
						KKGEPHHELPPGSTKRALPNNT
		1				SSSPOPKKKPLDGEYFTLOIRGR
		1				ERFEMFRELNEALELKDAQAG
		1				KEPGGSRAHSSHLKSKKGOSRL
1		1				GTRFLCOPAVTVIPVKIVRVTG
		1				DTVIRPHAEGAVRVOLRVGOA
		}				VTCRVCGIRDADIQIRCGGVNA
		1				GOPAGGAVAVTPGLARAADAD
						EFAVVVPGQPFHGGQAVRYTA
						VROPLRVGRMSGLMLAKTCFR
1		1				LQVMHRLTLTVFSQKVFTESIE
		1				VVEALKVNLMRVFLRRMDLRC
						HRKMIMIDNYIAYTGSMNMVD
		1				PRYFLRDALPHCPNPLTGPTFA
						VLEKLGYPHTFVSTDFNTVALD
		1	l			VKTFGIKANDDKAKLKALGEIA
						HACVDATIIYCKSPTVAGLVAR
		1			1	ELIKLGHGTPTENPHVYWSPLE
1		1				TVLACILARYRGHCSNTLATNS
		1			i	MLENCAFCSAPPRSLKESTLSL
		1	İ			NTVVIYDNRDGTRSIDKFNRFCI
						HAFPKIIRNAIYEVEQHT*RACR
						YQ*DVGWFNIYQPGISLAASKH
1	1	1			1	CSTSSR*RWI*LDWI/CASASLL
						DEATAAAEAMAMAKRVSKLK
		_				NANRFFVASDVHPQTLDLMSY
18091	48459	Α	18198	643	776	
18092	48460	Α	18199	1	1257	
18093	48461	Α	18200	3	346	
18094	48462	A	18201	1120	1335	
18095	48463	A	18202	312	1108	
18096	48464	Α	18203	1	744	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
18097	48465	Α	18204	381	1112	GVEPSPPTNPPPATAIPRATCVA
	İ		ŀ			AARAASPSPS*SHQPHPPPLAYD
	Į.					RCST*PTPTTTAGQDHDHGRR
	1					WRSAPAPRSDHLSDMLQE/RSM
	1					SLLPLILSSTRSGSNPLRSTFLSR
	1					SRSISKNCSAEV*SNNSAGVGTI
	İ					STS/RSTYDINRADTQVRRAVN
						NYDIIVMSNSFNGQSEHQVWIG
						GQF/ILHQICPLTQFQYGAEPDR
	1			1		KE*CQAPASKWALLHK*HRPFP
	1					QDRKAGECLLHEYEDLYPSVIH
18098	48466	Α	18205	2	307	HPARHKFVKGSSEHRKSPVKPP
						PIPSH*PP*PENTNPMRPLAPTDP
						VTNLRSLMTGRQRFTPYNNVS
						RSDPSTTARSSSADRVNASEYP
				l		TSSEETSGRSSR
18099	48467	В	18206	1	723	
18100	48468	С	18207	127	1410	
18101	48469	Α	18208	1	1773	MGKKQSRKTGNSKNQSASPPP
		l			1	KERSSSPAMEQSWTDNDFDEL
		1				REEGFRRSNY\SSY*EEIRT*WQ
	1	1				TSLKALKRN*MMM/ILLASPSR
		ı				TPISGPNGDPAGPKFVKAAATT
						GKARQRFHPATTTFHGRTPAPP
						LAHPAPTVSTPASTQHPARRHQ
						VARPDRSSTPLPARIALRVFCPT
						PSTAPPEHPRQNPNPAPQTDSA
		1				LPGADDVRVSTTDPERRHPHPT
						NTTTPGPGRVLRKELNRPRRPI
						HHRRRRFHVQRAWQLPVPHRH
	İ					HHLDHTSHTRRRLRMTDVRLD
						RPQPQRPPRITITTVGGDQRLRL
						DRSYQPESPCDGDLRQLQMAG
						RAPCSPLSMLVLEKCDNLKTCH
		1				TSHGSVMAETAVINHKKRKNS
1						PRIVQSNDLTEAAYSLSRDQKR
						MLYLFVDQIRKSDGTLQEHDGI
						CEIHVAKYAEIFGLTSAEASKDI
						RQALKSFAGKEVVFYRPEEDA
						GDEKQNAKNEHGTTSSLPTQFK
						TDHMESQKDHPHKEETSPKVP
						HLVQESQKDHLHKEATNLKVP
						HPHPGKPQGPPPQEGNKPQRPP
1						PPGRPQGPPPPGGNPQQPLPPPA
	L					GKPQGPPPPPQGGRPHRPPQGQ

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	eodon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	Sequence		33.340,227	scquenec	or pepade sequence	describe, a possible additioned institution)
18102	48470	Α	18209	944	1577	RLCCLEISSTGYPKSSISSSKYPQ
		l		l		IPRAGAQCSQAV*SGSNPLRSTF
		1		l	ŀ	LSRSRSISKNCSAEV*SNNSAGV
		l		l		GTISTS/GSTYDINRADTQVRRA
		l				VNNYDIIVMCNSFNGQSEHQV
		l				WIGGQF/ILHQICPLTQFQYGAE
		l		ŀ		PDRKE*CQAPASKWALLHK*H
		l		l		RPFPQDRKAGECLLHEYEDLVP
		l		ľ		IRDTLRLFPGGRYLPRAKHVAP
						SEPDPTHHAYD
18103	48471	Α	18210	3	634	DRVFDSGSKWRSEQDWAAAK
		l			\	AVGQCSENGDWRCCGNGRYP
		l				ARGPAVPA*PSLCLHHPR*RCT
		_				CCMPVYR
18104	48472	Α	18211	3	255	
18105	48473	A	18212	101	547	TSVELMDLCPIRLCRTFSGIPAY
		l				SMCIA*EWRNVCGVTGTENVT
	l				PSAAAAATASPIQVLTVLSVTS	
		l				QIRAFSVLPVRRLRRSMSLSRIN
		1				TCRTEYPRCAVVCLLWKDAVS
		l		İ		CLSTTFCARLCGQNTWLPRPCR
						HVNRAASDASVSLSTVT
18106	48474	В	18213	1	1113	
18107	48475	В	18214	220	1173	
18108	48476	A	18215	1	509	MPNHKAILIKFKKTEIIPITLLDH
						STIKIEINIKKIAQNHTITWKLNN
						LLLNYFWPLTVSLCEMCKDFYS
						LGIEFSRFPLQELQNKDCALEK/
						HSHWAQMWP*YPCPAKHWWS
						CRREHVLVVN/DCSTS*NSYWH
						FSD*LRAMKRRNEQCKR*AIRS
		L_				LSRSLPARQDLKLLS
18109	48477	A	18216	3	281	
18110	48478	A	18217	878	1135	
18111	48479	С	18218	1	1602	
18112	48480	Α	18219	33	608	VDSLRFQSPSCSVYSTDTR*ISE
						T**NKL*PPKPVIACPKMWIQV
	1		1	l		GQKFRQKAAATP*KAR*SPRPIP
	1		1			SH*QP*PKIQTRCGPQPPQIRSPT
						QKPHDRQTALSHRTTTFHGPTP
						APPLAHPAPTVSTPASTQHPAR
						RHQVARPDRSSTPLPARIALRVF
						CPTPSTAPPEHPRQNPNPAPQTD
						SALPGAVRG

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /-possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	l		l	sequence		
18113	48481	<del>  -</del>	18220	3	893	NPRKRTEOGKAONKVOWWLT
18113	46461	Α	18220	3	893	RTPVMVQKRPTIVSLKSSPDSPL
			l			ETYSMFLFLGMWVGVGVEM/C
1			l			SVKLEEQVNTYHYQRILLGISS
1						DNAILLEEESEEGRPMHISTIKE
1			}	l		PSPDSPILYLTLNLKLLTSLILFH
			1			YGESWNLLRADQRLIFAKSWP
						RASRYQQGHQDLFILRSDLPSQ
						VFIRDKLMERRNRRTGRTEKAR
				ļ.		IWEVTDRTVRTWIGEAVAAAA
				1		ADGVTFSVPVTPHTFRHSYAM
				ŀ		HMLYAGIPLKVLQSLMGHKSIS
				İ		STEVYTKVFALDVAARHRVQF
		<u> </u>				AMPESDAVAMLKQLS
18114	48482	A	18221	1	327	LISLRQRQQRTPGKPGKGPRPIP
						SPWPP*PENTNPMRPPSPTRSGH
						QPRSLMTGRQRFHTAQQRFTV
						RPQHHRSLIQRRPCQRQRVPNI
	10100	_				QRGDIRSLVQIGHQRRCLRG
18115	48483	В	18222	1	1419 2784	
18116	48484	A	18223 18224	936	1157	Protect occupance of the contra
18117	48485	l^	18224	936	1157	RTSTGLSGCIRCG\CASEGGQAV
		l				FV/WPRGPPETPCSRCPAAEGSP
	1	l				G*SPPREDPSSGSPGKRQTCTQT
18118	48486	В	18225	67	1314	SARSPS
18119	48487	A	18225	302	1423	CRWRFRFIMPFVMASMSAECL
10117	40407	<u> </u> ^	18220	302	1423	MNYNSTAMSGKTGLONDTTLI
		[				ARPWVKPYLGLEIMRIVGN*PH
						LTWCFPCTMYIPLFSQLLCCPVS
		1				FGOCGAFRNPGHPPSPNPEFFLG
	İ					PRRCNPSLGHKALVQEAASDTP
						GKS\PGKSPPGPIPKPIGPP*PGK
						HKPDAAPSPHRSGSPNPEAS*PE
ĺ						DSAFTPHNNVFTVRPQHHRSLI
		l		l		QRRPCQRQRVPNIQRGDIRSLRF
				i		GCFARHHPRHHRNIHDRTRTRP
		١.				RRLTRHSRGLFEDDVRVSTTDP
				l		ERRHPHPTNTTTPGPGRVLRKE
						LNRPRRPIHLRRRRFHVQRAWQ
						LPVPHRHHHLDHTSHTRRRLR
			ĺ			MTDVRLDRPQPQRPARITITAV
10100	40 400		10007	1931	2202	GGDQRLRLDRITKPRARPN
18120	48488	A B	18227	1731	2392 1422	
18121	48489		18228	1		
18122	48490	В	18229	298	1464	
18123	48491	В	18230	1	1800	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18124	48492	A	18231	745	1250	HTONORSGRSONDF*RRRKNIS ERSAVYR*ROLYIRROPYAERP SLR*RORP*IPCIRSOHGNRKRIP RRRIFI*OSVLRRRHELLP*RKPE
						ASAERHKTRC*VSERRPRYHRV
						KYDYH*KSIYSR*AHGAA*PSH
		l				RKDRESADLGSDGQNGQDLDC
						RGGCQPLLLTV
18125	48493	Α	18232	1	1661	MAETAVINHKKRKNSPRIVQSN
						DLTEAAYSLSRDQKRMLYLFD
						DQIRKSDGTLQEHDGICEIHVA
	ŀ					KYAEIFGLTSAEASKDIRQALKS
						YAAKEVVLYRPEEDAGDEEGY
					i	ESFPWFIKRAHSPSRGLYSVHIN
						PYLIPFFIGLQNRFTQFRLSETKE
						ITNPYAMRLYESLCQYRKPDGS GIVSLKIDWIIERYQLPQSYQRM
						PDFRRRFLOCINAGHEMTKAIA
						AQFNDDSPEARKITRRWRIGEA
						ADLVGVSSQAIRDAEKAGRLPF
					i	PDMEIRGRVEORVGYTIEQINH
			ŀ			MRDVFGTRLRRAEDVFPPVIGV
						AAHKGGVYKTSVSVHLAQDLA
						LKGLRVLLVEGNDPQGTASMY
			l			HGWVPDLHIHAEDTLLPFYLGE
						KDDVTYAIKPTCWPGLDIIPSCL
						ALHRIETELMGKFDEGKLPTDP
						HLMLRLAIETVAHDYDVIVIDS
		l				APNLGIGTINVVCAADVLIVPTF
						AELFDYTSALQFFDMLRDLLKN
			l			VDLKGFEPDVFIRDKLMERRNR
			l		i	RTGRTEKARIWEVTDRTVRTW
						GEAVAAAAADGVTFSVPVTPH
			ŀ			TFRHSYAMHMLYAGIPLKVLQ
						SLMG*YVHCKALWMDCAHV**
						TKEKIHSLLHRRHPLQGDKEPL
						PSPRNSSMPAVYPYWLPQRSIRI
18126	18101	-	19222	162	446	FQHI
18126 18127	48494 48495	A B	18233	162	2537	
18127	48495	C	18235	1	873	
18129	48497	A	18236	700	1198	PFFGTDFFPWARWCIOLRHKFW
1.0.2	1.0.57	ļ.,	1.0220	1	1	SKGKORTTKKAPVKPPGPSPAI
		1	1	I	1	DHP*PGKHKPDAAPSPHRSGHO
			1	I		PKTSMTGRQRFHTAQQPFHGPT
			1	I		PAPPLAHPAPTVSTPASTQHPA
				I		RRHQVARPDRSSTPLPARIALR
				I		VFCPTPSTAPPEHPRQNPNPAPQ
		1	l			TDSALPGAVRG

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
18130	48498	A	18237	363	940	LQTVLQGYSNENSMFVKQKGS
.5,50		Γ.		1	I	PPGKPGKKKPCFWGAPKNGAD
		l				IPSOSWRPSGNPGTTPPLPKPPSF
		l	1			FPGAPRMGQSQAWGHKGFWF
						KKGKPTEPPGKKARVKKPPGG
						OSPKAIGPTRGPGKPPKPDMRA
						PKPPTDSGHQTQKPS*PADSAFT
			1			PHINVSRSDPRTTARSSSADRVN
						ASEYPTSSEETSGRSSR
18131	48499	A	18238	861	1517	SLRPHLSGFYQARTL*DQRS*A
18131	48499	^	10230	801	1317	DHE/DISKNCSAEV*SNNSAGV
						GTISTS/RSTYDINRADTQVRRA
		l				VNNYDIIVMSNSFNGOSEHOV
						WIGGQF/ILHQICPLTQFQYGAE
						PDRKE*CQAPASKWALLHK*H RPFPQDRKAGECLLHEYEDLVP
						IRDTLRLFPGGRYLPRAKHVAP
						SEPDPEQDEQKLRFCKRHLYGQ
10122	40500	_	10000	1014	2227	QPRSPVEIRLQHVAIAYQTHHA
	48500	В	18239	1014	2337	DUTE OF DOVOLUGE & ON A DOOL
18133	48501	Α	18240	1495	1947	IVTLCFPSYCLHCEAGP/LPCGH
						PWLWLC*VLGSPG*TQRTGSW
						AMPGVQASKPACG*KVAPAAR
						RVPHPLHMLPHSGHSAASGGA
						SCPLCRG*ATGSDQVLKHAFRK
						GRSSNCASNGTPPPNADFLGQD
						VHPARHKLRQKSASEPRKKAR
	48502	В	18241	1	2055	
	48503	A	18242	1	909	
	48504	В	18243	184	395	UPPER PROGRAMMENT IN THE
18137	48505	A	18244	447	667	HRPRRRFQIKPQSQVPEHAPLPL
		ı		l		PTASDPP/AHSPRCPSESRLSPGG
						QRLGFPSSVLNCSKCSWQLAAC
		Ļ.				MGFSF
	48506	Α	18245	265	890	
	48507	В	18246	1	551	
18140	48508	Α	18247	407	636	RIMVHATGLMKHASSPGCWDL
						NRRTRRCGVRRVTE*QRAS*KR
			İ			*/ERDYISIMPKPDGLTAAKNLA
						EAFEHYNECIRI
	48509	Α	18248	1	1448	
	48510	A	18249	817	930	
	48511	В	18250	303	461	
	48512	Α	18251	612	3359	
18145	48513	A	18252	1	462	

SEO ID	SEQ ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
					L	
18146	48514	A	18253	268	749	RGGIEYLLLVVFILTRTRFIQAV
		1				EHRRNGRRVAEKIVPELITHFM
					İ	AEIRDLLQRTGVAL/W*HQSAA
		l				YLPG*QICALA**IHPGVAAGEY
			ľ			ORRSIOENGGKVOESGOTAS*M
						RG*MSVESRSGIAARCPESDAO
						SGVVHRSRWNQSLPARFGAGR
			İ			DYREAS
10115		١.	100.51	1700	0100	
18147	48515	Α	18254	1793	2193	TQRIPAAQKQGSRCIVDSSAEA
						LSAALAIGNIELVKPSRTMS/DK
			ŀ			AAQEIVNSGKAKRVVVSLGPQ
					1	GALGVDSENCIQVVPPPVKSQS
						TVGAGDSMVGAMTLKLAENA
		1	ŀ			SLEEMVRFGVAAGSAATLNQG
		1				TRLCSH
18148	48516	В	18255	1	1557	
18149	48517	A	18256	606	1123	ORDNPSGTDGGRNRAFGAGNI
1		l				HTRGAAQAVERLVDSFPAQEK
1		l	l			DPGESTGRTDSLPSSRPOKVAY
		l				PVHRNDRR/ERLWFAAPSSPSN
		1	ŀ			ATWGNAEWTLNFSSSDSVTGA
		l				
		1				SSER*NLLFRLATVRCTLPSSVS
		1				ADGAIVAALATHIGEAELTLES
		_				QCGAWRATFSSTCSSLPLNPN
18150	48518	Α	18257	110	318	TALKLPLPMSTKVTRCLSNLLK
			l			PKFNLPPLVQPPKKMLPRHLSR
1	1	1	l			*APNTKTSRVLKKN*PIPIPTRR
1		1				KT
18151	48519	Α	18258	2	3062	_
18152	48520	Α	18259	4435	4954	
18153	48521	Α	18260	1	1959	
18154	48522	Α	18261	2	715	
18155	48523	A	18262	1	756	MIRRVSVASGNEYPMRPASYIR
		1			1	TAPTVYPSSSPAGTWFAGNAPA
		i .	l			SSCGFRDRYLIVCSHOTPHVPG
		ı	l			KREEVNYETGIYWLRHYGYTD
		i .			}	YSRNAKORLORNNLAPILFTTT
		1	l		}	
		ĺ				VPLGGRQYNNSQHLPQRQSLE
		l	l			RIRHHTQAFTALIPHGAAGQGC
		ı		1		GSGDLHYLSLEDVAVSSKATPD
1		1	1	l	i	GSGVTRKASANLRVTIQIGGFQ
1		1	1	I	1	LRTCGFGPSCRGCHPALQISRAL
1		1	l	l		AVAAHQQAADNNMEFANYGP
		1		l	1	FELLQ\ARQLIES
18156	48524	Α	18263	1	799	
18157	48525	A	18264	i	270	
18158	48526	A	18265	2	188	LGFFFORPLGFGQELSKL*EQVL
1.5150	1.0520	ľ.		l~	1	LAPEEVGHLGEHLLFRHASEWP
1		l		I		APRVQLLLLVRVQDLQE
	L			L	L	AL KY YELLEV KY Y Y DE YE

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
18159	48527	Α	18266	2791	3274	SKIFPRHDDLLLWRSHRNGDDL
						RTAGMNAFKORLTLLGFKITIL
				ĺ		TANDYLFADGQ/RSVRKKYPQ
						AQVSRVAGADLWEELMARAG
						KE/GTPVFLVGGEPEVLAQTEA
	Ì					KLVRSSSATSAIAWPLLIPCAISS
		1		l .		WIRSTAFCCCSWVSEGKPADRS
1				ļ		PAPSRTWLRC
18160	48528	Α	18267	202	627	
18161	48529	Α	18268	1	2390	
18162	48530	Α	18269	1081	1911	
18163	4853 I	Α	18270	86	272	
18164	48532	Α	18271	674	2808	FILKLRTRRR*RHRLIRPWELFQ
		ı				TARNAEVMKA/LVRHLWLEVK
	1	1				GVDLGRFPERRYGSDKPDLRNI
1		1		1		MELTDVADLLKSVEFAVFAGP
						ANDPKGRVAALRVPGGASLTR
	l	1		1	ŀ	KQIDEYGNFVKIYGAKGLAYIK
		ı		1		VNERAKGLEGINSPVAKFLNAE
1		ı				IIEDILDRTAAQDGDMIFFGADN KKIVADAMGALRLKVGKDLGL
1		1		1		TDESKWAPLWVIDFPMFEDDG
				1		EGGLTAMHHPFTSPKDMTAAE
				1		LKAAPENAVATLGDPLESPDDC
	1			1		LHNRISTHGCFYVLCGISTNIGV
İ						ESTARNAWELGFNLVIAEDACS
1		1		1	l	AASAEQHNNSINHIYPRIARRG
		1		1		RDPORVMIYIGLPOWSHPKWV
					i	RLGITSLEEYARHFNCVEGNTT
		1				LYALPKPEVVLRWREQTTDDF
	1	1	l			RFCFKFPATISHQAALRHCDDL
						VTEFLTRMSPLAPRIGQYWLQL
1			1			PATFGPRELPALWHFLDSLPGE
i						FNYGVEVRHPOFFAKGEEEQTI
		1				NRGLHORGVNRVILDSHPVHA
1		1		1		ARPHRKLGGTAVWEWEPEGA
1		1		1	1	HWVGDEPGWFSSGDLSKAEY
				1	1	WAQKAADSGDADACALLAQIF
1	1			1	1	ITNPVSLDYPQAKVLAEKAAQ/
1		1	1	1		GSKEGEVTLAHILVNTQAGKPI
		1	l			YPKAISLLENASEDLENDSAVD
1		1		1		AQMLLGLIYANGVGIKADDDK
1				1	1	ATWYFKRSSAISRTGYSEYWA
1				1	1	GMMFLNGEEGFIEKNKQKALH
18165	48533	Α	18272	532	2103	
18166	48534	В	18273	1	4401	
18167	48535	Α	18274	343	765	
18168	48536	Α	18275	447	709	

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
l			1	sequence		
18169	48537	ĪΑ	18276	1	1571	MIEVKHLKTLOALRNCGSLAA
						AAATLHOTOSALSHOFSDLEO
	l					LGFRLFVRKSQPLRFTPQGEILL
	İ	1				OLANOVLPOISOALOACNEPO
		1				TRLRIAIECHSCIOWLTPALENF
		1				HKNWPQYSVIFKSGVTFDPHFI
					l .	FQQGELDPERAFDDFGIKPMAS
						ASIAOVHSARFNSNGHEVVIKV
		i i				IRAETLPVIKADLKLIYRLARW
		1	1			DAAFAAGWSPPAANLSCAGST
	1	1				KIHRLMNRTCCRNLPTPFSFGA
	l .					
		l l				KPGLYLVEAMVGGYRATTVV
						VSDTVALSKVSGIELLVWGAG
		1			1	KKQGEANAGSEILWTDGLGVN
		1				TRGVTDDSGTLQLQHISPERSY
		1				LGTLAMVQLREDMAKRQAAG
		1				IAPRSGRRMHRTQHKPPMTTE
	1					MGPRAVLREDTIPFLEALKASC
	į.			1		KQRILLTNAHPHNLAVKLEHT
						LDAHLDLLLSTHTFGYPKEDQI
						LWHAVAEATGLKAERTLFIDD
		1				EGDAMKEKPAVEVRLDKWLW
	l	1				AAR/SL*NPRAGP*ND*RR*GAI
		L				QRAAHEAEQNRRAECHAHSAF
18170	48538	Α	18277	2080	2274	RFQVVYFDHEKPSLRHE*FALE
						EYTGTRN*GCVNLLDR*KPFPF
		_				KFMERWLAFSPPGLTLESSRG
18171	48539 48540	B	18278	1	3126 341	MLDRLESEILADRVSEESRRWI
18172	48540	I <sup>A</sup>	18279	1	341	
	1					ASCGLTVEQMQNQMDPVYTPA
	İ	1			l	RKIHLYHCDHRGLPLALISKEG
l		1				TTEWCAEYD/GMGQPAE*REP/
		ı				SAAAAYPPAGAAV**GVRPVL
		<del> </del>				QPPPLL
18173	48541	A	18280	945	1484	
18174	48542 48543	A	18282	703	1149	
18176	48544	A	18283	161	476	LLPWRSCILRSDPLAAHPVI/LV
18170	46344	l^	10203	101	470	P*ACIFIARNCYPRPSCDSACKL
	l					RRESCG*FG*TRMVSAQATFSI
l		1				ITSA/LPFCEHLPGKRSGDFDTG
l						
10155	10515	+-	10004	ļ. ——	442	EDNALSGQRPEFRHG
18177	48545	Α	18284	1	443	MLSEPALRELATAIAGVRKGE
	1	1			1	DIAVENIIGANIFNIVIVLGLPAL
1			1	1	1	TPGEIDPLAYSRDYSVMLLQAG
		1		1		
						TLACEKMFWCKGKVVVMGM
						TLACEKMFWCKGKVVVMGMC KS/RAILGEKWPRNVCQHRIAN
18178	48546	A	18285	3	550	KEVLAIERECLAELDQYINQNF TLACEKMFWCKGKVVVMGMC KS/RAILGEKWPRNVCQHRIAN HENRDSIRKICCYHR

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
18179	48547	IA	18286	2157	2504	LVSLAGAAYRSPODPVPYMPIS
18179	48347	A	18280	2137	2304	PGLDWVRQIVCCVMASDAD**
ļ.						RVPRQNALLLPVCTSGPYHALA
						TGCGFRRGQMLKTTVLPRHYK
		ŀ				LYLGASSGMRYSTPATALMPLP
		1				LPHLAER
18180	48548	Α	18287	1	621	EITEAER
18181	48549	A	18288	1	423	
18182	48550	В	18289	li	1551	
18183	48551	Ā	18290	1171	2757	-
18184	48552	Ā	18291	347	690	
18185	48553	В	18292	1	528	
18186	48554	A	18293	i	1417	
18187	48555	A	18294	292	699	
18188	48556	A	18295	859	1377	
18189	48557	Α	18296	1	3036	
18190	48558	Α	18297	1	942	
18191	48559	A	18298	1	2124	
18192	48560	Α	18299	1955	2797	GGISIDRSGDH*GRGAVYHVAG
İ		1				R*NAGRTAELYFASRPTCG/RW
	1	1				LVAAVQGAATARISTIEMSVW
		1		İ		AQL*QMCRGKIRAT/ISLPEATA
İ		1				QVISSGSGATKVEDGLGDLNKP
		1				VSNQNLVTGIDTPVYNAPSAGS
		1				APFGVLADNMRYPILHKLKDR
		1		1		LNQTWYQIRIGDRLAYISALDA
į .	1	1				QPDNGLSVLTYHHILRDEENTR
		1				FRHTSTTTSVRAFNNQMAWLR
i	1	1				DRGYATLSMVQLEGYVKNKIN
		1				LPARAVVITFDDGLKSVSRYAY
1		1				PVLKQYGMKATAFIVTTRIKRV
18193	48561	Α	18300	1	1191	
18194	48562	Α	18301	1	298	MPVVFTVFFLWFPSGLVLYYIV
1						SNLPRYAEYLTVKDADGSVLD
						QGIALWFP\GPNSFTGEDVLELQ
1						GHGGPVILDLLLIRILTVCGLRI
		_				ARPACSPRSL
18195	48563	Α_	18302	I	1011	
18196	48564	A	18303	I	1845 755	MSPVIDKMYVDAYOPFSEEKIS
18197	48565	Α	18304	l'	1'33	MOEALEKGAOPLREFMLROTR
	1	1				EADLGLFARLANTGPLQGPEAV
						PMRILLPAYVTSELKTAFQIGFT
	1	1		1		IFIPFLIIDLVIASVLMALGMMM
		1				VPPATIALPFKLMLFVLVDGWQ
					1	
		1				LLVALVTGLIISILQAATQINEM TLSFIPKIIAVFIAIIIAGPWMLNL
		1				LLDYVRTLFTNLPYIIGRTMLQ
	į .	1				VTSEO/CAILVKPVLLAVTARA
		1				GADLHRADSERTQRTKTGGGF
		1			ľ	CRYWAG
L.	1	1		I	L	CK t WAU

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
18198	48566	A	18305	1	1977	
18199	48567	Α	18306	1	630	
18200	48568	Α	18307	1715	1996	LFRLLKTLTGRRKRSNKSWITT CRGFWGTWCAGWSRP*VVQK CRIYTMWR*WQHAQR*VSPAT LNGLMLITISRKNPHTRKGAGK HCPFSGPS
18201	48569	Α	18308	517	675	
18202	48570	Α	18309	480	626	
18203	48571	A	18310	757	1146	
18204	48572	Α	18311	318	724	
18205	48573	Α	18312	1	1743	
18206	48574	A	18313	1	1197	
18207	48575	A	18314	161	613	LLRQGFIVISAGGKRVEGQIKLV FPAKFEAGFRHGVIANLRLYPF PEEKIGEMATAPLSTSGDCRT* YALIGIQ/PTDGDARGSPRYKPA LALLPACVGSAKSTPHGRTPIPA IYVPSSPT*FRALASDSVAQT*Y CRPASQTRRASPARSL
18208	48576	A	18315	177	425	SRYFSATSTWPLVMSIPVTCPFS PASWLST*QSLPLPLPRSKIQQF CRCSGITRPQP*YPDPKSSSFVD AQGSPDHSHNILGLLLRVHFAR LPECAWGPAWLW
18209	48577	A	18316		576	ADSSKIADIISVIDGIAFOTNIL ALNAAVEAARAGEQGRGFAVV AGEVRNI.ASRSAQAAKEIKALI EDSVSRVDTGSVL.VESAGETM NNIVNAVTRVTDIMGEIASASD EQSRGIDQVALAVSEMDRVTQ QNASLVQESAAAAAALEEQAS RLTQAVPRSVWQPAHSPINRK HHPVLPIATGALMPGCGS
18210	48578	Α	18317	121	1819	
18211	48579	Α	18318	1	2151	

NO: of peptide sequence load in t.SSN post-docation of first codos for peptide sequence codos for peptide sequence load of peptide sequence codos for peptide sequence codos for peptide sequence codos for peptide sequence codos for peptide sequence codos for peptide sequence codos for peptide sequence codos for peptide sequence codos for peptide codos for peptide sequence codos for peptid	SEO ID	SEQ ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
18212   48580   A   18319   3   1127   GTPYASQPVIRPVEGSKPLIKQ   LDIGAHGTDKTIAGKLARVAR   MHEARQRLAAVATTACSAQON   IALMEEIAANFSYEMIRLTECII   GFTWNRLYQGINVHNAERYR   LAHDGHELVYVPCHRSHMDY   LLSYVLYHQGLVPPHIAAGNI   NIEWPAGPIFRRLGAFFIRTIKK   NIKLYSTVFREYLGELFSRGYS   EYFVEGGRSRIFGRLIDPKTG   LRGGTRPITLIPHYGVEHVMES   GTYAKELRGATKEKESLPQMI   RGLSKLINLLQQCYVNIGEPM   LMTYLNQHVPDWRESIDPIEA   RRPAWLTPTVNIAJADLMVRIN   NAGANAMMILCCTALLASRQ   SLTREQLTEQLNCYLDLMRNN   NAGANAMMILCCTALLASRQ   SLTREQLTEQLNCYLDLMRNN   HGWTLSTMHGCPPHEIBAICRS   MLEEKGLNTFVKLNPILLGYA   RVREILDVCGFGYIGLKEESFE   HDLKLTQALEBHLEPMALAK   KSLGGVKLTNTLGTINNKGA   PGDSTSGVIRTVERLITAWM   TCPCADEHQRGSVKLATALT   WW.RGSQNRDEITKDGFQSNI   AGGILGGISSQQIAHMALKP   SIDVPGRTINRGGEVEMITK   RHIPPCVGIRAVPIAEAMIAHV   MDHLLRQRAQNADVKTDFR   AQSIGSSNGCIVGADTLIFON   HYQVMRTDQRRYFGHPDLW   FIQRLSSQVSNLGMGTVLIGD   GMPAGGRINGGIASHQGIAD   DIFLQPKTRWTSAQLLRQAJ   DLVSRDGKHVVSTLWKPEIFS   KILAAQDKDVTRIFVNPAIKQC   LCLDAGTIATGCAKCDPOVSK   AYAYLLTRAQCIAHDLPDPL   PLEIDGTLLPRYVFINGGRAPGR   KGGVNPPLRMLNGVQKFAVW   WLCGRSFKFRSVSLERMAD   HTCROSFYRESSYSVSLERMAD   HTCROSFYRESSYSVSLERMAD   HTCROSFYRESSYSVSLERMAD   HTCROSFYRESSYSVSLERMAD   HTCROSFYRESSYSVSLERMAD   HTC	NO:			in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
18212 48580 A 18319 3 1127 GTPYASQPVIRPVEGSKPLIKO LDIGAHGTDKTIAQKLARVAR MHRARQRLAAVATTACSAQN IALMEEIAANSYSMIRLITECII GFTWRILYQGINVHNAERVR LAHDGHELVYPCHRSHMDY LLSYYLYHQGLVPPHAAGRIN NEWPAGPIFRRUGELSPROYS EYF VEGGRSRTGRLLDPKTOL LROGTRYLTUPIYIGYEHVMEN GTYAKELRGAFFIRRTEK NKLYSTVFREYLGELFSROYS EYF VEGGRSRTGRLLDPKTOL LROGTRYLTUPIYIGYEHVMEN GTYAKELRGATKERSELPQMI RGLSKLRNLQQGYVNFGEPMI LMTYLNQHYPDWRESIDPIEA RPAWLTPTVNNIAADLMVRIN NAGANAMNLCCTALLASRQ SUTREQLTEQLACYLDLMRNN HAGGARKERSLQALPARIPTSM HGYTLSTHAGCPPHGEALCRS MEERGLNTFVKLNPTLLGYA RVREILDVCGFGYGIGKEESFE HDLKLTQALEMLERKALAK KSLGFGVKLTNTLGTINKGA PODSTSOVLRTYERLLTAWMI TCPCADEHQRGSSVKLATALT WWLRGSQNEDETTKDGFQSNI AGGILGGISSQQIIAHMALKP SIDIVFGRTINRGGEVEMITK RHDPCVGIRAVPIAEAMLAIW MDHLLRQRAQNADVKTDIFR AQSIGSSNGCTYALEAML WHOTH CONTROL TO THE PROPERTY OF THE PROPERTY O		sequence	l	09/540,217		of peptide sequence	deletion, \=possible nucleotide insertion)
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RHDPCVGIRAVPIAEAMLAIVI MDHLLRQRAQNADVKTDIPRI AQSIGSFSNGCIVGADTI-PQSS HYQVMRTDQRRYFGHPDLVM FIQRLSQVSNLGMGTVLIGDB GMPAGGRFNGGHASHQTGLD DIFLQLPKTRWTSAQLLRPQAI DLVSRDGRHVVSTLWRPEISS IKLAAQDKDVTRIFVNPAIKQC LCLDAGTIATGCAKCDPGVSIK AYAYLLTLRAQCLAHDLPDPL PLEIDGTLLPRYVFIHGGRVF YYTPKEESIKLPHDYLDLHRSS PNILDVQMVPVSVMFGRAPGR KGEVNPPLRMLNGVQKFRAVI WLGRDSFVRFSPSVSLRRMAD HGTDKTIAQKLARVARMHFF RQRLAAVGPRLPARQDLFNKL		İ	1				
MDHLLRQRAQNADWKTDIPRI AQSIGSFSNQCIVGADTLPIQSE HYQVMRTDQRRYFGHPDLWW FIQRLSSQVSNLGMGTVLIGDM GMPAGGRINGGHASHQTGLD DIFLQLPKTRWTSAQLLRPQAI DLVSRDGKHVVSTLWKPEIFSI IKLAAQDKDVTRIFVNPAIKQC LCLDAGTTATGCAKCDPOVSI AYAYLLTRAQCALHDLPDPL PLEIDGTLLPRYVFIHGGPRVF YYTPKEESIKLFHDYLDLHRSN PNLDVQMVPVSVMFGRAPGR KGGFVNPPLRMLNGVQKFFAVI WLGRDSFVRFSSVSLRRMAD HGTDKTIAQKLJARVARMHFA RQRLAAVGPRLPARQDLFNKL		İ	1				
AQSIGSFSNGCIVGADTLPIQSE HYQVMRTDQRFYFGHPDLVM FIQRLSSQVSNLGMGTVLIGDM GMPAGGRFNGGHASHQTGLD DIFLQLPKTRWTSAQLLRPQAI DLVSRDGKHVVSTLWFPEISS IKLAAQDKDVTRIFVNPAIKQC LCLDAGTLATGCAKCDPOVSK AYAYLLTLRAQCLAHDLPDPL PLEIDGTLPRYVFIHGGRVF YYTPKEESIKLPHDYLDLHRSS PHLDVQMVPVSVMFGRAPGR KGEVYNPPLRMLNGVQKFAVI WLGRDSFVRFSPSVSLRRMAD HGTDKTIAQKLVARVARMHFF RQRLAAVGPRLPARQDLFNKL			1	ļ			
HYQVMRTDORRYFGHPDLVM FIRRLSQVSNLGMGTVLIGDM GMPAGGRIFNGGHASHOTGLLD DIFLQLPKTRWTSAQLLRPQAI DLVSRDGKHVVSTLWKPEISE IKLAAQDKDVTRIFVNPAIKQG LCLDAGTIATGCAKCDPGVSIG AYAYLLTRAQCLAHDLPDPL PLEIDGTLLPRYVFIHGGRVF YYTPKEESIKLFHDYLDLHRSS PNLDVQMVPVSVMFGRAPGR KGEVNPPLRMLNGVQKFFAVI WLGRDSFVRFSPVSLRRMAD HGTDKTIAQKLJARVARMHFF RQRLAAVGPRLPARQDLFNKI			1				
FIQRLSSQVSNLGMGTVLJGDM GMPAGGRFNGGHASHQTGLD GMPAGGRFNGGHASHQTGLD DIFLQLPKTRWTSAQLLRPQJA DLVSRDGGHVVSTLWKPEIFS IKLAAQDKDVTRIFVNPAIKQC LCLDAGTHATGGAKCDPGVSK AYAYLLTLRAQCLAHDLPDPL PLEIDGTLLPRYVFIHGGPRVF YYTPKEESIKLFHDYLDLHRSS PHLDVQMVPVSVMFGRAPGR KGEVNPPLRMLNGVQKFFAVI WLGRDSFVRFSPSVSLRRMAD HGTDKTIAQKLJARVARMHFF RQRLAAVGPRLPARQDLFNKL			1				
GMPAGGRPNGGHASHQTGLD DIFLQLPKTRWTSAQLLRPQAI DLVSRDGRHVVSTLWKPEISS IIKLAAQDKDVTRIFWPAIKQC LCLDAGTIATGCAKCDPGVSIG AYAYLLTLRAQCLAHDLPDPI PLEIDGTLPRYVFIHGGPRVF YYTPKEESIKLFHDYLDLHRSS PNLDVQMYPVSVMFGRAPGR KGEVNPPLRMLNGVQKFFAVI WLGRDSFVRFSPSVSLRRMAD HGTDKTIAQKLJARVARMHFF RQRLAAVGPRLPARQDLFNKL			1				
DIFLQLPKTRWTSAQLLRPQAI DLVSRDGKHVVSTLWKPEIFSI IKLAAQNKDVTRIFVNPAIKQC LCLDAGTIATGCAKCDPOVSIG AYAYLLTLRAQCAHDLPDPL PLEIDGTLLPRYVFIHGGPRVF YYTPKEESIKLFHDYLDLHRSN PNLDVQMVPVSVMFGRAPGR KGGFVNPPLRMLNGVQKFFAVI WLGRDSFVRFSPVSLRRMAD HGTDKTIAQKLVARVARMHFA RQRLAAVGPRLPARQDLFNKL							
DLVSRDGKHVVSTLWKPEIFS IKLAAQNEDVTRIFVNPAIKQE LCLDAGTIATGCAKCDPOVSK AYAYLLTLRAQCLAHDLPDP, PLEIDGTLLPRYVFHIGGPRVF YYTPKEESIKLFHDYLDLHIKS PHLDVQMYPVSVMFGRAPGR KGEVNPPLRMLNGVQKFFAVI WLGRDSFVRFSPSVSLRRMAD HGTDKTIAQKLVARVARMHFA RQRLAAVGPRLPARQDLFNKL			1				
IKLAAQDKDVTRIFVNPAIKQC LCLDAGTIATGCAKCDPGVSIG AYAYLLTLRAQCLAHDLPDPL PLEIDGTLPRYVFIHGGPRVF YYTPKEESIKLPHDYLDLHRSS PNLDVQMVPVSVMFGRAPGR KGEVNPPLRMLNGVQKFFAVI WLGRDSFVRFSPVSLRRMAD HGTDKTIAQKLJARVARMHFA RQRLAAVGPRLPARQDLFNKL		İ					
LCLDAGTIATGCAKCDPGVSK AYAYLLTLRAQCLAHDLPDPL PLEIDGTLLPRYVPIHGGPRVF YYTPKEESIKLFHDYLDLHRSN PNLDVQMYPVSVMFGRAPGR KGEVPPPLRMLNGVQKFFAVI WLGRDSFVRFSPSVSLRRMAD HGTDKTIAQKLJARVARMHFA RQRLAAVGPRLPARQDLFNKL		1	1	l		l	
AYAYLTURAQCLA HDLPDPL PLEIDGTLLPRYVFHIGGPRVF YYTPKEESIKLFHDYLDLHKSK PNLDVQMVPVSVMFGRAPGR KGEVYNPLRMLNGVQKFFAVI WLGRDSFVRFSPSVSLRRMAD HGTDKTIAQKLVARVARMHFA RQRLAAVGPRLPARQDLFNKL		1	1	1		ŀ	
PLEIDGTLIPR VVFIHGGRAVF YYTPKESIKLFHDYLDLHRSI PPKLDVQMVPVSVMFGRAPGR KGGVNPPLRMLNGVQKFAVI WLGRDSFVRFSPVSLRRMAD HGTDKTIAQKLJAR VARMHFA RQRLAA VGPRLPARQDLFNKL		1	1		I		
YYTPKEESIKLFHDYLDLHRS\  PNLDVQMYPVSVMFGRAPCR   KGEVPPLRMLNGVQKFAV   WLGRDSFVRFSPSVSLRRMAD   HGTDKTIAQKLJAR VARMHFA   RQRLAA VGPRLPARQDLFNKL   18214   48582   B   18321   1   1460     1460			İ		l		
PNLDVQMYPVSVMFGRAPGR   KGEVYPPLRMLNGVQKFFAVI   WLGRDSFVRFSPSVSLRRMAD   HGTDKTIAQKLJARVARMHFA   RQRLAAVGPRLPARQDLFNKI   18214   48582   B   18321   1   1460		1	l	l	l		
KGEVNPPLRMLNGVQKFFAVI   WLGRDSFVRFSPSVSLRRMAD   HGTDKTIAQKLVARVARWHFA   RQRLAAVGPRLPARQDLFNKI   18214   48582   B   18321   1   1460		1	1		1	l	
WLGRDSFVRFSPSVSLRRMAD   HGTDKTIAQKL\AR VARM\HF4   RQRLAAVGPRLPARQDLFNKL   18214   48582   B   18321   1   1460		1	l		1		,
HGTDKTIAQKLARVARMHFA   RQRLAAVGPRLPARQDLFNKL   18214   48582   B   18321   1   1460		1	1		1		
RQRLAA VGPRLPA RQDLFNKL		1	l		1		
18214 48582 B 18321 1 1460		1	1	1			
							RQRLAA VGPRLPARQDLFNKL
18215   48583   A   18322   2   234	18214		_		-		
	18215	48583	A	18322	2	234	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
18216	48584	A	18323	282	422	
18217	48585	A	18324	1	1974	
18218	48586	A	18325	154	1944	
18219	48587	A	18326	18	386	KACEAVF*DQGLPLGPKVQGQ
18219	46367	^	16320	110	360	WDWFPGPGALRHQQSVAHQA
			ľ			GGFRSLWGYSGVSGQCRRHSD
	İ					*SRPGREARRRSVAG**SHAL
	i		ŀ			HROTALFGARSDADLPAAAPR
						YLLYRGLSAAHFRPQAG
18220	40500	-	10227	181	655	
18220	48588	Α	18327	181	655	KARSPEDQGFRPRVHIDGGVW
						HLDVGSSHPGAEVGPKGMAVR
						HLKWYASWV*NVVRQFGPYLP
	1					WALEN/WRGAAPSTRGHGVC/G
						ITVFGKSDGTT/SHDQY*TAPYG
						SPHPPGRWSLRHRYPAHLTSSA
						LAFSDARRNAARQPRRWNPLS
						GYSQVICLPAW
18221	48589	Α	18328	μ	658	MDDGTSIAPDGDLWAFIGDELK
						MGIPENDRIREQKQKYLRNKSY
						LHDVTLRAEPYMYWIAGQVKK
						RNMPMELVLLPIVESAFDPHAT
						SGANAAGIWQIIPSTGRNYGLK
			l			QTRNYDARRDVVASTTAALNM
						MQRLNKMFDGDWLLTVAAYN
						SGEGRVMKAIKTNKARGKSTD
						FWSLPLPQETKQYVPKMLALS
						DILKNSKRYGVRLPTTDESRAL
				l	1	ARVHLISPVKCARFSRFVFCPA
				ŀ		VCRDSGGADERRTDSDGCQYA
						GGVKPESVMGAEIVEGFSHISV
						TSA WSRGDNSPAPMAFSRLWL
			1			TVFSMVFKRRETVRSLSAVGA
						GELRGAAPSTRGPEWTHHWCS
			1	ļ		GCHANGTARSAVVPPDPMPNS
			1			EVKRRSADGSVGSP*RLITAAK
			ļ			VGS*ROLKRTKRVGNPRTSGRY
1		l				RCRRKRSSTCLKCWH*VIFSKT
				1	1	ASVMAYVCQRPMKAVLWRVC
18222	48590	Α	18329	642	1343	LCLHLPLPTRFPRLQL*EEGGPV
				l		OPAAMPOWRTLPGPGPRPALPL
						PRRLRGSSLRARPGRLRGPRLR*
ł		1				RRHVCGGRRRAPLLLRAGLRRP
1		l		1		RLPRARGPVRRAPLCSRRPLLR
1		l		l		PLLRPRLRLRSRLHGSAV*VPSA
1		l				PRRRKRLARGPAGPQARGPSAL
1		l		1		
1			1			PFASGSGTARGRGRGRRCALA
						GPRAPPWPLPGCWVSLAGWDP
		l		l		GAVSPRTPGCTQQPKDAGGFR
10007	10501	<b>!.</b>	10220	ļ. —	010	GWSEAGVHDAQTV
18223	48591	Α	18330	1	810	

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				1		
18224	48592	Α	18331	236	717	ALPVGAAFSSTTGFGSGFGAGG
l		1			\	ASTFGLGGSTGFGFGGATGAGS
		1				GSNSVLLAAIVAGSSDGAAASP
	1					ARTSSAAPSGGCD/QERRIVDFK
	į.	1				RNKDGIPA VVERLEYDPNRSAN
						IALVLYKDGERRYILAPKGLKA
		1				GDQIQSGVDAAIKPGNTRLSYG
				i		QHREAWR
18225	48593	Α	18332	49	291	
18226	48594	Α	18333	75	839	
18227	48595	Α	18334	1	579	
18228	48596	A	18335	223	563	
18229	48597	Α	18336	1	1219	
18230	48598	A	18337	157	864	RGNRQLQQFPRHWRSNRLDGL
						LLQIQLQILGGHTVERHLVVQI
		1			1	ALVVNGHPGHADGMWILCIRV
		1				LLSLQQNGFRRVPSIGHWTGH*
			· ·			AATDQARLMLGGHINAQFAGI
						QRLEDLGTQLLHTTNGLVEVE
						ARRQILQLGLPLFLLLNQTDVW
		1				AIPGVHVLRFDVVGRDPS/EVLI
						DPRQNAGLLWKVFATFRPEPTR
						PAVCCPRGGQSGDDRRAGCAC
		_				NHVELVARHRRSCPWHSDRH
18231	48599	A	18338	1	219	
18232	48600	A	18339	11	2226	
18233	48601	A	18340	46 382	228	
18234	48602	A	18341	1	1431 2400	
18235 18236	48603	В	18342 18343	1	912	
18236	48604 48605	A	18344	2267	2539	
18237	48606	B	18344	1797	3411	
18239	48607	A	18345	1842	2560	
18240	48608	A	18347	1	1284	
18241	48609	A	18348	1	792	
18242	48610	Ā	18349	1	978	
18243	48611	A	18350	757	1011	LFGRFSNGFLIVVCORLROAVV
10243	48011	ľ	10330	/3/	1011	NEOFLPETATLTHRGELLFHSP
						A*LPGVFRYLAOM*RHAVIOVF
						RATGVPEPERCRORRPHER
18244	48612	A	18351	148	679	RMSDDKFDAIVVGAGVAGSVA
10244	40012	<u> </u> ^	10331	146	079	ALVMARAGLDVLVIERGDSAG
		1				CKNMT\GGRLYAHTLEAIIPGFA
						VSAPVERKVTREKISFLTEESAV
		1				TLDFHREOPDVPOHASYTVLRN
		1				RLDPWLMEQAEQAGAQFIPGV
					I	RVDALVREGNKVTGVQAGDDI
					1	LEANVVILADGVNSMLGRSLG
1		1				MVPAS
18245	48613	A	18352	1168	2241	MITING
18245	48614	A	18352	1 108	1344	
10240	140014	14	10000	1,	11277	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
18247	48615	Α	18354	440	886	
18248	48616	A	18355	1	2876	MAGVPGFEPGNAGIKNRCLTA
1		l				WRYPIRTTLSGEWCGRRDLNSQ
		l				EATLQQPLLQAIDLKKHYPVKK
İ		l				GMFAPERLVKALDGVSFNLER
i		l			İ	GKTLAVVGESGCGVLACTLFA
1		1				WNRNYFVLLFVGVFLSSFGSTA
		1				NPQMFALAREHADKTGREAV
		ı				MFSSFLRAQVSLAWVIGPPLAY
		1				ALAMGFSFTVMYLSAAVAFIV
1		1				CGVMVWLFLPSMRKELPLATG
						TIEAPRRNRRDTLLLFVICTLM
		1				WGSNSLYIINMPLFIINELH
18249	48617	A	18356	606	726	
18250	48618	Α	18357	1271	1726	
18251	48619	В	18358	1	1633	
18252	48620	Α	18359	1	407	
18253	48621	Α	18360	427	2307	
18254	48622	Α	18361	120	694	
18255	48623	A	18362	804	1087	KRQHLCTHSGAIRLRIAGVGSW
		l		l	\	KG/GRPNWRKMAVRWRVPASA
				l		VVSGWLRRWHCWPVAMPSAE
		l				SPRIRCGAGCCICRLPLFRCGCC
						TPARLTISH
18256	48624	A	18363	216	436	
18257	48625	Α	18364	476	577	FRRWYWGCCSTTRLSHCLTR*
						M*CMRWSLAVCC
18258	48626	Α	18365	1159	3744	
18259	48627	В	18366	169	743	
18260	48628	Α	18367	2811	3513	SLPRGWFQPEYGNLEIMEKTYN
		l				PQDIEQPLYEHLGFPRVGLRRE
		l				LKKAQESYWAGNSTREELLAV
						GRELRARH\WDQQKQAGIDLLP
		l		1		VGDFAWYDHVLTTSLLLGNVP
		1	l	I	i	ARHQNKDGSVDIDTLFRIGRGR
1		1		I	1	APTGEPAAAAEMTKWFNTNYH
	ĺ	1	l	I	1	YMVPEFVKGQQFKLTWTQLLD
	1			1		EVDEALALGHKVKPVLAGPGT
		1		l		WLWLGKVKSEQFYRLSLLNDI
			l		L	LAGYQQGLAETGVGPDDIVTA

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
18261	48629	Α	18368	1	2810	MKQTVYIASPESQQIHVWNLN
						HEGALTLTQVVDVPGQVQPMV
						VSPDKRYLYVGVRPEFRVLAY
						RIAPDDGALTFAAESALPGSPT
						HISTDHQGQFVFVGSYNAGNVS
						VTRLEDGLPVGVVHVVDGLDR
						LARQLIKNLATLKAGNARVVN
						SNAMSFLAQKGTPHNIVFVDPP
		1				FRRGLLEETINLLEDNGWLADE
	1					ALIYVESEVENGLPTVPANWSL
						HREKVAAFAGAEPYHYLNHTL
						GFPRVGLRRELKKAQDSYW
18262	48630	Α	18369	2279	2563	MNFGASLNSPTPRSYLSLGGEK
	ļ					KAPVWEHTLGVPSRRPAAGKL
		1				KKAPERYWGGEHPPVKKWLG
						G*ARKCRPRPWETL*KSHLRRR
						PSLGPWAGGL
18263	4863 I	Α	18370	481	1020	
18264	48632	Α	18371	1	998	MNENFGTQICVNNRLSFTDCSG
		l				YVTRYDHDRFGQVTAVHREEG
		l				LSQYRAYDSRGQLIAVKDTQG
		l				HETRYEYNAAGDLTTVIAPDGS
						RNGTQYDAWGKAICTTQGGLT
ļ		l				RSMEYDAAGRVIRLTSENGSHT
		l	İ			TFRYDVLDRLIQETGFDGRTQR
	ļ	l				YHHDLTGKLIRSEDEGLVTHW
		l				HYDEADRLTHRTVNGETAERW
		l				QYDERGWLTDISHISERHRVTV
						HYGYDSKGRLASEHLTVHHPQ
1	Ì	l				TNELLWQHETRLAYKRTGLAN
	:					RCIPDTCPPVNAYLGTACCQHE
		l				ICDTPWLSYRDPFTGKSWLSGR
	ļ.	l	l			YELHKRIYGITAKERKDVDVW
		l			1	HPDVRFFELYDENNELRGSFYL
		l				DLYARENKRGGAWMDDCVGQ
		l	l			MRKADGSLQKPVAYLTCNFNR
		l				PVNGKPALFTHDEVITLFHEFG
		l				HGLHHMLTRIETAGVSGISGVP
		l			İ	WDAVELPSQFMENWCWEPEA
		l				LAFISGHYETGEPLPKELLDKM
		I	l			LAAKNYQAALFILRQLEFGLFD
		l				FRLHAEFRPDQGAKILETLAEIK
1		I	1	l	l	KLVAVVPSPSWGRFPHAFSHIF
		ı	l	Į.		AGGYAAGYYSYLWADVLAAD
		1			l	AFSRFEEEGIFNRETGQSFLDNI
		1	l	l		LSRGGSEEPMDLFKRFRGREPQ
			l	l		L*HTVVELPRPFHREILAFRPL*I
	I	1	Į.	l	1	TQAYLRHHR*RA*RC*CLASGC

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		ŀ	İ	sequence		
18265	48633	A	18372	1409	1533	TGNDAPVPAQSAQYRYLQ*SV
18265	48633	l <sup>A</sup>	18372	409	333	RNFCRLSFRLGINLSLPYPHVDD
		1				VIPLMAEGKILPYLDIPLQHASP
						RILKLMKRPG
18266	48634	Α	18373	222	659	SAGSVKTQRSGANKQRRTRSRL
		ĺ		1		ASFC/ETLSSVSFPAWRKISFLIP
		l				VGLPISNNYVCSLNPVWCAMR
		ł	ł			LNMPPMSKSICWQKHWKSTVS
İ		1	l	1		RWITTRHSFVQTLISTACWRRSP
	1					VTQSSWRSTFACSTGLLSHAPP
						LPIRHCTNITNVWY
18267	48635	В	18374	ī	1527	
18268	48636	Α	18375	1	1005	
18269	48637	Α	18376	2	314	WVSYCSGSTTL/LLRALQECQR
	1	1		ŀ		QQGPWASAGDPGEGAGERERL
l		1		1		PQALASPPLQVKPARQ/RDPGL
				ł		RTPDPGDTASPALNGHIFALPA
						GTAGDCFPRPPRGRKNSGT
18270	48638	A	18377	3	576	
18271	48639	A	18378	189	563	OGRGSSRPGCGHLDPGGEEWL
102/1	40037	ľ^	10570	100	303	PORPGLOHLC\PSAYILIFAGVL
		1				VMVTGFLGFGAILWERKGCLS
		1		i .		TTTGDRFWKDRQPWTCR/WQT
			1	l		SHRNQSGAGGQWDRFRSHQGH
1						RDHEGRTSNWGSGFPREVA
		1				RUHEUKISNWUSUFFREVA
18272	48640	A	18379	1	531	A A COMPANY A PERCENT AND A SERVICE AND A SE
18273	48641	A	18380	1385	1673	AASTDRAAETG**KTR/HRWFL
						SVKLRTSTPTAVSPKK*KRLAW
1		1				TRCMTPPSKR*KKRVITPSSSPT
						SLTSTLPGATVATSPVMPRVWN
		1		ļ		CSTAVCRS
18274 18275	48642 48643	A A	18381	1	921 2115	
		A	18383	2	149	ARRNESRRGGR*HPCRPIT*TGT
18276	48644	A	18383	2	149	
1	i	1	l			VNQRPAGFRRFAGPFRYSGKPG
		ļ.			1000	RERL
18277	48645	Α	18384	482	1655 776	MENACVLLMGVLSTFLVSWLG
18278	48646	Α	18385	1	//6	
		1	Į.	1		KDAMAGVGLADNFNMVIMAF
		1		1		FAAIDLGTTVPGAFSLCKRDRR
				1		QARVATRQSLVIMTFLPVLLAP
1		1	1	1		LIHHFGEQIIDFVAGDATTEVKA
1	l	1	1	I		LALTYLELTVLSYPAAAITLIGS
1			1	1		GALRGAGNTKIPLLINGQVAML
		1	l	I		MQAPYYFQEAQIEAAIAAMDV
1		1	1	1		APEYADIRQVESSTAVLYLFSE
		1	1			RFMTYGKAYGLCEWFEGSRLSI
		1		I		AHIPVTDNDNETQYHFFRQSCQ
		1		1		HC/DRCSVHRRLPDGGVVA
			1			INCOMES VINCE DOG VYA

NO.	SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
18279   48647   A   18386   1017   9228   FGRCAGVCQ*RGRDGQRRDE GDGRLRARL*ALYQTITHDLE YRHKNLYRKLASQRVTEHV RAGLRYSYQYEKDCITITIOSL/HNKVLHTQGEAGLRXVVK& HADGSVTQSQPDAVGRLRAQDDAAGRTTEYSPDVVTGLITRII PDGRASAFYYNHHNQLTSAT PDGLELRREYDELGRLIQETAI DGDTTRYRYDPHSDIPCATE ATGSRKTMTWSRYGQLLSFTI CSGYVTRYDHDRFGQMTAV     18280   48648   B   18387   1   1431							
18279   48647   A   18386   1017   9228   FGRCAGVCQ*RGRDGQRRDE GDGRLRARL*ALYQTITHDLE YRHKNLLASQRVYEHV RAGLRYSYQYEDAVGCHITIDSLJ. HINK'ULHTIQGEAGLKRVVKKE HADGSVTQSQFDAVGRLRAQ DAAGRITEYSPDVVTGLITRII PDGRASAFYYNHHNQLISAT PDGLERREYDEGRILIQETH DGDTRYRYDMPHSDLPCATE ATGSRKTMTWSRYGQLLSFIT CSGYVTRYDHDRFGQMTAV LVRVMRPIVTCRRSRSILLRSI. HLCKWRVSTKSPULWTILSN RLEWKSWR*NGLOSKYODG EVQKGSVRYRAFALLGPAM AHRITGRERRYRYDSDGRVT QULMPAGLSTYTQVEKDRITTIT SLDRREVLHTQGEAGLKRVVK KEHADGSVTQSOFDAVGRRE QTDAAGRTTEYSPDVVTGLITTI TITTPDGRASAFYYNHHNQLTS TGPGGLELRREYDGEAGLGPAW VHREGLSQYRAYDSRGQLIC KDTQGLETRYRYDDSDGRVT QULMPAGLSYTYQVEKDRITTIT SLDRREVLHTQGEAGLKRVV KEHADGSVTQSOFDAVGRRE QTDAAGRTTEYSPDVVTGLIT TITTPDGRASAFYYNHHNQLTS TGPGGLELRREYDEGGRALGPAW VHREGLSQYRAYDSRGQLIC KDTQGLETREYPDEGGRAGV VREPHADGSVTQSOFDAVGRRE QTDAAGRTTEYSPDVVTGLIT TITTPDGRASAFYYNHHNQLTS TGPGGLELRREYPDEGGRAGV VREPHADGSVTQSOFDAVGRRE QTDAAGRTTEYSPDVVTGLIT TITTPDGRAGGAKRVV KEHADGSVTQSOFDAVGRRE QTDAAGRTTEYSPDVVTGLIT TITTPDGRAGGAKRVV KEHADGSVTQSOFDAVGRRE QTDAAGRTTEYSPDVVTGLIT TITTPDGRAGGAKRVV KEHADGSVTQSOFDAVGRRE QTDAAGRTTEYSPDVVTGLIT TITTPDGRAGGAKRVV KEHADGSVTQSOFDAVGRRE QTDAAGRTTEYSPDVVTGLIT TITTPDGRAGGAKRVV KEHADGSVTQSOFDAVGRRE QTDAAGRTTEYSPDVVTGLIT TITTPDGRAGGAKRVV KEHADGSVTQSOFDAVGRRE QTDAAGRTTEYSPDVVTGLIT TITTPDGRAGGAKRVV KEHADGSVTQSOFDAVGRRE QTDAAGRTTEYSPDVVTGLIT TITTPDGRAGGAKRVV KEHADGSVTQSOFDAVGRRE QTDAAGRTTEYSPDVVTGLIT TITTPDGRAGAKRVV KEHADGSVTQSOFDAVGRRE QTDAAGRTTEYSPDVVTGLIT TITTPDGRAGAKRVV KEHADGSVTQSOFDAVGRRE QTDAAGRTTEYSPDVVTGLIT TITTPDGRAGAKRVV KEHADGSVTQSOFDAVGRRE QTDAAGRTTEYSPDVVTGLIT TITTPDGRAGAKRV TURGGATAR KAHVEN TURGGAT AND THE A		sequence		09/540,217		of peptide sequence	deletion, \=possible nucleotide insertion)
GDGRLRARI.*ALYOTITHDLE YRHKNLYRKLASQRVTEHV RAGLRYSYQYEKDCHTITIDS.LI HNKYLHTQGEAGLKRYVYKK HADGSYTQSQFDAYGRLRAQ DAAGRITEYSPDVVTGLITRI PDGRASAFYYNHHNQLTSAT PDGLERREYDELGRLIQETAI DGDITRYRYDNPHSDLPCATE ATGSRKTMTWSRYQGLLSTI CSGYVTRYDHDRFGQMTAV    18281		1			sequence		
GDGRLRARI.*ALYOTITHDLE YRHKNLYRKLASQRVTEHV RAGLRYSYQYEKDCHTITIDS.LI HNKYLHTQGEAGLKRYVYKK HADGSYTQSQFDAYGRLRAQ DAAGRITEYSPDVVTGLITRI PDGRASAFYYNHHNQLTSAT PDGLERREYDELGRLIQETAI DGDITRYRYDNPHSDLPCATE ATGSRKTMTWSRYQGLLSTI CSGYVTRYDHDRFGQMTAV    18281	10270	10647	<u> </u>	10206	1012	loase	ECRCAGVCO*RCRDGORRDEA
	18279	48047	A	10300	1017	9226	
RAGLRYSYQYEKOCITITIOSL  HNKVLHTQGEAGLKRVVKKR  HADGSVTOSQFDAVGRLRAQ  DAAGRITEYSPDVVTGLITRII PDGRASAFYYNHHNQLTSAT  PDGLELRREYDELGRLIQETAI DGDTTRYRYDNPHSDLPCATE ATGSRKTMTWSRYGQLLSTAI DGDTTRYRYDNPHSDLPCATE ATGSRKTMTWSRYGQLLSTAI CSGYVTRYDHDRFGQMTAV   REFERENCE     REFERENCE							
HNKVLHTQGEAGLKRVVKKH		1					
HADGSVTQSQFDAVGRIRAQ   DAAGRTTEYSPDVVTGLITRI   PDGRASAFYYNHHNQLTSAT   PDGLELRREYDELGRLQETAI   DGDTTRYRYDPMPSDLPCATE   ATGSRKTMTWSRYGQLLSFTI   CSGVTRYDHDRFQQMTAV   SERVE   CSGVTRYDHDRFQQMTAV   SERVE   CSGVTRYDHDRFQQMTAV   SERVE   CSGVTRYDHDRFQQMTAV   SERVE   CSGVTRYDHDRFQQMTAV   LVRYMRPIVTCRSRSILLRISH   LVRYMRPIVTCRSRS					1		
DAAGRITEYSPDV-TIGLITRIT   PDGRASAFYYNHNQLTSATG   PDGLERREVPDELGRIQUETA   DGDITRYRYDNPHSDLPCATE   ATGSRITAMTWSRYGQLLST   CSGYVTRYDHDREGQMTAV     18280	l						
PDGRASAFYYNHHNQLTSATE		l		i			
PDGLELREYDELGRLIQETAI	1						
18280   48648   B   18387   1   1431							
RESEN   RESENTATIVES PROGRESS   RESENTATIVES PROGRESS			1	l			
CSGYVTRYDHDRFGQMTAV     18281							
18280   48648   B   18387   I   1431	1	1	1				
18281   48649   A   18388   575   835							CSGYVTRYDHDRFGQMTAV
LVRYMRPIVTCRSRSILLRSI					1		
HLCKWRYSTKSPVILWTILSN	18281	48649	Α	18388	575	835	
RLFWKSWR*NGLQSKYODG							
18282   48650			l				HLCKWRVSTKSPVILWTILSN*
FHPSDPWALGRSQGGAGL(0PEVQKGSVRYRAFALLGPAM			l				RLFWKSWR*NGLQSKYQDG
EVOKGSVRYRARFALLGAM   AHRHTGRPEIRYRYDSDGRVT   QLNPAGLSYTYQYEKDRITTI   SLDRREVLHTQGEAGLKRVV   KEHADGSVTQSOFDAVGRIR   QTDAAGRTTEVSPDVVTGLIT   ITTPDGRASAFYYNHNNLTTS   TGPDGLELRREYDELGRLQE   APPGDITRYRYDDPHSDLIPC-   TEDATGSRKTHTWSRYGQLL   ETDCSGYVTRVDHORFGQMT   VHREEGLSQYRAYDSRGQLIC   KDTQGHETREFYNIAGDLDGC   APEGGRNGTQYDAWGRRT   QQGDADDRSAGGTRARKGH   SFRSVGDRTVSRHGYPGRNLIR   RMYRSSVPLYRLTASIAPVPQ   YRPPHQSEEVY     18281   48651   B 18390   1   2640	18282	48650	Α	18389	1207	2465	ASTAQQHQLLSPAKEETTGWRI
ARRITGREIRYRYDSDGRV1			1				FHPSDPWALGRSQGGAGLIQPP
OLNPAGLSYTYQYEKDRITITI   SLDRREVLHTQGEAGLKRVV    KEHADGSVTQSCPDAVGRIR     QTDAAGRTTEYSPDVVTGLIT   ITTPDGRASAFYNHHOLTS     TGPDGLELRREYDELGRLIQE   APBGDITRYRYDNPHSDLIPC/   TEDATGSRRTMTWSRYQQLL     FTDCSGYVTRYDHDBTGQNT   VHREGLISQYRAYDSRQQLIC     KDTQGHETRFEYNIAGDLIDG   APBGGRNGTQYDAWGRRT     QCGDADDRSAGGTRARKOH   SFRSVGDRTNSRHGYPGRILL     RMYRSSVPLYRLTASIAPVPQ  YRFPPHQSEEVY     18283   48651   B   18390   1   2640     18284   48652   A   18391   1   2640     18285   48653   A   18392   1   549     18286   48654   A   18393   290   389   HLGGPRTAR*ARFWHL*RAYC     L*SGECRRAGSV   L*SGECRRAGSV     18287   48655   A   18394   1095   1268   HLGGPRTAR*ARFWHL*RAYC     L*SGECRRAGSV   L*SGECRRAGSV   RRSAHAGRFLQTAS     18288   48656   A   18395   1056   2178   RRSAHAGRFLQTAS     18289   48657   A   18396   1   669     18290   48658   A   18397   1628   1856     18291   48650   A   18399   1   3186     13186   13186   13186     COLONDO			1				EVQKGSVRYRARFALLGPAMV
SLDRREVLHTQGEAGLKRVV.   KEHADGSVTQSQFDAVGRLR   QTDAAGRTTEYSPDVTGLT   TITTPDGEAGSTYNNHHNQLTS   TGPGGLELRREYSPDVTGLT   TITTPDGEASAFYYNHHNQLTS   TGPGGLELRREYSPDELGRLIQE   APPGGITRYRYDMPHSDLIPC/. TEDATGSRKTMTWSRYGQLL   FTDCSGYYTRYDHDRGQMT   VHREEGLSQYRAYDSRGQLIC   KDTQGHETREFYNIAGDLIDG   APEGGRNG/TQYDAWGRRR   /QGDADDRSAGGTRARKGH   SFRSVGDRTVSRHGYGGNL   RMVRSSYPL/YRLTASIAPVPQ   YRFPPHQSEEVY   SFRSVGDRTVSRHGYGGNL   RMVRSSYPL/YRLTASIAPVPQ   YRFPPHQSEEVY   SECONDAR   SFRSVGDRTVSRHGYGGNL   SECONDAR   SFRSVGDRTVSRHGYGGNL   SFRSVGDRTVSRHGYGGNL   SECONDAR   SFRSVGDRTVSRHGYGGNL   SFRSVGDRTVSRHGYGGNL   SFRSVGDRTVSRHGYGGNL   SFRSVGDRTVSRHGYGGNL   SFRSVGDRTVSRHGYGGNL   SFRSVGDRTVSRHGYGGNL   SFRSVGDRTVSRHGYGNG   SFRSVGDRTVSRHGYGGNL   SFRSVGDRTVSRHGYGGNL   SFRSVGDRTVSRHGYGGNL   SFRSVGDRTVSRHGYGNG   SFRSVGDRTVSRHGT   SFRSVGDRTVSRHGT   SFRSVGDRTVSRHGT   SFRSVGDRTVSRHGT   SFRSVGDRTVSRHGT   SFRSVGDRTVSRHGT   SFRSVGDRTVSRHGT   SFRSVGDRTVSRHGT   SFRSVGDRTVSRHGT   SFRSVGDRTVSRHGT   SFRSVGDRTVSRHGT   SFRSVGDRTVSRHGT   SFRSVGDRTVSRHGT   SFRSVGDRTVSRHGT   SFRSVGDRTVSRH					1	1	AHRHTGRPEIRYRYDSDGRVTE
REMADGSVTQSQFDAVGRIR   QTDAAGRITEYSPDVVTGLIT   ITTPDGRASAFYYNHINQLTS   TGPDGLELRREYDEUGRLIQE   APPDGITRYRYDDHISDLIQC   TEDATGSKETMTWSRYGQLL   FTDCSGVVTRYDHDRFGQNT   VHREEGLSQYRAYDSRGQLIC   KDTQGHETRFEYNIAGDLDG   APPEGRNRGTYDAWGRRIT   VQGDADDRSAGGTRARKGH   SFRSVQDRIVSSRHJYCPGNLIC   RMVRSSVPLYRLTASIAPVPQI   YRFPPHQSEEVY   VRFPPHQSEEVY   VRFPPHQSEEVY   SFRSVQDRIVSSRHJYCPGNLIC   RESST   SSS   SS			l				QLNPAGLSYTYQYEKDRITITD
OTDAAGRTTEYSPDVYTGLIT   ITTPDGRASAFYYNHHNQLTS   TGPDGLELRREYPDELGRLIQE   APPGDITRYRYDDPHSDLIPC- TEDATGSRKTHTWSRYGOLL   FTDCSGYVTRYDDPHSDLIPC- TEDATGSRKTHTWSRYGOLL   FTDCSGYVTRYDDDRFGQMT   VHREEGLSQYRAYDBGGLIC   KDTQGHETREFYNIAGDLDGG   APEGGRNGTQYDAWGRRT   QQGDADDRSAGGTRARKGH   SFRSVGDRTVSRHGYPGRNLI   RMYRSSVPLYRLTASIAPVPQI   YRFPPHQSEEVY   18284   48652   A   18391   1   2640   18285   48653   A   18392   1   349   1   2640   18285   48654   A   18392   290   389   HLCGPRTAR*ARFWHL*RAYC   L*SGECRRAGSV   L*SGECRAGSV   L*SGECRRAGSV   L*SGECRRAGSV   L*SGECRRAGSV   L*SGECRRAGSV   L*SGECRRAGSV   L*SGECRRAGSV   L*SGECRRAGSV   L*SGECRRAGSV   L*SGECRRAGSV   L*SGECRRAGSV   L*SGECRRAGSV   L*SGECRRAGSV   L*SGEC			l				SLDRREVLHTQGEAGLKRVVK
ITTPDGRASAFYYNHINOLTS   TGPDGLELRREYDELGRLIQE   APDGDITRYRYDMPHSDLIPC-   TEDATGSRKTMTWSRYQOLL   FTDCSGYVTRYDMPHSDLIPC-   TEDATGSRKTMTWSRYQOLL   FTDCSGYVTRYDMPHORQMT   VHREGLISQYRAYDSRQOLIC   KDTOGHETREFYNIAGDLOG   APEGG/RNGTQYDAWGRRT   QGGDADDRSAGGTRARKGH   SFRSYODRIVSRHGYPGRALL   RMVRSSYPLYRLTASIAPVPQ   YRFPPHQSEEVY   TESSY   TES			İ				KEH\ADGSVTQSQFDAVGRLRA
TGPDGLERREYDELGRILOE							QTDAAGRTTEYSPDVVTGLITR
APGGITRYFYDNPHSDLPC/ TEDATGSRKTMTWSRYGQLL FTDCSGYYTRYDHDRFGQMT VHREEGLSQYRAYDSRGQLIC KDTOGHETREFYNIAGDLDG APEGGRNG/TOYDAWGRRAT //QGGDADDRSAGGTRARKGH SFRSVGDRTVSRHGYPGRNLI RMVRSSYPL/YRLTASIAPVPQI YRFPPHQSEEVY    18283							ITTPDGRASAFYYNHHNQLTSA
TEDATGSRKTMTWSRYQQLL   FTDCSGYVTRYDHDRFGQMT							TGPDGLELRREYDELGRLIQET
FTDCSGVYTRYDHORFGQMT			1				APDGDITRYRYDNPHSDL\PCA
FTDCSGVYTRYDHORFGQMT			l				TEDATGSRKTMTWSRYGOLLS
RDTOGHETREFYNIAGOLDGG	i		l				FTDCSGYVTRYDHDRFGOMTA
RDTOGHETREFYNIAGOLDGG			1				VHREEGLSOYRAYDSRGOLIGV
APEGGRAGTOYDAWGRRAT			ı				
Record   R			l				
RSPRSVGDRTNSRHGYPGRILL   RMYRSSVPLYRLTASIAPVPQ  YRFPPHQSEEVY   RS284   48652   A   18390   1   2604			İ				
RMVRSSVPLYRLTASIAPVPQI   T8283   48651   B   18390   1   2604			l				
YRFPPHQSEEVY			l				
18284   48652   A   18390   1   2604			l				
18284   48652	18283	48651	В	18390	1	2604	
18286   48654   A   18393   290   389			-				
L*SGECRRAGSV	18285	48653	Α	18392	1	549	
18287   48655   A   18394   1095   1268	18286	48654	Α	18393	290	389	HLCGPRTAR*ARFWHL*RAYG
L*SGECRAGSVAENARSACR   RRSAHAGRFLQTAS   18289   48657   A   18396   1   6669   18290   48658   A   18397   1628   1856   18291   48659   A   18398   227   668   18292   48660   A   18399   1   3186   1			l_			<u> </u>	
RRSAHAGRFLQTAS	18287	48655	Α	18394	1095	1268	HLCGPRTAR*ARFWHL*RAYG
18288     48656     A     18395     1056     2178       18289     48657     A     18396     1     669       18290     48658     A     18397     1628     1856       18291     48659     A     18398     227     668       18292     48660     A     18399     1     3186			1				L*SGECRRAGSVAENARSACRC
18289     48657     A     18396     1     669       18290     48658     A     18397     1628     1856       18291     48659     A     18398     227     668       18292     48660     A     18399     1     3186			1				RRSAHAGRFLQTAS
18290     48658     A     18397     1628     1856       18291     48659     A     18398     227     668       18292     48660     A     18399     1     3186	18288	48656	Α	18395	1056	2178	
18291         48659         A         18398         227         668           18292         48660         A         18399         I         3186		48657	Α	18396	1		
18292 48660 A 18399 1 3186	18290	48658	Α	18397	1628	1856	
	18291	48659	Α	18398	227	668	
18202 48661 4 18400 201 621	18292	48660	Α	18399	1	3186	
110293  40001  A  18400  291  031	18293	48661	Α	18400	291	631	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	uf peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
18294	48662	Α	18401	1	1437	
18295	48663	A	18402	345	727	
18296	48664	Α	18403	870	1043	
18297	48665	A	18404	1	2175	
18298	48666	Α	18405	1	1332	
18299	48667	Λ	18406	1	1566	
18300	48668	В	18407	1	921	
18301	48669	В	18408	1	2487	
18302	48670	В	18409	1	2919	
18303	48671	В	18410	1	2214	
18304	48672	Α	18411	1714	1979	RLAWRLAGRWWAGSWRTSTIF
		1				PAAACSRLRCSPPSKFCSAWCR
Į.	İ	1				WCSTRACSSCCRSTSSPMPAWR
		1				PSAGS*LSTARRRAPPSALVLRI
		1				
18305	48673	A	18412	1201	2118	PSRQADKENRPHPGRGYPARM
						MSGLTGTITTVSTGWCTTRGHN
						MKSRWSKVAIFTTRWGRRVAK
i						RVWRRERDLTGWMSLSRKPQV
		1				TWYGWDGDRLTTIQNDRTRIQ
	1					TIYOPGSFTPLIRRIPVLGGGDTT
		ŀ				MDCLRTSIRLNAASVTCAYRRE
		1				QISMPGSRKEVVNAREEGVEFQ
		1				FNFQPQYIACDEDGRLTAVGLI
		1				RTAMGEPGPDGRRRPPPVAGSE
		l				FELPADVLIMAFGFQAHAMPW
		l				LOGSGIKLDKWGLIOTGDVGY
	1	l				LPTOTHLKKVFAGGDAVHGAD
						LVVTAMAAGRQAARDMLTLF
	1	l				DTK*PGTAGTATG*PQYRTTEP
		l				ASRRFISRGASRHSSEGS/SVLG
		1				GGDTT/MGLFADFHPPQCRQRD
		1				L\PYRRDQISMPGSRKEVVNAR
						EEGVEFOFNFOPOYIACDEDGR
		1				LTAVGLIRTAMGEPGPDGRRRP
						PPVAGSEFELPADVLIMAFGFQ
1		1			I	AHAMPWLQGSGIKLDKWGLIQ
1				1	1	TGDVGYLPTQTHLKKVFAGGD
					1	AVHGADLVVTAMAAGRQAAR
1						DMLTLFDTKAS
18306	48674	В	18413	1615	1656	
18307	48675	Α	18414	1287	5056	
18308	48676	Α	18415	1	271	
18309	48677	Α	18416	1	588	
18310	48678	Α	18417	2150	2332	
18311	48679	A	18418	1	238	LEELGVIGAVLVGFSL*VLWAP
1						LQLPKAGGRVKVAGIQLGEVE
1	1					WKVS\KSCSSPDPPPGVMAAKIS
						ISQALQPPQSTR
18312	48680	В	18419	1	2721	
					·	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
18313	48681	Α	18420	712	1031	PVMRQRGVFRSVILIKIRSARCC
		1				QMIQPRVISHAMYSLSPFFALR
ŀ				i		RSTKSPKRFSMNNS*ASRSSGST
						SRDTSAIS*ARRSISSRTSRLLIRS
						LISLISSLLVNVV
18314	48682	A	18421	1	1779	
18315	48683	Α	18422	693	921	
18316	48684	Λ	18423	758	1183	ALTAASRSECAVIMMTGRTSCC
						DIVEKWIPARCCQMIQPRVISH
						AMYSLSPFFALRRSTKSPKRFS
						MNNS*ASRSSGSTSRDTSAIS*A
						RRSISSRTSRLLIGWRSLWYTILI
						NSIPPTNRAKSMKPEPSPNACSK
						VKRCC
18317	48685	В	18424	1	708	
18318	48686	Α	18425	1	2436	
18319	48687	A	18426	1382	I813	
18320	48688	A	18427	900	1028	AGYAAPGRTDRRSSPSG*GYRY
						SGCYQICRQPGRLGSRKSPV
18321	48689	Α	18428	1	881	MTPSRFAKKNGSLVKRCPMGI
l						DAEVTMIKPIAARPKVSHSKVR
				1		SYMIRLSVSFSREPITQPFSAVEI
						QTRIRYGVSGFFLRRVDTEHHP
						DRHAARALQYHITGSNRCDAIN
						AVQFDTAGGECTNRRMAEDHG
						RNVAVIQMLIRLVIKQAFREVP
						SELWTNRKQACPFLDFDCGENS
			İ			AIAANNYDWFGNMNVLTFLRD
						IGKHFSVNQMINKEAVKQRLN
		1				REDQGISFTEFSYNLLQGYDFA
						CLNKQYGVVLQIGGSDQWGNI
					Į.	TSGIDL/NPSSASESGVWPDRSA
						DH*SRWHQIW
18322	48690	Α	18429	1	3270	
18323	48691	A	18430	1	374	MKTCWQILEIESTTQIDIIRQAY
				1		LARLPLCHPETDPQGFKALRQA
				1		YEEALRLAVNPVEEADDEEKD
ĺ				1		AAAEHEILRAFRT/FTGFRK*SFS
	1	l		1	l	AFRLAEIYSAIKYLEHGGCRSIT
					l	LAAVCNRHRSAI

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleatide location of lust	Amino acid sequence ( X=Unknown,
	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
			L			
18324	486 <b>9</b> 2	Α	18431	63	1272	LRRSCNAVYCW*CVATCPS\GE
				1		EDGIVLIDQDKCRGWRMCITGC
				l		PYKKIYFNWKSGKSEKCIFCYP
						RIEAGQPTVCSETCVGRIRYLG
				l		VLLYDADAIERAASTENEKDLY
						QRQLDVFLDPNDPKVIEQAIKD
			İ			GIPLSVIEAAQQSPVYKMAME
						WKLALPLHPEYRTLPMVWYVP
						PLSPIQSAADAGELGSNGILPDV
1				l		ESLRIPVQYLANLLTAGDTKPV
				l		LRALKRMLAMRHYQRAETVD
				ĺ		GKVDTRALEEVGLTEAQAQEM
				l		YRYLAIANYEDRFVVPSSHREL
l				l	ł	AREAFPEKNGCGFTFGDGCHGS
				l		DTKFNLFNSRRIDAIDHOOEMF
1						EAIAASKNLPKEDAHALGIFLR
						DLTTMDPLDAQAQYSELFDRG
1						RATSLLLFEHVHGESRDRGQA
						MVDLLAQYEQHGLQ
18325	48693	Α	18432	2	859	WPLRRSPYSIINGSGKSAASGSV
100220	1.00,5	· ·	10.55	ľ		MQVAQFNSHYQYDPKFERGM
						YLYEHRRCFNNIIDYCNSLCYH
						AWLVAHKDDIERNYRGPLVOV
						VGWCDAIFGAEELGISRAQFDQ
						FLRMMOGGAOFGGGYOOOTG
1			İ			GGGRPGGHFFEKRRLLRMVDR
İ						LNARFTGGVLVSFKGPLLEGFG
			ŀ			PWQGLSPWVIGPDLGLPG/CLG
						AWGAVSVCHCPWVCKTGSPFR
						WVPHRRFHPPPG*KFPENWMG
			İ			FCSSRTCSGLFSHPHSPTMAFKN
			ŀ			FELGHGTPPRGTRNRPTMSSNT
İ				l		YRPHRFO
18326	48694	A	18433	479	601	CWRPLPAEKRWWYLAANWW
18320	48094	^	10433	479	001	RLAARFVFPMLCVRQ*PSSMIW
			l	i		
				l		TTPDADIAIGTWRSCCAVLRGR KMPVSSITMRRRCY*CWRPLPA
			1	I		
			1	I		EKRWWYLAANWWRLAARFVF
	10.505	١.	10101	-	ļ	PMLCVRQAAPYTK
18327	48695	Α	18434	69	194	ATYENMLANPRN*KHDANRHY
						PPGLSCSLTVVSSRNRSARV
18328	48696	Α	18435	173	298	ATYENMLANPRN*KHDANRHY
						PPGLSCSLTVVSSRNRSARV
18329	48697	Α	18436	ı	1734	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1	1	sequence		
		<u> </u>				
18330	48698	Α	18437	851	2202	RQKRLIFCCVKGKNWPP*WRW
		l			1	LNEKLPCSLMLLPTLPPSVLGIR
		1				LQNQLQRQFVRQGGVWMPGD
						EVKKVTCKNGVVNEIWTRNHA
						DIPLRPRFAVLASGSFFSGGLVA
1		1	l	l		ERNGIREPILGLDVLQTATRGE
1		l				WYKGDFFAPQPWQQFGVTTDE
		l				TYARHRQGKPLKTCLPSVRCW
						ADLIPSPRDAAAVFVPSVLYMP
1		l				LNRLPNAOEANNE
18331	48699	В	18438	1	5301	Britas (111QE/11111)
18332	48700	Ā	18439	710	889	
18333	48701	Ā	18440	1622	2615	
18334	48702	A	18441	1	1309	
18335	48702	A	18442	1	266	PRQCGFMKKRLENGDDYFAVN
18333	48/03	Α.	18442	1	200	PRGRCLHCCWMTVLC*RKRSD
		l				
		1	ŀ			YAVSCRQRPRPPVLAPVNSISRS
		1				VSPYTPEEYKPTVRAQLEKNCN
		_				М
18336	48704	Α	18443	267	395	
18337	48705	Α	18444	1	3807	
18338	48706	Α	18445	1	2193	
18339	48707	Α	18446	1278	1846	SCRSAPRNRHQIPGTYRSRLPRH
						TTPPGYDHNRKNPNLYISTRQK
	İ	ŀ			i	RDAFFAVQYHSLLYYRQTLLPN
						DHNQSVDR*FVFRL*NQNGYNS
						GRHLYWRYHSYNAWL*LCHR
		1				HPVYYRLYYIFLQPVQMQMPQ
1						CPSPLMPECSFSFSFLILINA/SNI
1				į		QRESPVENRKVFNLRLLKIYYR
			l			LIIFLKCGNLLNL
18340	48708	Α	18447	1	2106	
18341	48709	A	18448	881	1401	
18342	48710	A	18449	1	233	MMGFDGTVOYMASLGAPMPM
1.05 12	1.57.10	Γ.		l'	I	LAA/MYCGSYGSARRDINRAW
1		1				LFHPSAGGAVYFLHAGYGGDW
		1				SPLLGYDRRCGWAKYD
18343	48711	-	18450	1	1960	OF BEG (DIRROGWAR 1D
18343	48711	A	18450	563	928	PO A HACODA A O A L WITH IT TO A CO.
18344	48/12	Α.	18451	263	928	FSAIKSSPKAQALWHVLHY*AV
1		l				N*TNIFKTEKPIFNRGKRFRPTP
1						TRQLRECWIVWGSASCQLTKQ
1		1				AVVARWTIILMRRRKGWHGRA
1						IILMPGGPRLKQVPRQFCKPPA
		L				AAARLSKSMGRC
18345	48713	A	18452	1	828	

SEQ ID	SEQ ID NO:		SEQ ID NO:		Nucleotide location of last	
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	ļ					
18346	48714	Α	18453	1	1327	MMQKPATVDEEESPRETHRYS
	l	l				VRRRGELIVEAGGRAENTVVT
		i				GAGWLKVATGGIAKCTQYGN
		1			l	NGTLSVSDGAIATDIVQSEGGAI
		l				SLSTLATVNGRHPEGEFSVDKG
	l	1				YACGLLLENGGNLRVLEGHRA
		1		l		EKIILDQEGGLLVNGTTSAVVV
		1				DEGGELLVYPGGEASNCEINQG
	1	1		l		GVFMLAGKASDTLLAGGTMN
	į.	1		l		NLGGEDSDTIVENGSIYRLGTD
		1				GLQLYSSGKTQNLSVNVGGRA
					1	EVHAGEVTGDIHVEITDASRQT
					1	LCNALKLQPDEGGSSRVIPTCK
						ASRLRIDANFKRFVDEEVLPGT
	1					GLDAAAFWRNFDEIVHDLAPE
						NRQLLAERDRIQAALDEWHRS
	i	l				NPGPVKDKAAYKSFLRELGYL VPOPERVTVETTGIDSEITSOAG
l		1	l		Į.	POLVVPAMNARYALNAANAR
						WGSLYDALYGSDIIP\QEGAMV
	l	1				SGYDPQREAMECP
18347	48715	В	18454	71	4995	SOTOFQREAMECE
18348	48716	A	18455	1	3572	MARKRKSRNNSKIGHGAISRIG
10340	40/10	l^	10433	ľ	3372	RPNNPFEPCRNRYAQKYLTLAL
		l				MGGAAFFVLKGCSDSSDVDND
		l				GDGTFYATVODCIDDGNNADI
		l				CARGWNNAKTAFYADVPKNM
		l				TOONCOSKYENCYYDNVEOS
		l				WIPVVSGFLLSRVIRKDRDEPFV
		l				YNSGGSSFASRPVWVPSSIVIMS
		i	ľ			YGLASYVIAVAFLERDRIQAAL
		l				DEWHRSNPGPVKDKAAYKSFL
						RELGYLVPQPERVTVETTGIDS
		1				EITSOAGPOLVVPAMNAR
18349	48717	A	18456	485	1999	
18350	48718	Α	18457	44	270	
1835I	48719	Α	18458	1	2223	
18352	48720	Α	18459	290	756	
18353	48721	Α	18460	8	314	
18354	48722	Α	18461	2	686	
18355	48723	A	18462	1	732	
18356	48724	Α	18463	1	780	
18357	48725	Α	18464	101	435	
18358	48726	A	18465	805	993	
18359	48727	A	18466	452	2180	
18360	48728	Α	18467	691	1443	
18361	48729	Α	18468	1	320	DPRDCRLKVGKEMFTLFGPQF
						VRELQQRGFDIFLDLKFHDIPNT
					1	AAHAVAAAADLGVWMVNVH
						ASGGARMMTAAREALVPFRPD
L _					L	APLLIA VPV*RSIKASDLVVPL

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18362	48730	A	18469	632	796	
18363	48731	A	18470	129	425	TDIITRQNGTGANIDAIEIIATKA
		ŀ				STGLFVYQPRFARCPRVMSSGY
						HTATRGSSGTRTVRARVCHTA
			1	l		AGVYGSSKQTQF*NRFCQRKCF
						RYPDGCRRA
18364	48732	A	1847I	1	1062	
18365	48733	A	18472	I	996	M DINGSON BIR CHANCEN
18366	48734	Α	18473	1	1004	MLRVYHSNRLDVLEALMEFIV
		1				ERERLDDPFEPEMILVQSTGMA
						QWLQMTLSQKFGIAANIDFPLP
				1		ASFIWDMFVRVLPEIPKESAFN
						KQSMSWKLMTLLPQLLEREDF
						TLLRHYLTDDSDKRKLFQLSSK
					1	AADLFDHVSGASVSSKVEQLR
		1				AQLNERILVLDGGMGTMIQSY
	1				1	RLNEADFRGERFADWPCDLKG
		1			1	NNDLLVLSKPEVIAAIHNAYFE
		1			1	AGADHETNTFNSTTIAMADYQ
		1				MESLSAEINFAAAKLARACADE
		1				WTARTPEKPRY\VAGVLGPTNR
		1				TASISPDVNDPAFRNITFDGLVA
		1		1		AYRESTKALVAGIVLMPAIPAL
18367	48735	A	18474	606	846	WEAEPGGCA
18368	48736	A	18475	3042	3933	GPHPPAPGGPA\CHYDVHQPYL
10500	10,30	1	10475	5012	3,33	RORTEDRATTRHYLAQSFAQYSL
		1				RQWAFHFLLDNITPDIQQIVIAH
		1		İ		TRRTGGFTITASEAAIEMLLCFK
		1				RDFVALQHLFNQIDAPARAVQF
		1		1		IAOKLIGWACCEAARKNOLPH
		1		1		NTTKRSLLMSILYEERLDGALP
		1			3	DVDRTSVLMALREHVPGLEILP
		1				TDEEIIPYQCDGLSAYRTRPLLV
		1		İ		VLPKOMEOVTAILAVCHRLRV
		1				PVMVFPGLRLSREAFLTTAEFG
		i				TOELRRPAOLRLOVYRLLSTAG
						RHHPAQNSPIRVLEVDIDLLGG
		1				TOELWGWKETH
18369	48737	A	18476	869	1639	ICSRCKSTRTSPTRCRKAIKVIL
	1	1				VCFVIRELLVVAPELTIIGLPEG
		1				NWITVSKGMLAKSPVDSNSTQ
						LKEAEEERLKAAOYGLOLVES
		1		1		ONELONOLDKCRNEMMTMTE
		1		1	l	MOLRNKKRRRELGNLIKRFRSG
				1		AESLPDAVVLTTEEGGIFWCNG
		ı		l	1	LAQQILGLRWPEDNGQNILNLL
		1		l		RYP/EVYAISENA*FFSPAQSGA
		1		1		OHRAASGNSRHALYPOTVADG
		1	1			GA*CHANASTGRGAA*LFCQRE
	1	1	ł	i	ı	P*VTYAIDRVTGLPGDDE

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			1	sequence		
18370	48738	A	18477	388	2356	
18371	48739	A	18478	137	318	GGOLSSWAMDFCHL/PAFWNS
1.0371	10737	1.	1.0.,,			MTWHLQRLWGACGYFWHAQ
		1				WERLLTTFEGNEWILIFIGGIL
18372	48740	A	18479	923	1149	WEIGEET IT EGIVE WIELINGGIE
18373	4874I	A	18480	I	373	
18374	48742	A	18481	168	360	
18375	48743	A	18482	1	147	
18376	48744	A	18483	161	440	
18377	48745		18484	277	2172	
18378	48746	A	18485	164	406	LFRREGSYDRYLLMDDYCRRK
183/8	48 /46	I <sup>A</sup>	18483	104	406	DDSYFDRYRDSFDGRGPPGPES
		1	1			
						QSRAKGKVAETVYSYY**NTL
		<del>  _</del>				QKREETNNQYPHLKKG
18379	48747	Α	18486	405	999	
18380	48748	Α	18487	64	288	
18381	48749	Α	18488	159	550	CAVCHISFQDTPVLVSSNVTMQ
		1			İ	FGSKPLFENISVKFGGGNRYGL\
		1				IGANGSGKSTFMKILGGDLEPT
	1	ı				LGNGSLDPNERIGKLRQ\DQFAF
	1	1			ŀ	EEFTVLDTVIMGHKELWEVKQ
						ERDRIYALPEMSEEDGYKVAD
18382	48750	Α	18489	3	481	
18383	48751	Α	18490	2	233	
18384	48752	Α	1849 I	2	3026	SVPTIIFFFLPVLRFWRPGIQQA
	1	1				KKCHLFATGTQSRRNTLRQRT
	1		l			AKGIPQQRMTAKREEISIGILHV
			İ		1	TPQQRRECRGDNRFTARFRRTP
	1					WRLLGHCVSAAVTGVLPAVAG
		ł			1	SPLAYSDTDEFYPVAGGTMSQ
		1				HLPLVAAQPGIWMAEKLSELPS
	į.		l			AWSVAHYVELTGEVDSPLLAR
	1	ļ				AVVAGLAQADTLRMRFTEDNG
1	1	1				EVWQWVDDALTFELPEIIDLRT
	1				i	NIDPHGTAQALMQADLPQDLR
1		1			1	VDSGEPLVFHQTTLGFI
18385	48753	A	18492	2714	3079	RLIGLRMVREFVGLIRRASVAS
1	1	1			1	GSWHCCRMRRKRLIRPKPSILQ
	1	1	1		l	SMLWSPSTRRMFFTLVPIFSIEE
1	1	1	1			LPFTFRSLMMVTLSPSASRLPLA
	1	1	l	I		SLTISSSLSCAGSASFHS*AHSG
		1	l	1		OMYMPLSS
18386	48754	A	18493	I	888	
18387	48755	Α	18494	1778	2025	
18388	48756	A	18495	1	1425	
18389	48757	Α	18496	3	96	FVGRIRRLRRIRRY*FTPLTD*LS
10206	10750	Ļ.	10407	420	955	CAHQVP
18390	48758	Α	18497	420	ככען	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X-Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18391	48759	A	18498	533	1006	RPSIFACVSP*RINHSRIMPQTN AKNAKPNPAQVMRGVISRRRR AMLESNSAITRTPTTSFTMAITS ASSSPPAVKVSICPHGINTPTNIC NTTSCFRLIPHFMTPKPLPLYSE SGPSCSSCSASARSNGSLPISIKV ANAQAQSASTSGMLWLSGQ
18392	48760	Α	18499	3	418	EWHYLSADRRQCAFQOVSRKT ATVCHHPVDYYAGSLYRLYFT DRLRARLAGHAAES/OTPASHA VFQLVLE*L*SPLFSPVSTSGGR TANSTVLIMKSCMSGAVERQPT NWQAILMFLIFVVFTLGITYWA SNAYVLAG
18393	48761	С	18500	63	500	
18394	48762	A	18501	1	1107	
18395	48763	Α	18502	1	153	
18396	48764	Α	18503	88	510	
18397	48765	Λ	18504	204	654	
18398	48766	Α	18505	241	771	
18399	48767	Α	18506	1655	1909	
18400	48768	Α	18507	2	48	
18401	48769	Α	18508	1	585	
18402	48770	A	18509		723	LQPPGRRWAPAVSGLSRQVV SVIEGRYATAL\YYAASRQNKL EQVEKGILLRVAQILEGTYEWA SAVLESPMLAFPLEVKEPK ITTAKVGGSLPLTYQTILNFALL ENGSP*GNYPESPSGLFLTYGTLNFALL GVFHSRERVPCTVITSGIFL*EG RPQFSEFKNCSSRGFLRSRAKFL KLGAKYTDPSILGGMIVRIGEL KYDMSVKTKIQKLGRARREI
18403	48771	Α	18510	400	894	
18404	48772	A	18511	1	1023	DROLAWOTHON OT A WAY OF THE
18405	48773	Α	18512	73	424	RPGMWSTRSPNSTA WPLSLEPD PGMASACTTMHTTTIAEPDPG MSGWPDGRMETSSPTIMDIVVI *CAIAAEAIVLVSLLFVMLRYM YRHMGTYHTNEAKGTGVADS ADACPAGDPA
18406	48774	A	18513	141	563	RPGMWSTRSPNSTAWPLSLEPD PGMASASTTMHTTTIA\EPDPG VSIGLP\DGRMETPTPHP*LTMV VIAGV\IACL\WPFVLSLPSSFVM VALTLLTGHK\GARTTPNEAKG\ TEFAES\ADAALQ\G\DPAL\\QDA \GDSSRK\EYFI

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
18407	48775	A	18514	182	935	QAFELHCPCRPKFSTLPSPAWPF
						RHTDLRKRGRRTAQ*YAGNES
	1			i		HPPSLPRYLRRSRH/SRMQAPSS
	1			l		TCSYSHTSLQCSPAPQNH/AQHF
	1					*PALEELACG/SPSVSSPYLVLSS
	İ					CQEQPHHCCPPSTPRPSW/CPSS
				1		GDAICYSPGQ/CPRSRGPLP\EDS
						SDSPPAEQVLPPSSGSHNTLYLR
						CKRFSAFILNCEPPSK\C*KPGHR
	1	1				CRS*AGILTLLPPG/ERGP/GDGP
						CSTGRQSASKTPPPPSHPHTGHS
						LWSEEK
18408	48776	A	18515	48	676	KARLTWQQTREESLCRETPPYK
						TIRSRETYSLPREQHGKDLPP*F
	ı					NYLPPSPSHNTICPG*QDQGRFT
					1	Q\PLYLRCKRFSAFILNCEPPSK\
l						C*KPGHRCRS*AGILTLLPPGGE
		ļ	1			AQHFKVKHPSIPL/REGGEVGIK
		1	1			PKKTSPGTELLMQP/CHQPSPRT
	İ	-				CQPAPRKSNRP/LGCLSPLMKHS
						TLGYLLWLQKAIWLKGFGTSG
		L.				W*M*GRFHL
18409	48777	A	18516	86	92	TANAALHQPSPRTCQPAPRKSN
				1		RPQAA*ALNC
18410	48778	В	18517	1	2031	
18411	48779	A	18518	98	367	DLFLYLSWQHCHPYSHCHPNQ
	1	1				KPGRFLMKLSS\ETVTIELKNGT
		1				TRSHGT\IHQVWDVQ\MNTH\L
	1	1	1			KAVKMTLKNREPVQL\ETLSIR
						GNNIR\YFILPD/SVYPLDTLLVD
		1				VDPKVKSKKREAVAGRGRRRG
		ـــ	L			RG/TRDVARGR*RGNNIR
18412	48780	A	18519	1	310	
18413	48781	A	18520	37	136	RRRPSSSWALPPSRGPSST*AER
L	ļ	١		<u> </u>	205	GAQHQQPVPA
18414	48782	Α	18521	3	305	FFTLCLQWGLFSCESPICSGVGR
		1	1			YWA*VCLCFLQIEAIELPMDPK
	1	ı				LNKRRGFVFITFKEEEPVKKVL
	1	1				EKKFHTVSGSKVRCSQLCLASC
		_	I			AAGELALRGMG
18415	48783	В	18522	249	367	
18416	48784	Α	18523	1	1008	
18417	48785	В	18524	17	835	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
18418	48786	A	18525	2	1188	SLIKLNSPPPRGGGTARYGAWL
						LVGGFPCGGGQGGDTVGAAP
i	ĺ					WADWGEASAAASFDVLAEAC
						ARLSSLRVGDEAGSRGVIWRAR
						SPPRLGLALSEAG\EE\QPMETT
		1				GASENGHEAVPE\ASR\GRGCW
1						TPLRRGLEARPRRPRAGIRTAPR
ł						D/QRINASKNEEDAGKMFVGGL
				ŀ		S\WDTSKKDLKDYFTKFGEV\V
		ļ				DCTIKMDPNT\GRSRGFGFILFK
				1	,	DASSV*K\VLDQKEHRLDGRVI
				1		DP\KKAMA\MKKAPVKKIFVGG
		i				LNPESPTEEKIRESFGEF\GEIEAI
						ELPMDPKLNKRRGFVFITFKEE
1		i		ŀ		EPVKKVLEKKFHTVSG\SKCEIK
				l		VAQPKEVYQQQQYGSGGRGN
		1		İ		RNRGNRGQ/GGGGGGG*GQGS
			l			TNYG\KTQ\RRGGHQ\NNYKPIL
						EAGRQERPT
18419	48787	A	18526	3	784	
18420	48788	Α	18527	3	1990	PAMNGLSLSELCCLFCCPPCPG
		1				RIAAKLAFLPPEATYSLVPEPEP
l .		1		ŀ		GPGGAGAAPLGTLRASSGAPG
		ŀ				RWKLHLTERADFQYSQRE\RST
i		l				IEVFPTKSARGNRVSCMYVRCV
1		l				PGARYT\VLFSHGNAVDLGQMS
1		l				SFYIGLGSRLHCNIFTYDSSGYG
		l				ASSGRPSERNLYADIDATWQAL
1		l				RTR*GRPLVGRVRARWRPRLTL
1		l				LRRRQVRHQPGQHPSCTGRSIG
						HGAHRGTWPRATSVPRWCCTR
		1			ł	RSTSGMRVAFPDTQERPTASTP
	1		1	I	1	FPYIRERCPRLTSPRAHHPTGTK
1	l				1	DEVIDFLEAGWRSTRRCHQGG
1		l				GAAVGGGGPGHNDIELYSQYL
		_				ERLASLSFSQELPSQRA
18421	48789	Α	18528	82	406	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first eodon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18422	48790	A	18529	2	1474	ARASGSSSSGQGKMGOSQRG GHGSGGGKKDDKDKKKXYEPP VPTRVGKKKKKTKGPDAASKL PLVTHPHOCRLKLLERIKDY LLMEEEFIRNQEOMKPLEEKQ EEFRSKVDDLKGGFRLSVGNL KSFLDNHAUVSTPVQSEN KVEKAPGDYLDKOGFLSVGNL KVHAVIGVLMGDTDPLVTVM KVHAVIGVLMGDTDPLVTVM KVHAVIGVLMGDTDPLVTVM KVHAVIGVLMGDTDPLVTVM KVHAVIGVLMGDTDPLVTVM FORWILLSFVDENGLENDQN EIKESVELPLTHPEYVEEMGIP FGKVILLVPPGTGKTELPKAP FGKVILLVPPGTGKTELPKAP FGKVILLVPGTGKTELPKLAP FGKVILLVPGTGKTELPKLAP FGKVILLVPGTGKTELPKLAP FGKVILLVPGTGKTEVDSNSGGER EFQRTMLELLNGLUGFDSNG DVKVIMPTNIETLDPALIRP PAFDRKYEFPLCPDEKTKKRIF QISHKS/RMTLADVGTPWTTLI MAKDDLSGA*PSKANCTEAGL MALRENRRMKYPNEDFKKS KENVLYKKGCGTPEGVVSLM
18423	48791	A	18530	2	274	PWLVIRKMVGRFLNP WQDLICRMAASVKEQSTKPIPL PQSTPG/ESHSLSTSGKSEVRDL FVAEROFAKEOHTDGTLKEVG
18424	48792	A	18531	3	844	EDYQIAIPDSHLPVSEERWALD ALRN

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SEQ ID	SEQ ID NO:		SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=1)nknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
8425	48793	A	18532	261	2814	VRFRNLIRIYCNIKICAVSHCPP
		l				KVFKLNSLFFLHRFDSVAFGES
		1				OSEDEOFENDLETDPPNWOOL
		l				VSREVLLGLKPCEIKRQEVINE
		1				FYTERAHVRTLKVLDOVFYOR
		1				VSREGILSPSELRKIFSNLEDILG
	ŀ	l				LHIGLNEOMKAVRKRNETSVII
		1				QIGEDLLTWFSGPGEEKLKHA.
	İ	ı				ATFCSNOPFALEMIKSROKKDS
		l				RFQTFVQDAESNPLCRRLQLKI
		ı				HPTOMORLTKYPLLLDNIAKY
		l				EWPTEREKVKKAADHCRQILN
	1	1		ŀ		FVNQAVKEAENKQRL/EEDYQ
		l		l		RRLDTSSL\KLSEYPNVE\RLRN
		1		l		MDLTKRKMIHEGPLVWKVNR
		l				DKTIDLYTLLLEDILVLLQKQD
		i		1		DRLVLRCHSKILASTADSKHTI
		ı				SPVIKLSTVLVRQVATDNKALI
		l				VISMSDNGAQIYELVAQTVSEI
		l				TVWQDLICRMAASVKEQSTKI
		l				PLPQSTPGEGDNDEEDPSKLKE
		ı				EQHGISVTGLQSPDRDLGLEST
		l				LISSKPQSHSLSTSGKSEVRDLF
		l				VAERQFAKEQHTDGTLKEVGI
		l		l		DYQIAIPDSHLPVSKE\RRALDA
		l		l		LRNLGLLKQLLVHQLGLTEKS
		l				LENWQHFPRYRTAFQGPQTDS
		l		l		VIQNSENIKAYHSGEGHMPFR
		l				GTGDIATCYSPRTSTESFAPRD
		1				VGLAPQDSQASNILVMDHMIN
		1				TPEMPTMEPEGGLDDSGEHFF
		1				AREAHSDENPSEGDGAVNKEE
18426	48794	Α	18533	90	383	ILQLHSSGPCLLWL*LSFRSLST
		1	l			TAV/CQCCRPAADFHPSGSSRV
		l			1	AVLLIQ/HRRPLPLPIGLKACYF
		1				ALSLQTSLTCLGLVVLLDFPKE
		1				AASLDKV
18427	48795	A	18534	ī	456	
18428	48796	A	18535	830	1092	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18429	48797	A	18536	391	1824	GSGADASGFISDAGLIFKKASSK GPKRLEKFSDERAAVFRCYHKL FLLFSSLCYGTYHLVVLPTLKP REDEDWISLCLRIFCLMOKDTH SMLGECGERREGKKOKTGALG SSLSLEDAKHLLPFIPALPFSWN ALPODLCNVFKLLWDYRIRVD FSPIAGTLIKBUTDPOGGESHVN FGRIWSDTIKSORCQGLRQPPDR PIPILLMYKGQHVWPSQLDKAG IGEVTELNNYKNVARLPKSTKK HAIGIYFNDDTSKTFACESDLEA DEWCKVLQMECVGTRINDISL GEPDLLATGVERGESERFNV YLMTSP*LRMLHGIECALQVIT YLEYICLWGRGTPWFNYQAGR MCQTGEGLFIPQTRDGEAIYQK VHSIAALAIAEQHERLLGSVKN SMLQMKMSERAASLSTMVPLP SKAYWGMITGHSTGOLYVLO
						DVSSPLKLHRTETFPSLQDS
18430	48798	С	18537	22	620	
18431	48799	A	18538	48	413	EDSKSKTISHPWRDCGDYCHH QGLERCRGGDSHHTPVQLS*LA CAED\NKSWRMT\GIIVSLTKC* LQMQLLYQMWFHCLSKLTHLL GISTLQLCVTILFREILITFPLHKI SHWSITLMTLR
18432	48800	Α	18539	23	124	QWVIISLTKW*LQLQLLYQMW FHCLSKLTRLLP
18433	48801	Α	18540	I	1860	
18434	48802	A	18541	209	3816	QGPTFRERKYREHHKDTPREE QLQDT*SSDSPKLK*RKKC*GQ PERKYKLPTKGSPSD*KKISRQ/ KTLQARRQSWFFEKINKIDRQ ARLIKKKREKNQIDTIKNDEQ ARLIKKKREKNQIDTIKNDEQ EVESVNRPTGSEIEATINSLPTK KSPGPDGFTAEFYQRYKEELVP FLLKLPQHEKEGILPNSFYEASII LIPKPGRDTTKKGNFRISLMNI DAKIL
18435	48803	Α	18542	1	1521	
18436	48804	В	18543	1	2265	
18437	48805	В	18544	1	1716	
18438	48806	Λ	18545	1	1704	
18439	48807	A	18546	1	3618	
18440	48808	A	18547	1	3087	

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	eodon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
		<u> </u>				
1844I	48809	Α	18548	277	350	SPVEKELKLWKNRHKLLSC*W LTC
10110	10010	١.	10540	107	422	
18442	48810	Α	18549	197	422	IVNKVVLPQGGPASPSLKGFWV
		ı				YKLAQVWKLIEGP*FPIFIIQISL
		1				LSI*PRSFLFV*IK*ECSRLPISFTS SGR
10440	48811	١.	18550	1	3171	MVKGSIQQEELTILNIYAPNTG
18443	40011	Α	18330	['	31/1	APRFIKOVLSDLORDLDSHTLI
		1				MGDFNTPLSTLDRSTRQKVNK
		1				DTQELNSALHQADLIDIYRTLH
		1				PKSTEYTFFSAPHHTYSKIDHIL
		1				GSKALLSKCKRIEHTNYLSDHS
		1				AIKLELRIKNLTOSRSTTWKLN
		1				NLLLNDYWVHNEMKTEIKMFF
		1				ETNENKDTTYONLWDAFKAVC
		1				RGKFIALNAYKRKEERSKIDTL
		1				TSQLKELEKQEQRHSKPSRRQE
		1				ITKMRAELKEIETO
18444	48812	la	18551	209	2432	QGRPTFRFRKYREHHKDTPREE
10.111	1.00.2	ľ	1.000.			OLODT*SSDSPKLK*RKKC*GO
		1				PERKVKLPTKGSPSD*KRISRQ/
		1				KTLOARROSWFFEKINKIDRPO
		1				ARLIKKKREKNOIDTIKNDKGD
						ITTDPTEIQITIREYYKHLYANK
						LENLEEMDKFLDTYTLPRLNQE
		1				EVESVNRPITGSEIEAITNSLPTK
						KSPGPDGFTAEFYQRYKEELVP
		1				FLLKLFQPIEKEGILPNSFYEASII
						LIPKPGRDTTKKGNFRPISLMNI
						DAKILNKILANQIQQHIKKLIHH
		1			i	DQVGFIPGMQG\WLEVLARA/IR
						QEKEIKGIQLGKEEVKLSLFAD
		1				DMIVYLENPTVSAQNLLKLISN
		1				FSKVSGYKINVQKSQAFLYTNN
						RQTESQIMSELPFTIASKRIKYL
		1				GIQLTRDVKDLFKENYKPLLNE
		1				IKEDTNKWKNIPCSWIGRINIVK
		1				MAILPKVIYTFNAIPIKLPMTFFT
						ELEKTTLKFIWKQKRSHIAKSIL
		1			1	SQKNKAGDITLPDFKLHYKATV
		1			ł	TKTAWYWYQNRDIDQWNTTE
		1	i		1	PSEIMLHIYNHLIFDKPDKNKQ
		1				WGNDSLFNKWCWENWLAICR
			l	1		KLKLDPFLTSYTKINSRWIKDL
1		1		1		NVRPKTIKTLEENLGNTIQDIG
		1	l	1		MGKDFMSKTPKAVATKAKIDK
		1		1		WDVIKLKSFCTAKETTIRVNRQ
		İ		1		PTEWEKIFATYSSDKGLISRIYN
		1				ELKQIYKKKTNNPIKKWAKDM
L	L	L	L	L		NRHFSKEDIYAAKRHMKKCSSS
18445	48813	Α	18552	1	3255	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleatide insertion)
				sequence		
18446	48814	A	18553	li .	3139	
18447	48815	Α	18554	I	3210	MVKGSIQQEELTILNIYAPNTG
					1	ALRFIKQVLRDLQRDLDSHTIIM
						GDFHTPLSTLDRSTROKVNKDI
						QELNSALHQEDLIDIYRTLHPKS
						TEYTFFSAPHHTYSKIDHIVGSK
				1	1	ALLSKCKRTEHTNCLSDHSAIK
	ł					LELRIKNLTONRSTTWKLNNLL
						LNDYWVHNEMKAEIKMFFETN
					l	ENKDTTYQNLWDTFKAVCRGK
						FIALNAHKRKOERSKIDTLTSOL
						KELEKQEQTHSKASRRQEITKIR
						AELKEIETO
18448	48816	Α	18555	I	3345	
18449	48817	В	18556	1	3127	
18450	48818	Α	18557	1	3325	
1845 I	48819	Α	18558	I	3145	
18452	48820	Α	18559	I	548	
18453	48821	A	18560	I	3229	
18454	48822	Α	18561	I	3352	
18455	48823	Α	18562	I	1965	MGDFNTPLSTSDRSTRQKVNK
					1	DTQEMNSALHQADLIDIYRTRH
	1					PKSTEYTFLSAPHHTYSKTDHIL
1						GSKALLSKCKRTEMITNYLSDH
						SAIKLELRIKKLTQNCSTTWKL
						NNLLLNDYWVHNEMKAERKM
						FFETIENKDTTYQNLWDAFKAV
						CRGKFIALNAHKRKQERSKIDT
						LTSQLKELEKQEKTHSKTIRRQ
		1				EITKIRAELKEIETQKTLQKINES
						RSWFFERINKIDRTLARLIKKKR
l						EKNQIDRIKNDKGDITTDPTQIQ
	l					TTIREYYKHLYANKPENLEEMD
1	1					KFLDTYTLPRLNQEEVESLNRPI
	1					SGSEIVAIINSLPIKKSPGPDGFT
ŀ						AEFYQSYKKELVPLLLKLFQSIE
					1	KEGILPNSFYEASIILLPKRGRDT
					I	TKKENFRPISLMNIDAKILNKIL
	1				l	AKRIQQHIKKLIHHDQVGFIPG
ŀ						MQ\GIKYLGIQLTRDMKDLLKE
						NYKQLLNEIKEDTNKWKNIPCS
1		1				WVGRINIVKMAILP/KELEKTTL
		1			1	KFIWNQKRACIAKSILSQKKKA
					1	GGITLPDFKLYYKATVTKTARL
					1	YTKHGTSICCGSFGELLPMQKA
		1			1	KRELAHHMAKAGARVKGQLG
	1	1			1	HVTQHQLGSIEWFNKYSLSTYY
		1				TVDTKPQFSHPTKDNKTGLTCR
		1			I	NRTTVGVDLQAKGNLVVKHLS
l		L	L	<u> </u>	L	SLQHCYEFICHI

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
18456	48824	Α	18563	1	3099	MGELITPLSTLDRSTRQKVNKD
						TQELNSALHQGDLIDIYRTLHP
						KSTEYTFFSAPHHTYSKIDHILG
						SKALLSKCKRTEIITNYLSDHSA
	1		ŀ	İ		IKLELRIKNLTQNRSTTWKLNN
	1					LLLNDYWIHNEMKAEIKMFFET
			l			NENKDTTYQNLWDAFKAVCR
						GKFIALNAHKRKQERSKIDTLT
						SQLKELEKQEQTHSKASRRQEI
ĺ						TKIRAELKEIETQKTLQKINESR
						SWFFERINKIDRPLARLIKKKRE
						KNQIDTIKNDK
18457	48825	A	18564	1	3253	MGDFNTPLSTLDRSTRQKVNK
						DTQELNSALHQGDLIDIYRTLH
	ľ					PKSTEYTFFSAPHHTYSKIDHIV
						GSKALLSKWKRTEIITNYLSDH
						SAIKLELRIKNLTQSRSTTWKLN
						NLLLNDYWVHNEMKAEIKMFF
						ETNENKDTTYQNLWDAFKAVC
						RGKFIALNAHKRKQERSKIDTL
						TSQLKELEKQEQTHSKASRRQE
						ITKIRAELKEIETQKTLQKINESR
						SWFFERINKIDRPLARLIKKKRE
		$oxed{oxed}$				KNQIDTIKNDK
18458	48826	Α.	18565	1	3095	
18459	48827	Α	18566	2	2678	

SEQ ID	SEQ ID NO:	Met		Nuclcotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop eodon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
18460	48828	A	18567	1	2478	MKAEIKMLFETKENKDTTYQN
10.00	10020	ľ	10001	ľ		LWDALKAVCRGKFIALNAHKR
			l			KQERSKIDTLTSQLKELEKQEQ
		1				TLSKASRRQEITKIRAELKEIET
		l		l		OKTLOKINESRSWFFERINKIDR
				1		PLARLIKKKREKNOIDAIKNDK
			l	l		GDITTOPTEIOTTIREYYKHLYA
				l		NKLENLEEMDKFLDTYTLPRLN
				l		QEEVESLNRPITGAEIVAIINSLP
				l		TKKSPGPDGFTAEFYQRYKEEL
						VPFLLKLFQSIEKEGILPNSFYE
				1		ASIILIPKPGRDTTKKENFRPISL
	1		ŀ	1		MNIDAKILNKILANRIQQHIKKL
						IHHDQVGFIPGMQGWFNIRKSI
			l	1		NVIQHINRAKDKNHMIISIDAEK
		1	l			AFDKIOOPFMLKTLKKL\EIKYL
	İ					GIQLTKDVKDFFKENYKPLLKE
	ĺ	İ				IKEDTNKWKNIPCSWVGRINIV
						KMAILP/KELEKTTLKFIWNQK
				l		RACIAKAILSQKNKAGGITLPDF
l			i	1		KLYYKATVTKTAWYWYQNRD
			l	ł		IDQWNRTETSEITPHIYNYPIFD
				ł		KPEKNKQWGKDSLFNKWCWE
l	ļ	1	ł		-	NWLALCRKLKLDPFLTPYTKIN
		1	i	l		SRWIKDLNVRPKTIKTLEENLGI
						TIRDIGMGKDFMSKTSTAMAT
ĺ	l			l	1	KAKIDKWDLIKLKSFCTAKETT
	l					IRVNRQPTKWEKIFATYSSDKG
						LISRIYNELKQIYKKKTNNPIKK
				l		WAKDMNRHFSKEDIYAAKKH
	ļ					MKKCSSSLAIREMQIKTTMRYH
				1		LTPVRMAIIKKSGNNRTPTRPIQ
18461	48829	В	18568	1	3403	
18462	48830	A	18569	2	2976	APRFIKQVLSDLQRDLDSHTIIM
		l				GDFNTPLSTLDRSTRQKVHKDT
						QELNSALHQADLIDIYRTLHPK
						STEYTCFSAPHHTYSKIDHIVGS
				i i		KALLSKCKRSEIITNCLSDHSAI
				i		KLELRIKKLTQNRSTTWKLNNL
		ŀ		1		LLNDYWVHNEMKAEIRMFFET
			İ			NENKDTTYQNLWDTFKAVCRG
						KFIALNAHKRKQERSKIDTLTS
						QLKELEKQEQTHSKASRRQEIT
			l			KIRAELKEIETQKTL\QKINE\SR
L				L		SWFF\ERINK
18463	48831	Α	18570	472	829	AIASESASPKAWQLPCGAAQQF
				l		AALPGLGNYKFPLTLITGYGSN
		1		I		KSPP*GYLVFQTYSSLPLLRLPP
		1	1	l		GHFGFLLPLSQ\RLRRELQCWL
				l		G*LTQTIKMKSVYHSTTEVRKS
1	ı	1	I	ı	I	MHGIQEIH

			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN 09/540,217	location of first	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/540,217	codon for peptide sequence	or pepude sequence	deletion, (=possible nucleonae insertion)
18464	48832	В	18571	1	2293	
18465	48833	Α	18572	1	3810	
18466	48834	В	18573	1	4107	
18467	48835	В	18574	87	3161	
18468	48836	A	18575	1	3192	
18469	48837	Α	18576	1	1983	
18470	48838	A	18577	1	3156	
18471	48839	В	18578	1	3471	
18472	48840	В	18579	ı	2337	
18473	48841	Α	18580	1	3852	
18474	48842	A	18581	1	3057	
18475	48843	A	18582	1202	2004	SGIYMIGFEOVLKAOPPLSSPNO PMNKVATVVGMEVMHOLSNM DFHSRRLTWLRPLPGFTGPG/Y QGVKVEVAPLITITSDPLAKFL LLISATSTSLEVTVPEGEMLPPR DTTKIATFGTOTGFLAU,CLADG LWDLVIIPGKGKPSRDLVESPS PYSTYEGIDGWPDEPAPTATKP PVMPAPALPPDTRSGSKAPTVP TYPYOMEHHQVQLASNNSNTE ALGHLSPQSSWVQTPGQNSGP AIPNHLGKDMISPPQMAPAGVK WESQKY
18476	48844	A	18583	1	2832	
18477	48845	A	18584		3702	MQKKHDKIRNSFMIKTLKLIKT EGIYLNTIKATYKKPITNIILNGE NQKAFALRSOTRFWILALCQM SRLRKLTNYISDHSAIKLELRIK NPTQSRPTTWILNNLLINDYW VINEMKAEIKMFFETNENDT TYONL WDAFKA VCRGKLIALN AHRKQERSKIDTLTSQLKELE KQEQTHSKASRRQEITKIRAEL KETETQKTLQKINESRSWFFER NKIDRPLARLIKKKREKNQIDTI KNDKGDRITARLIKKKREKNQIDTI KNDKGDITTDPT
18478	48846	Α	18585	1	3139	
18479	48847	Α	18586	2	2918	
18480	48848	В	18587	1	3242	
18481	48849	Α	18588	1	3640	
18482	48850	Α	18589	371	522	
18483	48851	В	18590	1	3918	
18484	48852	A	18591	1	3057	

SEO ID	levo m ve	INC.	SEQ ID NO:	[Marchaelide	Nucleotide logotion -61	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
NO.	sequence	nou	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1	bequence	l		sequence		
1						
18485	48853	Α	18592	1	3233	MGKKQSRKTANSKKQSTSPPP
	l					KEHSSSPATEQSWTENDFDELR
						EEGFRRSNYSELREDIQTKGKE
						VENFEKNLEECITTITNTEKCLK
1			l			ELMELKAKAOELREECRSLRSR
1		1	1			CNOLEERVSAMEDEMNEMKRE
	l					GKFREKRIKRNEQSLQEIWDYV
	l		1			KRPNLRLTGVPESDGENGTKLE
				i		NTLODIIOENFPNLAROANIOIO
1		1	1			EIQRMPQRYSSRRATPRHIIVRF
		1	1			TKVEMKEKMLRAAREKDRSTR
1						OKVNKNTOELNSA
18486	48854	Α	18593	965	4165	TWKGTTSTSRCKIMPKYRSTRQ
10400	40034	Α.	16393	903	4103	KVNKDTQELNSALHQADLIDIY
		l				RTLHTKSTEY/TFFSAPHHTYSK
				İ		IDHIVGSKALLSKCKRTEIITNY
						LSDHSAIKLELRIKNLNQSRSTT
		1				WKLNNLLLNDYWVHNEMKAE
1						IKMFFETNENKDTTYQNLWDA
		1			ŀ	FKAVCRGKFIALNAHKRKQERS
İ		1				KIDTLTSQLKELEKQEQTHSKA
						SRRQEITKIRAELKEIETQKTLQ
						KINESRSWFFERINKIDRPLARLI
						KKKREENQID
18487	48855	Α	18594	1	5093	MEGEMNEMKREGKFREKRIKR
1						NEQSLQEIWDYVKRPNLRLIGV
1						PESDGENGTKLENTLQDIIQENF
						PNLARQANVQIQEIQRTPQRYS
		1				SRRATPRHIIVRFTKVEMKEKM
						LRAAREKDRSTRQKVNKDTQE
		1				LNSALHQADLIDIYRTLHLKSTE
		1				YTFFSAPHHTYSKIDHILGSKAL
1		1				LSKCKRTEIITNYLSDHSAIKLE
1		1				LRIKNLTQNRSTTWKLNNLLLN
1		1				DYWVHNKMKAEIKMFFETNEN
						KDTTYQNLWDTF
18488	48856	Α	18595	1	131	
18489	48857	Α	18596	5382	9269	RAKSPANIIMTGSNSHITILTLN
		1			1	VNGLNSPIKRHRLASWIKSQDP
					1	SVCCIQETHLMCRDTHRLKIKG
						WRKIYOANGKOKK\AGVAILVS
				l		DKTDFKPTKIKRDKEGHCIKVK
		I		1	1	GSIQQEELTILNIYAPNTGAPRFI
1	İ	1			1	KOVLSDLQRDLDSHTLIMGDFN
1	1	1			I	TPLSTLDRSTRQKVNTDTQELN
1		1	1	1	1	SALHQADLIDIYRTLHPKSTEYT
1		1			1	FFSAPHHTYSKIDHIVGSKALLS
1		1		1		KCKRTEIITNHLSDHSAIKLELRI
				1	1	KNLTQS
18490	48858	A	18597	1	312	10.123
10490	40020	ΙΑ.	11037/	1'	1312	

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				- Cancille		
18491	48859	Α	18598	142	876	RKKGILPPKESLKELEEEAEEEQ
						RILQQSVVKTYEDMTLEELEDH
						EDEFNEEDECAIEMCRQQRLAE
						WKATKLKNKFGEVLEISGKDY
				ĺ		VQEVTKA/ERRALWVI\LHLYK
						QGIPLCAL\VNQHLSWTLPGSFP
			İ			DVKFIKAISTTCIPNYTDRNLP\T
						ILVYPGRRYQGLSLLVLWCLAG
					l	MNPDQEMSWEWKLSESGAIMT
		l			ĺ	DLEENPKKPIEDVLLVLSAALW
						SS*RGDSDSEGDLRATASITCRT
18492	48860	Α	18599	1	2310	
18493	48861	Α	18600	3	1124	LYNRRRRRRCSHCRHRCRRLSS
						GLRKEEVISLGASLGRVFVPCSP
						PTVSAARGPTGAPGGPNSKPLS
			i			GCCDDGFNLGRQQWGNPLPFC
					l	SKTISSSLHWTWSQVNLVEILP
			ł			AIFSSFLNLQHVNLWFLAAAM
						KAVTEQGHELSNEERNLLSVA
			l			YKNVVGARRSSWRVISSIEQKT
			İ			ERNEKKQQMGKEYREKIEAEL
		1				QDICNDVLVRGQCFCFEQWFL
		l				NSINLMYKCRLSNYFRYLSEVA
1						SGDNKQSK*YL*KEIRPVMEPV
				l		FFHRDFLTILIRLGLALNFSVFY
						YEILNSPEKACSLAKTVRKTLC
						DI*P*QNSACVINFILFLNILRDN
						LTVSTTSTGFIVSFLFTYLIIHCY
						LQEGICTIKCSYSFKLLNLL
18494	48862	Α	18601	340	1323	AARPQKRHNNHSSLLTGSHIH
						WKRGRVQNIIADVLQFCLYLLT
						VLFVPCSPPTGMTMDKSELVQ
						KAKLAEQAERYDDMACSSERH
						VTEQG\HE\LSNEEKKSCSLVAY
						K\NV\VGARRFLPGRVISSI*A*K
						QRRNEKKAADGQKSTREKIEG
1						RTCRTFCN*CFWELLGQISLFPN
1						ATQPRKVKVFYFEK*KGDYF\R
						YLF*KWQS*RQQTQPTCVGTSP
						ARAYPGSNLKI*LRKKMQP\TH
1						PNSVLVLAPKFPQSFYYEI\LNSP
1						\EKGLVSLGKNGHFD*SNLLNL
1						DTLEWKSLIKDSTSDSWQLLR\
10405	10062	ļ	10600	22	20	DN\LTLWDIRKTRGDEGDAGEG
18495 18496	48863 48864	A B	18602 18603	33 167	89 232	
10496	40004	ь	18003	107	232	

SEQ ID NO:	SEQ ID NO: of peptide		SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
NO:	sequence	noa	09/540,217	eodon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
18497	48865	A	18604	14	600	MAELAPASPSDIKASVSNGDTT
						LLCSRRQSCGMNEVRQVSLTYI
						GSPAPSHSLPLQPRSGGSLCPSR
		1				AW/PDPHQLFDDTSSAQSRGYC
		l				AQRAPGGLSYPAASPTPHAAFL
						ADPVSNMAMAYGSSLAAQGK
	l					ELVDKNVSGRGWWEWGDARC
						HRASDLSSASPD\HRFIPITKLKY
		_				YFAVDTMYVGRKLGLLFFPYL
18498	48866	В	18605	1	1230	
18499	48867	В	18606	41	931	DEPOSITOR DE CASO CONTRA CONTR
18500	48868	A	18607	3	166	PRPFPKSRLPPGIIGGEYD\QRPN
						PILP\GRGGPNDRFPF\RPSRGRP
	10010	<u> </u>	10000	2.0	1007	TDGRLSFM
18501	48869	A	18608	212	1881	CLRVLLLKRTWPVEVPETGARF
	ļ		İ			/TGGILRSH\LRQSLLCT\WGYSS
		1				NTRFTITLNYKDPLTGDEETLAS
						YGIVSGDLICLILQDDIPAPNIPS
		ı				STDSEHS\SLQNNEQPSLATSSN
		1				QTSMQDEQPSDSFQGQAAQSG
		1				VWNDDS\MLG\PSQNFEAESIQE
						NAHM\AEGTGFYPSRTPCSW*L
						NPVEGQVP\HSLETLYQLADCS\
						DANDALIVL\IH\LLMLESGYIPQ
		l				GT\EAKALSMPEKW\KLSGVYK
		1				LQYMHPLCEG\SSVT\LTCVPLG \NLIVVNATLKINNEVRKC*KGC
		1				SLLPESF\ICKEKLGENVANIYK
		1				DLOKLSRLFKDOLAHPLLAFTR
		1				OAL\NLPDVFGLVVLPLELKLRI
		1	ŀ			FRLLDVRSVLSLS\AVCRDLFTA
	1	l		l		SNDPLLWRVFYICVNFRDNTV\
		l		{		RVQ\DTDWERTVQGRRAHTKE
		l				KESPKGRVLWMLLAIROTH\TIP
		ŀ				FYSQPLWHPRGHFPKLPAFPPGI
		Ι.	l	1		YSGGWNMDQR\PTFPYVGRTQ
		1 :	1			SSSLNSWVLGETPKPSFLPLRPR
			İ	1		FDPVWPHFPGP*PPSLPRARAGE
	ŀ					NDQISPFRPQQGSGQLIGRLSIH
18502	48870	Α	18609	1	1065	THE QUELTIA QQUE OQUI OTTO THE
18503	4887I	A	18610	1	1513	
18504	48872	A	18611	1	2247	
18505	48873	A	18612	3	421	
18506	48874	Α	18613	1	103	
18507	48875	Α	18614	3	435	
18508	48876	Α	18615	268	501	QLECIPGTWELWKEEQERAMA
		I			l	GGGLKKIISATEKKLARMLLAP
			1	l		SASWCCSGP*VFHGST*WGKPG
	1			l		PVSVSLLQGVLGK

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon fur peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
18509	48877	Λ	18616	3	296	EAMEAVILTCDPATPAASYQW
		1				WMNGQSLPMTHRLQLSKTNRT
		1				LFIFGVTKYIAGPYECEIRNPS*V
		1				PAASDPVTLESPPLLFNGLATTE
		1				TLRKRGNP
18510	48878	Α	18617	3	1464	GAVRTWGRGFQTEKCQASLLN
						FWNPPTTAQVTIEAEPTKVSKG
		1				KDVLLLVHNLPQNLAGYIWYK
120						GQMKDLYHYITSYVVDGQIIIY
						GPAYSGRETVYSNASLLIQNVT
		1				REDAGSYTLHIVKRGDGTRGET
		1				GHFTFTLY\LIPWTLLYL*RSLA
		1				QVSHYETPGKTAPPCGSTA**L
		1				N*PPDLTLFSPVLFLLKYPVPGQ
		1			i	AFQYPKGLKTIGSSITHL*DVLG
		1				KGSCRENIPRAAK*D*N*EDSST
						ACSK*GPQVETPKPSISSSNLYP
		ı				REDMEAVSLTCDPETPDASYL
		1				WWMNGQSLPMTHSLQLSKNK
						RTLFLFGVTKYTAGPYECEIRN
		1				PVSASRSDPVTLNLLPKLPKPY1
		1				TINNLNPRENKDVLAFTCEPKS
		1				EN\YTYIWW\LNGQSLPGSVPR
		1				VKRPI\ENRVLIFTPCSRGIETG\P
		1				Y\QCEI\RDRYGGHPQLPSHPGM
		1				SSITTKHSGLYACSVRNSATGM
						ESSKSMTVKVSAPSGTGHLPGL
18511	48879	A	18618	79	1516	
18512	48880	В	18619	96	1730	FOR CERVITEOF LOCAL CREATIVE OF
18513	48881	Α	18620	9854	11033	ESLCFPKTEQEASQSLSP*IIIHLS
			1			CDTCTSYWLSRTHVG*QVGDA
ļ.		1				NSE*RMPVEESKVPHRTIFCYPH
		1				S\KLPMPYITINNLNPREKKDVL
		1				AFTCEPKSRNYTYIWWLNGQS
						LPVSPRVKRPIENRILILPSVTRN
		1				ETGPYQCEIRDRYGGIRSNPVTL
		1				NVLCEYPLFLCGPGHQLNSKRP EARPLSLSPVQV*TTLLLDIRPG
	i	1				HDSLPWEILGRHSLNOEYKGRG
		1				
1	1	1	l	I		ALVMGH*GPTACNERNRGIPQ AWA**T*MGFGCHLRLCLGSEG
1	1	1		I		HCVPLRDQEHPLPLDDITCGFIL
						FPPDGPDLPRIYPSFTYYRSGEN
	1	1	1	I		LDLSCFADSNPPAEYSWTINGK
		1		I		
	1	1	l	1		FQLSGQKLFIPQITTNHSGLYAC SVRNSATGKEISKSMIVKVSGK
l	i .		l	1		WIPASLAIGE
L		L	L	L		WIPASLAIGF

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon,/=possible nuclcotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
18514	48882	A	18621	3	1350	GRTAQLTAVLRKLLDPRLISTE
		1				ENTQAAETMGPLSAPPCTHLIT
		1	l			WKGVLLTASLLNFWNPPTTAQ
		1	l			VTIEAQPPKVSEGKDVLLLVHN
		1	l			LPONLAGYIWYKGOMTYVYH
		1				YITSYVVDGQRIIYGPAYSGREF
		1			i	VYSNASLLIQNVTQEDAGSYTL
		1				HIIKRRDGTGGVTGHFTFTLHL
		1				ETPKPSISSSNLNPREAMEAVIL
		1				TCDPATPAASYQWWMNGQSLF
		l				MTHRLQLSKTNRTLFIFGVTKY
			ŀ	l		IAGPYECEIRNPVSASRSDPVTL
			Ì			NLLPKLSKPYITINNLNPRENKD
		ŀ				VLTFTCEPKSENYTYIWWLNG
		l		l		QSLPVSPR\VKRPIENRILILPNV
		l				TRNETGPYQCEIRDRYGGIRSD
		l				PVTLNVLYGPDLPSIYPSFTYYR
		1				SGENLYLSCFAESNPRAQYSWT
		l				INGKFQLSGQKLSIPQITTKHSG
		1				LYACSVRNSATGKESSKSITVK
18515	48883	Α	18622	273	2271	CGSWLMTQFSMDKRQGRSRSV
		l				TITNTAVTSLEWVPFHAFAIPRS
						TLVSQQGATSHTDNTQEMDSP
		l				GQEPGFAKEVEVEPGFQPLPQM
		l				TLLVPAMCLLLHGACSAKGFC
ĺ		1				AAPHFLLASPMGKGQVPLNPFS
		1				FTLSEELDLPQSLKRNPKGCIAR
		1				RAKPILAAERHKRLILHTSTKEN
		1	1			TLLDNRVIECLTMEAVAKFNIM
1		1				KEREGPSHQPALSPPKARWHIL
		1				WQKLMFTASLLTFWEP\PTTAR
		1				VTTEAMPFNATEEEEEEFFLLA
		1				HNLPQNLTRATIW\YK\GQMRH
		1		l		LYHYITSYVVDGEIIIYG\PAYSG
	ļ.	ı	1			RETAYSNASLLIQNV\TRED\AG
	į	1				SYTLHIIK\RGDGTGGVTGRFTF
						TLYLETPKPSISSSNFNPREATE
	ļ.	1				AVILTCDPETPDASYLWW\MNG
		1				Q\SLPMTHSLQLSKANRTLYLF
		l				G\VTNYTAGPY\ECEIRNPVSAS
		l				RSDPVTLN\LLP\KLPKPYITINN
		l				LKPR\EE*GCLRPFTCEPKE*GTT
		l	l	l		PYIWWVKRFRSLPVSPGVKRPH
		l	l	1		LKNRI\LIPTPVFTRKWKQGPYS
		1	1	I		MWNYGDRYGG\IRSLPSSPWNV
			l			LLWVQDLPRILPFHFTYYRSGR
		l	l	Ì		KSSYLSCSGGTLNPP\AQYSWD
		l	1			N*WKSFQLTRGQKLFYSGHITT
		l				KHSGLYVC\SVRNSATGRESSK
	L	١.		ļ.———		SMTVEVSDWDITLNSTSTSNSIF
18516	48884	Α	18623	1	1131	

	SEQ ID NO:					Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN 09/540,217	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	acietion, (=possible nucleotiae insertion)
18517	48885	Α	18624	1	603	MDIADPFSGFPMGMGGFTNMN
						FGRSRPAQEPTRKKODPPVTHD
						LRVSLEEIYSGCTKKMYQED\K
		l				SHKRLNPDGKSIRNEDKILTIEV
		1		l		KKGISLPEALCG/TTVNVPTLDC
						RTIPVVFKDAIRPGMRRKVRGE
						GLPLPKTPEKRGDLIIELEVIFPE
		l				RIPQTSRTILEQILSSYLSYLSSP
	ŀ					GLTRDLSRAQGFLDLSTSCGP
18518	48886	Α	18625	3	1228	WSAAEPVDGDSGSAGRRRGPW
1						PKTTYHPWAVARGASEKEIKR
	l	l				AYRRQALRSHPDKNKEPGAEE
		l				KFKEIAEAYEVLRDPRKREIFD
						HYREEALKGSGPSGG\SGGGAN
		l				ATSFSYTFHGEPLAMFAEFFGG
		1				RNPFDTFF\GQ\RNGEEGMDIDD
						PFSGFPMG/LWGGFTNVNF\GRS
		1				RSAQEPARKK\QDSP\VTHDLRV
						SLEGDLTAAVPRRCTKKMKISH
						KRL/NTPDGKSIRNGDKILTIRSE
		l				RRGWKEGTQITFP\KEGDQTSN
		ł				NI\PADIVFVLKDKPHNIFKRDG
	1	1			İ	S\DVIYPARI\SLREA/LCVGCTV
						NCPHSGTGRT\IPVVFKECYQGL
						GMRRKSSWENGLPLPQNTREN
		1				VGDLII*GFEVIFP\ERIPQ\TSRT
		l				VLEAGSFQYSYLEVPQGLTRGP
						FPELKDFWDLFLPVVGP
18519	48887	Α	18626	321	1121	GDAVPSAPRRPSRRTPGCGSRG
		1				ALQPGPPPRA\PPPEP/PPRGAAA
		1				AAPPAGPAAPAARQPPRRPPAQ
		1	ŀ			PRSCPRRVRPTPAWSPPGRRGP
		1	ľ			RRSRRRPPGGPGPAAPLRLSRA
		1				HSPPAPPGSPYRPHGAGTSVAP
		1				WTRPPAARGTEADPGRCPVSAF
						GTAPGQMRGRGSATQRLHRGH
						STAPGAGGRCGRRPGGSGRPG
		l				AGAGPRRSTAAPPRCRRRSPTG
						PRSPRGPRSARPARGSVGGPRG
		1			ł	TPGKQPGPRRA*TSGPEPRCCG
						HARG
18520	48888	Α	18628	191	653	KLEIQRLLRMTTECIRHTKQKK
		1				FGSPGLQPPLPGNAKSRADSTA
		1				LPALPAQQKETKQQEPGESS*E
		1				PGGSSPSRMERAEAAPAQS/PA
		1				GGTGTGQGWGAPHLGPALARR
	l	1				VTGPPQHGSPGPRTRPTPYPAR
						C/PSRPIFVPAIVWSRLRAPPGLP
18521	48889	Α	18629	141	319	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18522	48890	A	18630	178	722	PLGNVSCSHRSFQTARVDYSLI YVLAWGQKKEVWELRNWQTH ALMKLANKLEPRTSVNKD/SP KSLLYSCSYSYFDEPVELRSSSF SSWDDSSDSEVETHLHLKLV* PNILAFVERFPTARRKPDVEPVE NTDEAQNSFCKTAHNLWSLTFP FFCLLYETRARLESWSLSCLR YEHISSG
18523	48891	A	18631	2	367	
18524	48892	A	18632	1	381	QRYSSRRATPRHIIVRFTKVERK ETMLRAAREKGRVTHKGKPIR LTVDLLAETLQARREWGPIFNI LNEKNFQPRISYPAKLSFISEGEI NPQMLR/DFVTTRPTLRDLLKE ALNMERNNRYLPGRPL
18525	48893	В	18633	1	846	
18526	48894 48894	A	18634	3	11170	VGSMTGEASGNLQSQRKAKRK EARLTCLEPVEPGSGTHPPMC LAPPMWKCQKPETGIKEGDR DHNSLPAREENQTENESDELTE AGFRRWYITNSSRLKEHVYTOC KEAKNFERSLKELLTRITSLEDN INYLMEPRNTAREHREAYSSIN SQIDQAEEKIPEIBODHNEIKRE DKIREKRMKRNKQSLQEIWDY KRPNLSLAGVPESDEEMGIK KNTLQDIQENFPNLAKQANIQI QENQRTPQRYSLRATPRHIIVR TFIXVEMKEKMILBAAREKGRIV THIGGRIFTADLSAETLQABY RTEWGPIFINLEKENFOCPRISYP AKUSFISEGEIKYFTDKQMLRD FVYTRIPALKRAPGKEGT*TLE RDMRYQPLQKHAKL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18527	48895	A	18635	73	1504	ODLRLEYLKDTMFSKLAHLOR FAVLSRGVHSSVASATSVATKK TVQGPPTSDDIFEREYKYGAHN YHPLPVALLERGKGILLMGM*E GRKYFDPLSSVSALSNQGHC HPKIVKCSGRVKWDKIDL*HLE AFYNNGTLVNMREPYY*TFST YHKVLPMNTGVEAGETAICKL ANRKWGLYTYKGGIQKYKCAKIV FAAGNFWGRTLSAISSSTDPTS YDGFGFFVARDFDIIPY**SCPH MEQCSSKDPKOGLAFHG'FDIPI GEAGVIVVPDFGYLMGSAESS GTRDQVLFICLMEIQTELARTW **PGLAVDYBVNRPDIVLLGKAL SGGLYPYSAVLCDDDIMLTIKA EVLEEENLAENADKLGIILLRNE LLMLTLPSMLVTARKKEKGIY LNAHLAIKGNQKIWDA/WGKV CLRLQDNGLLPKFTSVATLSRF
18528	48896	Α	18636	2	348	
18529	48897	A	18637	588	801	RTAYFCQYHTASVYSERAMPP GCPEPSQA*ELQETGHRQVALR RSGRPPKCAERPGAADTGAHCT STDGRL
18530	48898	A	18638	175	510	NSESPGPLWWLSCDNPAKDRIY STEADGLGLPDQSFVVHRAQL* CVAG*LGTHSRFQEWAV*D*SD LLKAQLHFKVGRCVWEAGGGL EWVLGGRCRCRVPQPLETLIQ WGPW
18531	48899	Α	18640	1	1431	
18532	48900	Α	18641	202	994	IRWGGGRLLLDSNIRLWVVLPIR YSTFFRRALIRHYVSILLAERQ RSFTQGNKYLDSSSPNFEGRVR FRGKLGNYIPKQSFFG/RRKFLF FPNPEDGIFSKKLIKREVVPPSPM TDPTMLTDMMKGNVTNVLPM LIGGWINMTFSGFVTTKYPFPL VTLRF*A*WLQQGNRSYSPFRCI PG*WFCIPGYFPQCILGFRSI/YT LWISGGKNORG WNQSRMM/DR SRMTGASHGPWPADSGRFFN KRWEALLELTDHQWALDAAGE DAA
18533	48901	A	18642	97	224	LPTKSTWVAGKK*KKRSNIKD YSTPLTSYRSIRSHAFKIVAS

SEQ ID	SEQ ID NO: Met   SEQ ID NO:   Nucleotide				Nucleotide location of last Amino acid sequence ( X=Unknown,			
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide		
	sequence		09/540,217	codon for peptide scauence	of peptide sequence	deletion, \-possible nucleotide insertion)		
				sequence				
18534	48902	A	18643	117	457	IWGDVEKGK\KVFYL*RCSOCH		
	10302	ľ				TV*/ERGGKHKTGPKSP*VSFGR		
						RTGQAPWDTLYTAANK\NKGII		
	İ					WG\EDTLM\EYLENPKKVHPLD		
						TKMIFVRHLRKREERADLIALS		
						SKKLLN		
18535	48903	Α	18644	411	1054	VTGAQRLVTCRMGKQNSK\LA		
						P\EVMED\LVKSTEFNEHELKQ		
		l				WYKGFLKDCP\SGRLNLEEFQQ		
						LYVK\FFPYGRRLPSFAQHAFPN		
		1				LSTRMGDGTI\DFREFICAL\SITS		
		1				RG\SFEQKL\NW\AFNMYGPGW		
						VMGKITRVEML\EIHRGLSYQN		
		i				G*GTVIMMKMNEDGLTP\EQRV		
1		l				GQDFSAR WVRNKDDQIYTGID		
				1		FKGSCQRADPFIV*LL\QCDIHK		
18536	48904	Α	18645	3	475	GAEGARGGGSSYSEMAETVAD		
i						TRRLITKPQNLNDAYGPPSNFL		
				ŀ		EIDTNLPIFKLKESTVRRRYSDF		
		1		l		EWLRSELERESKVVVPPLPGKA		
		l				FLRQLPFRGDDGIFDDNFIEGKK		
						TRGWEQFINK/VSLGHPL\AQNE		
						PLFFHMFLQDEIIDKSYTPSKIR		
18537	48905	Α	18646	1	695	LRARSLRDRCARAPCPHGGQQ		
		1		1		RRRRRLNAEGAEGARGGGSSY		
		1			i	SEMAETVADTRRLITKPQNLND		
Į.		l				AYGPPSNF\LEIDVSNPQTVGVG		
	1					RGRFTTYEIRVKTNLPCFQS*KN		
						LIVRR\RYSDFEWLAKWNLERE		
1		1	1	l	1	SK\VVVPPLPG\KAFLRQLPF\RG		
			1	l	1	DDGNILMDNFI*/EERKIRGWSS		
1		1		l	i	FLNKVA\GHPL\AQN\ERC\LHM		
				l	1	VFYQDEIIDKKLLLPSKNKAMP		
		<u> </u>				WKFGPRKGAKNVDY		
18538	48906	С	18647	3	474			

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon far peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
18539	48907	Α	18648	156	1254	RPLHTLEVLRRMTKRLVTKAA
						ASAARAQPAEPRDRKYDKHLS
						YLATWGRSAGRAGSPRGARGR
						ELARAPVSLPAGVPGRGSAAG
				1		HSSEARTGPNGKMGGSSREPGT
				1		EKVPCPRGLSPTREVGHQVHGT
		1				LGAGPNELHPSGPAGARCRPGR
		İ				REAKLGDAARSEAQSSAHKFHI
						DSLSLPWNPTAMEMLMPKKNR
				İ		\IAIYE\LLFK\EGVMVPKK\DVPI
		l				PKHPELAEQKCAPTFHVMK\A
	1	1		1		MQ\SLKSPRPT*KEQFAW\RHFY
	ł	İ				WYLT\NEGIQ\YLRDYL\HLPPEI
1		1				VPAHPYGRSPSRRLARPRPKKV
		1				WKGEATLRDFTRGEADSFLCH
		ŀ				S/DSYRRSAVPP\GA\DKKAEAG
				1		GLGQKPNFQF\RGGFVRGRGQ\P
18540	48908	В	18649	1	1053	
18541	48909	Α	18650	1	529	MGRYMEREPLQGNHRRSGLSG
				1		ERCSHMGGVLIERRELQTETRK
		1	1	1		EGVVEWCWLEKEVLATITKPV
						RGDKNGGTQVVKHRKMPRYY
1		ı	i		•	PTEDVPQKLLSHG\KKPFSQHM
		1		1		RKL/FLYRRHARNLSLPPQPELII
		1			1	SDVK/IPRHPADA*LEEQQLSEP
						E/HSEGTSY*RIPEKVLSYPAIRP
18542	48910	В	18651	258	363	
18543	48911	Α	18652	197	398	ARMSQEKDFHKVMSALKARTG
l						HLHFFCGGMSSVKVGQGFSLLL
		_		1		*FFSYFRPSGCILPL*ELPEARCP
18544	48912	Α	18653	215	932	GTQSCNQKVLNSANNLQELGIG
		1	ļ			PKFQMRLKPQLAPMQPNRGTS
		1		l .		LGRSIPCPPVLCSMRKIHLRPQV
	ŀ	1				LRPTSPRNISPILNRVSEVSDHA
1						GTPALVLHP*RQVPLFWGRGK
				i		YPNPFSLCLYPFSAFLGGKKHP
						TPSPSP*VASPLF*RSKYPNLVSL
						CPSPLFPRPDLLSLWPNPLF\RTP
						TSYISVPQSLISMPRPLISAPQPLI
						STTQPLSRFSGRSLLQVPEIWPP
10545	40012	١.	18654	1,	378	GQGMPAARDSS
18545	48913	A		114	380	
18546	48914	A C	18655 18656	228	260	
18547	48915	C	18657	99	335	
18548	48916 48917	A	18657	55	474	ROVPLFWGRGKYPNPFSLCLYP
18549	48917	A	18608	122	4/4	FSAFLGGKKHPTPSPSP*VASPL
1	1	1				F*RSKYPNLVSLCPSPLFPRPDL
1	1	1	1			LSLWPNPLF\RTPTSYISVPQSLI
			1	1		SMPRPLISAPOPLISTTOPLSRFS
		1	1	1		GRSLLQVPEIWPPGQGMPAAR
1	1 -	1 _	1	1		OKOLLO V FEI W FF GQ GW FAAR

SEQ ID		Met	SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
18550	48918	A	18659	ı	187	AELATGNVKVEASGTPEEKAG
		1				SVLG*ACFAGP*ERCCWQNN*D
		1				GIISIQSYCLCNLGCFIQT
18551	48919	С	18660	1	357	
18552	48920	Α	18661	3	148	
18553	48921	Α	18662	1	312	
18554	48922	Α	18663	149	457	
18555	48923	В	18664	1	675	
18556	48924	С	18665	110	928	
18557	48925	Α	18666	495	817	LTSPSRCTHEKSCSSLPPL*DKP
		l				QPHLQHTRTSKRLNCSSQVFLQ
		l				NLLPEELATSSRNLATGPRNAC
	Ì	l				SPGFLLSHIPSVWDPTGNRTVQ
						LTWQPLPEPLELWPKAL
18558	48926	Α	18667	228	3021	VFDRTQNVQGRIMEAPEYLDL
	1	l				DEIDFSDDISYSVTSLKTIPELCR
	l					RCDTQNE\DRSVSSSSWNCGIST
		l				LITNTQKPTGIADVYSKFRPEKR
	ŀ	l				VLPLKHQPETLENNESDDQKN
	Į.					QIVGEYQKGGESDLGPQPQELG
	l					PGDGVGGPPGKSSEPSTSLGEL
		l				EHYDLDMDEILDVPYIKSSQQL
						ASFTKVTSEKRILGLCTTINGLS
		l				GKACSTGSSESSSSNMAPFCVL
	l	ı				SPVKSPHLRKASAVIHDQHKLS
	l	1				TEETEISPPL
18559	48927	Α	18668	1440	1764	ERSTYNLRSSDQP/RPRNILTNF
						KS/VDKGDTFYPWTHNSGASH
	ŀ	1				GLGR\RLPWC*ELATSARNLTP
						RPRTAGSPGFLLSHVPSVWDPT
						ANRTVQLTWQPLPEPLELWPK
18560	48928	Α	18669	1	3255	MLTLTGAGGESWIIRPGNLLEQ
ŀ	l					LGAEETLGRRQEPGDEVTAHFL
	l					LQGVINMGPVPYPGAHSSNMP
	l	1				GSVSPILGHSVKLFEEYYPVGD
İ	i	1				PLMGSGRPHTPRKKIWSDLNA
						HSDLYLALDWTPLPEQSEPGPG
		1		i		LAAWKPFQAEEYTCKCAEGNE
		l		l		NTPFDLRKGTLPCPRNLERARO
	1	l				AYMHIEEKFPFELTEQHICEFQS
	1	1	l			MCYVLVRVLGACSOSTWLILEP
1	1	1		l		DGVSGPSKGASEAIGQCQSSAA
1	1	1				KPRRSGKESVREPWA
	<u> </u>	Ь		L	L	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				scquence		
18561	48929	A	18670	1	1442	CSEYEDSSPAPVPATDLSSTLSS
10001	10,2,	· `	1.0070	ľ		SVPQPQDTGTSQQLHPLDPWHE
						LLRAOELOGATNHKGYSHAEH
				1		EHAGLGVOGGNGALAFSNSGH
						RHAVPTISSGTGRRRTPSSSAFG
						LLNLHOWFVSGFOAFSDRLKA
						ALSASLLLRFGDSDWLPSSSAC
					1	KCLMLGLHFVIVGNICATLKEK
						YSSMLHLDVTMKKNGEKRTRL
						QKRKKGMPPHPA/S*GPKHSCH
						HSPCQCCPSSAK/SASELQGSWT
		l				PFGGLLTRTRMKFGAKTRDLD
		1				
						QGTSLGRSLPCPPTLCSMRKIHL
				į.		RPQVLRPTSPRNISPISNPRQRR
					1	QVLSMDPKLRHRSRTGK/DSLP
		1				LVFNHCRDTSLIIHPCFKGVRPR
				1	j	RDACLGPSPLAASPAFLEKGQD
						LINLAFKVYNNRKKLQFLASTV
		1	ŀ	!		RQTAATSPAHKNFQMPEPQRP
l		l		ŀ	ł	GVPPEPPPTGACYMCRKIWPLG
		1				QANARSPGFLLSRVPSVRDPTG
		_				NRTVQLTWQPLPEALELWPKA
18562	48930	Α	18671	140	327	
18563	48931	Α	18672	95	115	IIRHLCND*TPREGCLPSP*PAW
						SDTFETWVNNQASLQ
18564	48932	Α	18673	218	674	MPISRPTARFKRIKVYYHSPAT
		1				AWPSKAYKLPLQFPHFTCPKTR
				1		QGLQVTSGSAPYQPNCFVYPPR
				ŀ		VAKTKYSPILNTSLHNPLLCSGS
						QTCFLY/SFLCTFHPSLSSLSLGL
						TLTPIRLSKLRGLYCHKASQTA
						PITSIKPKFLPHLLPISA
18565	48933	Λ	18674	1	268	
18566	48934	A	18675	1	458	
18567	48935	Α	18676	3	461	LLLTQSLFGGLFTRTRMKFGAV
1		1		1		TRIGGPPLGNQSPSSCSLLHEKD
				1		PPTTSGPQTDQPKKHLTNFKSA
		1	l	l		ARPTFLGQGQVPLNPFSFTLS/E
		l			1	QVLLS*AARTPQSLISTPQPLISV
			1	l		PQSLISVPQPLLYFSGGQEPPPPP
l						LLCVSSLFSRLASFTM
18568	48936	С	18677	156	329	
18569	48937	Α	18678	449	667	
18570	48938	A	18679	79	311	
18570	48938	A	18679	79	311	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
		l		sequence		
18571	48939	A	18680	<u> </u>	693	MARTICK CORK CORRECTABLE
185/1	48939	^	18080	1	693	MAPTNCKGSRKCGRPHEQMPH PYLPLLTLFSDSARLHPGEINSR
		l				
		l				VPHTKPVWWSLHTDAYEIWYH
1		l	ĺ			DSDWGDLPWEINPLSSCSLLHE
						KDPPTTSGPQTNQPKEHLMNFK
		l			ŀ	SGPHWKSDCPTRQPLPGPLELW
		l	ŀ			PKA/HLTDSFPDLLSLAAED*CC
1		1				LIALEAPWTITDAELWITLTVED
1		1		l	ľ	SQLYEDTLAGRSVLIKNLTP*TL
i				ĺ		Q/PLDGLDPT*SSIVPQLPSACRI
10.570	10010	ļ	10001	220	865	LPTGFTVPE
18572 18573	48940 48941	A.	18681	328 451	1238	TALLI TOOL DOOL PROTESTANCE
18573	48941	A	18682	451	1238	TALLLTQSLFGGLFTQTRMKFG
		ł		l		AVTRIGGPPLGDQSPVLLFFVPR
				l		ERSTYDLGPQTDQPKKHLTNFK
				i		STSFVFSSCIPPP*PSSISLLPPW/T
					İ	TDHAPLTISL/TT*SPLPCSMPIS/
		ł		l		ASHSML*KD*SLLSLACYSMAF
				l	ŀ	*SL*TLLTIPPFYLS*NQRRFTG*
		ļ.				FRICALSTKLFCLSTPWCQTHIL
		ŀ				SYPQYLPPQSIILFWISNVLSLLF
						LCTLHPSLSSLSLGLTLTPFRLS
				l		KLPGLYCRKASQTAPITSVKPK
		_				FLPYLLPISA
18574	48942 48943	C	18683	933	1037 4323	L LOW COMPLETCH CHONCOVIC
18575	48943	Α	18684	933	4323	AASHLCGTPLEIGLSNSPGSHSQ
						SPWNSGPRLSDCFPDLLG*VAE
				l		D*HCPIASEASWTVT\ELWVTLT
				ł		VEVAATALILLEALKITSYAPLT
			1			LYSSHNFQNLFSSSHLT/PYTFC
						PQ/GPFSYTHSLLSLPQSPLLLA
		1	141			QTSIRPPTLFLIPHLTPMTVSL*S/
		1		[		ILTFIPFPHISFFPVPHPDHTWFID
				}		GSSTRPNRHTPAKAGYAIVSST
		1				FIIEATALPPSTTSQQAKLIALTQ
						ALTLAKGLLVNIYTDSKYAFHI
18576	48944	-	18685	849	1944	WOUNT ESCHOLUMINESSOLUM
18576	48944	A	18085	849	1944	WQVPLFSGRGKYPNPFSPCLYP
1		1		l		FSAFPGKRQELATSARNLSDHQ
1		1		1		AKECLQPRIPPKPCPIFAGPHWK
1						SDCSTSPGQPLPEPLELWPKA/H
		1		1		LTDSFPDLLGLAA\ED*HCPIAS
1		l		ĺ		EAPETITDAELPVTLTVEGKSIP
1		l		i		CLIDTGATHSTLPSFQGPVSLAP
1		l		l		ITVVGIDGQASKPLKTPPLWCQ
l		l		l		LGQHSFMHSFLVIPTCPLPLLGR
						NILTKLSASLTIPGVQLHLIAAL
L.						LPNPKPPLCPLTSPQYHPLPQDL

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \= possible nucleotide insertion)
				sequence		
18577	48945	A	18686	2	377	KGATIVYALDTLFIMEMKHEFE
						EAKSWVEENLDFNVNAEISVFE
						VNIRFVGGLLSAYYLSGEEIFRK
						KAVELGVKLLPAFHTPSGIPWA
İ						LLNMKSGIGR\NWAWASGGSSI
						LAEF\GTLHLEFMHL
18578	48946	Α	18687	215	1135	PITLRRHLFFSGIGRNWPWASG
						GSSILAEFGTLHGMKIVF*/HFH
						GNILFSI\KVMNIRTVLNKLEKH
						YLN*KLNHSKIHFPLFPDHVSV
						GGLGDSFYEYLLKAWLSINLRR
						DYKMLKNKCFSQAIETHLIRKS
1						SSGLTYIAEWKGGLLEHKMGH
						LTCFAGGMFALGADAAPEGMA
ŀ						QHYPVSTVQENNPYSFIPCPLV
						MKLGPEAFRFDGGVEAIATRQ
						NEKYYILRPEVMETYMYMFRL
						SGSDFFSSFLLLPPQASSCFQTLF
ļ						DLFKVPDSLCSILEFRRHSSRQP
						YSTDQPFIYLVGKRILFCPLT
18579	48947	C	18688	304	400	
18580	48948	A	18689	16	450	GHSMDMRVPAQLLGLLLLWLP
18581	48949	A	18690	<b>]</b> 1	l'''	GARCVIWMTQSPGTLSLSPGER
		l				ATLSCRASORVNSNYLAWYOO
		l		l		KPGKTPKLLIYGASNLETGVPS
		l				RFSGSGSGTDFIFTISSLOSEDIA
		1		l		MYYCOQYNNWPHPS\TFGQGT
		1				KLE\IKRT\VAAPSVVHLPGPSD
		1				EOLKIWELPSACVPA*NNF\YPO
		l	ŀ	i		SRPKVQWEGGITPLQ\SG*LPQE
		1				SVHRGRTROGTAPYSPOOAPW
		1		i		TVRQSRITEETQSLTACEV\TPS
		1				GALRFRPVHKGAFNRGESF
18582	48950	Α	18691	3	688	HASADAWAANAEEHRHDRPR
		l				GTLR\EYKV\VGRCLPTPK\CHT
		l				PPLLPACEIFAPNHVVAKS/RAF
		1				WYFVSQLK\KMKKVFQGKIGL
		1				LVGQVF*ESSPLR/V*KNFRGSW
				I		LAAMDSRERAPTNMLPGNNRG
		1				P*PPAGGCSTQLLTRDNGVAPG
		1	1	I		TGAPKPHFHFRFIERLEGRFAG
						QQSCRRP/ALVQSSFH\DSKIKFP
				1		ACPNGVL\RRQHKPRF\TTKRPN
						TFFLGAGPSSGVCPK
18583	48951	A	18692	1	784	
			-	·		

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last eodon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18584	48952	A	18693	t	4713	MQGPYLLLWLPDSLEEGKEGL YLGNCIHTCLVTVPEDAFFPHF LTQHSGTHLPPSSDIPSHFMNNS TGRLAQRILGTSTEAFLSPEVM VFVHARNATVRTAMSLIERAK
						NCGHIPFFFPTQGHDYVLAEKQ VQRSRNKQVRELFPDGFSIHHA
						GMLRQDRNLVENLFSNGHIKV LVCTATLAWGVNLPAHAVIIKG
						TQIYAAKRGSFVDLGILDVMQI FGRAGRPQFDKFGEGIIITTHDK LSHYLTLLTQRNPI
18585	48953	A	18694	313	489	SSCFKLHFQQLFKNCNTQMRN QIGFLRF*NNLVMLLSSSSVTNQ LELQKKIILLTCKMQ
18586	48954	A	18695	I	851	ACGWALAQRPARRAMVAGID AGRS\LGVLSVVCLLHCFGFISC
						FSQQIYGVVYGNVTFHVPSNVP LKEVLWKKQKDKVAELENSEF\ RAFSSFKNRVYLDTVSR*PSLST
						T*TSSR*KMKYEMESAKIVTD\T MKFLPYVP*VSFQSPTLT\CALT NGSIEVQCMIPEHYNSHRGLIM
						YSW\DCP\MEQCKRNSTSIYFK MENDLPQK\IQ\CSLSNP\LFNTT SSIILTTCIPSSGHSRHRYALIPIP
						LAVIPTCIVLYMEWVF*KCARN PDRTQLQLIGNRRMKTTA
18587	48955	С	18696	35	181	
18588	48956	A	18697	75	344	PQVLRPTSPRNISPILNRVSDHA GTPALVLHP*RQVPLFWGRGK
						YPNPLYLCAPIPYFRT/HNLISLR PNPLCPHPDLVSLCPDPFPAFLE
18589	48957	Α	18698	I	268	
18590	48958	A	18699	39	376	QYISELQFLASTVRQTPATSPAH KNFQTPEPQQPGIPPEPPPPGAC YKCWKSGHQAKECLQPGIPRK PRPISGSHSQSPLELWPKA/HLT DSFPDLLGLAAED*HCPIASEAL
18591	48959	A	18700	2	295	CQTTQGRLLTAGTPL*SFTHVS RVSDHAGTPALVLHP*RQVPLF WGRGNHISGTQELPNT*TAV/V QAF/LPEPPPTG/CLLHVPEIWPL GQGMPAGQDSS
18592	48960	A	18701	81	402	VKFGPEIWCRDSDQGRGGVGT SLGRSIPCPPALCSVRKIYLRPL VLRPTSPRNISPILNRDPTVQLT WQPLPEPLELWPKA/HLTDSFP DLLGLAAEDRCCPIASEAP

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
18593	48961	A	18702	165	439	PPROAKMONLAAPGSHSOSPW
		1	1	1	\	TLRPKAL*LTPSOIFSA*RLKTD
						TARSPRKPPSFQGPVSLASITVV
						GIDGOASKPLKTPOLWCOLRO
						YSFK
18594	48962	Α	18703	284	511	IILVVKWANGLRCLTSRHSFTH
						QSLPS/PLCPVQLVPN\SRLSPQS
						QPQASLSLSNLPFLQTHLTSPFL
						PRLLLARPK
18595	48963	С	18704	414	557	
18596	48964	Α	18705	1	1284	MNFEGTETLHCNGHCKVIAMT
					1	LGNQEVNQRNFSTGTTGPMEG
						MWLLSSNSHHSLKYAGALAIL
						AFQYQERGSQAGHRDSWPETK
		1		1		ETHFICGPKTPALVTDWEGSLP
		1	l	1		LVFNHCRDASLIIHPRFSGVRPF
						RDACLGPSPLAATPQTITDTEL
						WVTLTVEVWDIST/LFPGN*SH
						A/TLPSH*NLITLTPLNANI/AIPO
						HALKGLKPVITRLLQHGLLKPI
						NSPYNSPILPVOKLDKSYRLVO
						NLRLINKIVSPIHPV VPNPPAFT:
						QITQAVSQALGIQWNLHIPYHP
						QSSGKVERTNGLLKVHLTKLSI
						QLKKDWTVLLPLALLRIRACPI
		ł		i	\	DATGYSRFELLYGRTFLLGPNI
				1		PDTSPLGDYLPVLQQARQAAN
						LLLPTPDPQPHEDTLAGRSVLV
						KNLTPQTLQPRWTGPHFIIYSTI
						TAVCLQDPPH
18597	48965	В	18706	1	933	
18598	48966	Α	18707	3	435	TKETGFIHGPKTPAPVTDWEGS
		1				LPLVFNHCRDTSLIIHPCFKGVF
		1				PRRDACLGPSPLAASPAFLEKG
			İ			QDLINLAFKVYNNRKKLQFLA:
			İ			TVRQTAATSPAHKNFQMPEPQ
		1				RPGVPPEPPPTG/CLLHVPEIWP
						LGQGMPAARDSS
18599	48967	A	18708	2	111	
18600	48968	В	18709	1	595	
18601	48969	С	18710	1	1344 385	VIDE DODLE LUDATE COST COST
18602	48970	Α	18711	227	383	VPILPQPLLLHPAIFLSPPLLTPG
						PAYSFVP*LALPHLPSNLLLKR WLEPKA
18603	48971	С	18712	148	258	
18604	48972	A	18713	215	693	
18605	48973	С	18714	1	816	
18606	48974	В	18715	1	513	
10607	48975	В	18716	1	1452	
18607				11	1432	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		ŀ		sequence		
18609	48977	A	18718	2	2107	IDMIFTPGPPSTPKHKKSQKGSA
	10511	i .		[		FTFPSOOSPRNEPYVARPSTSEI
					*	EDQSMMGKFVKVERQVQDMG
			l		i	KKLDFLVDMHMOHMERLOVO
l						VTEYYPTKGTSSPAEAEKKEDN
	İ				Į.	RYSDLKTHONYSETGPPEPPYSE
						HOVTIDKVSPYGFFAHDPVNLP
1						RGGPSSGKVQATPPSSATTYVE
						RPTVLPILTLLDSRVSCHSOADL
ł						OGPYSDRISPRORRSITRDSDTP
				ļ		LSLMSVNHEELERSPSGFSISQD
				ŀ		RDDYVFGPNGGSSWMREKRYL
				l		AEGETDTDTDPFTPSGSMPLSST
ļ				l		GDGISDSTVPLFLSSEILOKOVG
				1		OSITSMLGFLSRGPSMKLCMGL
			İ			ACVLSLWNTVSGIKGEAKKEK
						GMTFLPTTDSKKFFSLLSVTSYS
				1		SFAFHKFSVAVYNISNLKTVDP
		ĺ				AKFPTRYCYCLNNRTNDLSDFT
						ALLVDIIGNSTSYLTEIFKSTSIL
1						SVNQSNESDCIFICVMTGKSGR
		l				NLSDFWEIEEKYPIINYTFTSGL
						SGVLALLLTQSLFGGLFTRTRM
						KFGAVTRIGGPPLGNQSPSSCSL
						LHEKDPPTTSGPQTDQPKKHLT
				1		NFKSAARPTFLGQGQVPLNPFS
				l		FTLS/EQVLLS*AARTPQSLISTP
		l				QPLISVPQSLISVPQPLLYFSGG
ł						QEPPPPPLLCVSSLFSRLASFTM
1			1			GAFTHGTQTPSPTKATAPRYPQ
		1				TGDLSAEWPFTAGEEPVLVPRP
18610	48978	Α	18719	828	1063	RHSQAAED*HCPIALE/VPQTIID
		1				AELRVTLTVEGYSLPPGCLRGL
						MLSVSGFSRSTVQAVSGSTVLG
		i				SGGQWFSCASV

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
İ			ŀ	sequence		
10711	48979	_	18720	183	1140	LGSGDLPWEINPLSSCSLLCEKH
18611	48979	Α	18720	183	1140	
		l				PPTTSGPQTDQPKKHLTNFKSG
						ETKEMHFIRGPKTPVPVTDWEG
			•			SLLLVFNHCRDGLSDHSATFQG
1						CQT/MAGMPALVLHP*RQVPLF
		1				WGRSKLLLARLS*VPILPQPLLL
				i		HPIILLSPPLLTPGPAYSFVP*LS
		1				MSIHQVVLRPDEQGPGQEQQPP
		1				LYVMEPGEINSFIAHTKPVWWS
	1					LHTDAHEIWCHDSDRGTSLGRS
		1				IPCPPALCSVRNIRLRPQVLRPTS
		İ		1		PRNISPILNQERQRRCILFVDPK
						LRCQSRTGKAAFSWCLIIAGTA
			ļ			SLIIQPHFKGVRPCRDACLGPSP
					1	LAASPAFLGKEQAAPCQAELGP
						NSSSASAPPPYNPFITSPPHTRSG
	1	l	1			LQFRSVTSPPPPAQQFTLKKVA
1		1				GAKDIVKASLAPALAQGVPGTP
		1				QATASEGASLKSWECLCGVNL
				1		ATAQSARVKEACQEACQSLPRF
		1				QRMYEKAWVPKQKTTAEVELS
		Į.		į		QRASTRVVLRGNVGLESPSRVF
						SIALSSGAVGGVHCPSDHRMIE
l		ŀ				PAAFNLSMKNPQRQSCLRA
18612	48980	Α	18721	372	906	LRSADLPWEINPLSSCSLLHEKD
	1					PPTSSGPQTDQPKEHLTNFKSE
l						KKETRFIRGPKTPAPVMD*GRQ
						PSLGV*PLQGCLSDYSPRFQRC
		1				OTTOGHLPWSFTLSSKSHFSGG
		l				RGKSLLQVPEIWPPGQGMPAA
		1				QDSS*AV\PICAGPRWKSDCPTH
						LAATPKAPGTLAQGSLTPSQIFL
18613	48981	Α	18722	983	1980	KFGLVQLTLGKPLPEPLELRPK
		1				A/HLTDSFPDLLGLAAED*HCPI
1				1		ASEAA*TITDTELRVTLTVEVW
	1			l		DIST/LFPGN*SHA/TLPSH*NLIT
1						LTPLNANI/AIPQHALKGLKPVIT
						RLLQHGLLKPINSPYNSPILPVQ
						KLDKSYRLVQNLRLINKIVSPIH
						PVVPNPPAFTSQITQAVSQALGI
				l	1	QWNLHIPYHPQSSGKVERTNGL
		1		1	1	LKVHLTKLSLQLKKDWTVLLP
				l	1	LALLRIRACPRDATGYSRFELL
				l	1	YGRTFLLGPNLIPDTSPLGDYLP
1		1		1	1	
				l	1	VLQQARQAANLLLPTPDPQPHE
1				l	1	DTLAGRSVLVKNLTPQTLQPR
10616	40002	n	10722	ļ, —	271	WTGPHFIIYSTPTAVCLQDPPH
18614	48982	В	18723	1	271	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
18615	48983	A	18724	803	1158	CSWHDRFPDWKAGNLLSLAA*
						D*HCPIASEAP*TITDAELQVTL
						TVEGSGDLPWEINPPSSYTLLCE
						KDPPTTSGPQTNQPKKHSHQFQ
						IRDKGDTFYPWTHNSGASHGL
						GRQPSLGV
18616	48984	A	18725	1855	2506	GASPSVWDPTENRTVQLHLGS
						HSQSPWNTGQRSRDLTSFPDLL
i						GLAA\ED*HCPITSEAPLTITDAR
						AMG*LSTVEGKPVPFLINTEAT
		1				HATLPSFQGPVSLASIT\VVGID
		1				G\QAF*TSLKLPNSWCQH*TIRR
						FKHSFLVIP\TCQVPLLG\EDTLT
i						KLSASLTIPGLQLYLIATLLPNP
						KPPLCPPLVYPHLNPQV*DISTP
		1				SLGDRSCTPYHLIKT
18617	48985	Α	18726	2	979	TSTMAVGKNKRLTKG\GKKGA
1		l			İ	KKKVVDPFPR\KDWY*RRKHPL
	1	l				MFH\IRNIEKDVGSPRTPRDPKL
		1				QSDGLKGSVCLKVSPAELPE*L
		1				KFAFRKFK\LITEDVSGVKTCPD
		1				LTSHGAWDLYP*QNCCSMVQK
		1				MGRPMIEA\HVECSRLTD\GYLL
		ļ				\RLFCVGFYLKNRNISDHGRPSY
		l				AQPPNRVR\QIR\KKMMEIHDPQ
				1		RLQTNVP*KEVVNKLIPASIGK\
1		1				DI\EKACQ\SIYPL\QNVF\VKKV
		l				KMLK\KPKF\ELGKLMELHGEG
İ		l		-90-		SSSGKATGDETGAKVERADGY
		1				GPPVQESVGKFRLPIVGNRSGH
						CVKKEKQSSRRRDFGVSVHPRI
18618	48986	Α	18727	1	615	ASTAAPRMLLLFQPRYRTLQPQ
	ľ	1				RLLMPKKNR\IAIYE\LLFK\EGV
		1				MVPKK\DVPIPKHPELA\DRNVP
						NLHVMKAMQVSQSPRG\YVK\E
1		l			\	QFA/WKKISYWCLTN*GYQGVS
						ISSRDYL\HLPP\EIVPA/TPLRRS
		1				RPED/SGRPSA*KGLEG*SDLAR
						LHKNGEAGQRLPYRR\SAVPP\G
						\ADKKAEAGGLGQKPEF\QF\RG
L		L				GFVRGRGQ\PPQ
18619	48987	Α	18728	3	395	SAEVGAAETTLTELRRTVQSLEI
						DLDSMRNLKASLENSL\GILLHL
		1		1		ESELAQTRAEGQRQAQEYEAL
				1		LNIKVKLEAEIATYRRLLEDGE
				1		DFNLGDALDSSNSMQTIQKTTT
L						RRIVDGKVVSETNDTKVLRH

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \-possible nucleotide insertion)
18620	48988	A	18729	323	1973	PCMWIGFAAVRKGLKDSSSASC GCTRRVRGTWWQGLSRVCVA RNEEVRLWGLCWLGSSPPAGW
1						NNVFYMLISADVLACLEPRAN
1						KEAANELAGAVDLGWMANVR
						RNPRDMVTSTHLGTHFHLRKTP
						PRGEKTCELASQQPLIEATTKT
					1	KSVAVSHILTYTPPTLNGVAAV
						SSRVHFSFWPPTLQTGLEQGSM
						SFTICFTTSTNYQSLHSIQPHSHS
	l					VQFISSTAKVYAVLRGLGSRTS
						VSFSTSFWSGWGSGGLAAGMP
						GIDNARLAADDFRVKYKTELV
						MCLSVESNVRGLHKVTDDTNV
						TRLQLETEMEALKEELLFMKK
						NQEKEVKGLQALIASSELTMEV
			ŀ			NAPKSQDLSNIMADLPAQYDEL
						A\RKN*EELDKYWSQED/IEEHT
1		l				TVVTNTSLLEVWSC*DARLTEL
1						RRTSPGLWRFDLDSM\RNLK\AS
1						LENSL\REVEAPYAL\QMEQL\N
						GILLHLESQLGQTPRTEAQRQA
						Q\EYEALL\NIKVKL\EAEI\ATLP
1						GRLLGRMAKDFNL\GDS\LDER
			l			NSFQNL\QKTNTPPGNVDGKVV
		ļ				S\ETN\DTKVLRH
18621	48989	Α	18730	1	897	MGHHRRQSLSPVLSLYSPDSMS
						FTTRSTFFTNYQSLGSVQAPSY
						GARAVSSAASVYAGAGGSGSRI
						SVSRSTSFRGGMGPGGLAAGM
						AGGLAGMGGIQNKKTMQSLN
						DRLASYLDRVRSLETENRRLES
						KIREHLENKGPQVKDWSHYCK
						TIEDLRAQIFANTVDNACIVLHI
						DNARLAADDFRVKYETQLAMR
						QSVENDIHGLRKLETEIEALREE
						LLFMKNHEEEVKGLQAQIASFR
						LTVEVDAPKSQDLAKIMADIRA
						QYDDLAGKNREELDKYWPQQF
		_				EENTTVVT\QSAEVGAA
18622	48990	Α	18731	3	423	SLSPVLSLSPDSMSFTTRSTFST
1						NYRSLGSVQAPSYGARPVSSAA
		l				SVYAGAGGLATGIAGGLAGMG
1		1				GIQNEKETMQSLNDRLASYLDR
1	l					VRSLETENRRLESKIREHLEKK
		l				GPQVRDWSHYFKIIEDLRAQIF
						ANTV\DNAR

NO: of peptide sequence hold in USSN 69:540,217 codo for peptide sequence of peptide s	SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
18623   48991   A   18732   663   2089   AFTTRSTFSTNYRSLGISVQAI YGAGPGRAARPASYAGAGG SRISVSRSTSFRGGMGSGGLAG RELAGGLAGMGGIQNEKE AQALNDRLGI-FTWDRYSL. DRTRKLGRAKFREHFGRKK PQVRIDWSHYFKINIBELIRAC RKYLLDNAPHPFLQDLTIAPS LD*P*FFKY*GQSLAMRGFLV NDIPHGSAKVIDDTQVHTDL AWRQRFEAPQRRELALSMKF PRRRLKLKGLSSPALPSSWG*P VRLPPNFFQDLRQRSLADHDGF MNELGSKKNPRKLRQSTWS QI*GRAPQLVTTSLLEVGSL TTLTZGKRTSPGPWKIRPW MKKS*KAQLGRNSP*REVGR YGFYKMBASFKRGSLHP*S WYGTRFGAEGTAPQAFRSYE C*NKRSKLEA*PSPYPPALD DGED**SLVDPLDSKQHAK QKTTTPPG*VGLKVS LHAK QKTTTPPG*VGLKVS LLPSKGKFGLALAVAGGVN LLYNDAGGHRAVIFDRFRGV DIVVGKGTHFLIPWVQETQ FDLCRSRPRNIVPSQSTG*AKD QNVQHHTAASLFRACRQPSF IFTSIGEDYGWSVCLPSUTTER KVSVGSLWMLGELITRELU RQVSGDLTFRAATFGLILDE SLTHLTFGKDFT*AVEAKQV QQEAEKGQICWLEKAEQQW AAIISABGDSKAAELJANSLA* GDGLIELRKLJF*AAFDIAYQI GSRNITTYLTFGGSVLLQLPQ GSPLPTTSICGSUCQLPQLPQLPQLPQLPQLPQLPQLPQLPQLPQLPQLPQLPQ							*=Stop codon, /~possible nucleotide
VGAGPGRAARPASYAGAGG SRISVSRSTSFRGGMGSGLG RELAGGU-AGMGGJQNEKE A/QALNDRLGLFTWDRVRSL DRRTRKL GRAKFREHFORK PQVRIDWSHYKINEDLIRAG RKYYLDNAPHPLQDITAPS LD*F*EFKY*GQSLAMRQFLV NDIPLGSAKVIDDTQYHTDL AWRQRFEAPGRELALSMK* PRRRKLKGLSSPRLPSSWG*P VRLPPHFODLAGRSLADIPOP MNELGSKKNPRKLRQSTWS Q*I*GRAPQLYTTTSLLEVGSL TTUTQKLRRISPGPWKIRPW MKKS*KAQLGNSP*REVCR YGPYKMEASFRGSLLHP*S WQTRFGAEGTAPQARSYEC C*NIKSKLEA*DRYPPALL DIGEDF*SLVDPLDSKQLHAK QKTTTPPG*VGLGKVVS NFRVEAGVRGQVKTCAF* LESNIGKFGLALAVAGGVVN: LYNDAGHRAVIFDRFRGVC DIVVGKGTHFLIPWVQETQ FDCRSRPRNVPSQSTG*AKD QNVQHHTAGSLFRACRQFS* IFSIGEDYGWSVCLPSUTTE KVSYGSLWMIGELITRELU RQVSDDLTERAATFGILLDE SLTHLTFGKDFT*AVEARCY QQEAERGGJCWLEKARCY GDGJELRKLJF*AAREDJAYJ RSRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGQSVLLQLPQJ RSRRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGQSVLLQLPQJ RSRRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGGSVLLQLPQJ RSRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGGSPLLQLPQJ RSRNTITYLPTGGSPLLQLPQJ RSRNTITYLPTGGSPLLQLPQJ RSRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGGSPLLGLPGPPRLIN SLSFLLFTPERINGEIFMIGLK		sequence		09/540,217		of peptide sequence	deletion, \=possible nucleotide insertion)
VGAGPGRAARPASYAGAGG SRISVSRSTSFRGGMGSGLG RELAGGU-AGMGGJQNEKE A/QALNDRLGLFTWDRVRSL DRRTRKL GRAKFREHFORK PQVRIDWSHYKINEDLIRAG RKYYLDNAPHPLQDITAPS LD*F*EFKY*GQSLAMRQFLV NDIPLGSAKVIDDTQYHTDL AWRQRFEAPGRELALSMK* PRRRKLKGLSSPRLPSSWG*P VRLPPHFODLAGRSLADIPOP MNELGSKKNPRKLRQSTWS Q*I*GRAPQLYTTTSLLEVGSL TTUTQKLRRISPGPWKIRPW MKKS*KAQLGNSP*REVCR YGPYKMEASFRGSLLHP*S WQTRFGAEGTAPQARSYEC C*NIKSKLEA*DRYPPALL DIGEDF*SLVDPLDSKQLHAK QKTTTPPG*VGLGKVVS NFRVEAGVRGQVKTCAF* LESNIGKFGLALAVAGGVVN: LYNDAGHRAVIFDRFRGVC DIVVGKGTHFLIPWVQETQ FDCRSRPRNVPSQSTG*AKD QNVQHHTAGSLFRACRQFS* IFSIGEDYGWSVCLPSUTTE KVSYGSLWMIGELITRELU RQVSDDLTERAATFGILLDE SLTHLTFGKDFT*AVEARCY QQEAERGGJCWLEKARCY GDGJELRKLJF*AAREDJAYJ RSRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGQSVLLQLPQJ RSRRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGQSVLLQLPQJ RSRRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGGSVLLQLPQJ RSRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGGSPLLQLPQJ RSRNTITYLPTGGSPLLQLPQJ RSRNTITYLPTGGSPLLQLPQJ RSRNTITYLPTGQSVLLQLPQJ RSRNTITYLPTGGSPLLGLPGPPRLIN SLSFLLFTPERINGEIFMIGLK							
SRISVSRSTSFRGGMGSGGLA RELAGGLAGMGGQNEKE A/QALNDRLGLFTWDRVRSLL DRATTRL GRAKFREHFGRK PQVRDWSHYFKINEDLINAG RKYLLDNAPHPFLQDLTIAPS LD+P*FEKY*GQSLAMRGFLV NDIPLGSAKVIDDTQYHTDL AWRQRFEAPQRELALSMK: PRRKLLGLSSPRLPSSWG*P VRLPNFQDLRQRSLADIPGP MNELGSKKNPRKLRQSTWS QI*GRAPQLVTTSLLEVGSL TTLTOKLRKTSPGPWKIRPW MKKS*YAQLGRNSP*REVGR YGRAPQLVTTSLLEVGSL TVLTQKLRKTSPGPWKIRPW MKKS*YAQLGRNSP*REVGR YGRYKMEASFKRGSLHP*S W/QTRGAEGTAPQAFRSYE C*NKRSKLEA*DRPPYPPALI DGEDF*SLVDPLDSKQLHAK QKTTTPPG*VGLGKVVS LESNGKFGLALAVAGGVVN: LYNDAGHRAVIFDRFRGVC DIVVGKGTHFLIPWQETQ FDCRSRPRNIVPSQSTG*AKD QNYQHTAASLFRACRQPSF IFTSIGEDYGWSVCLPSUTTER KVSVGSLWMLGELITRELU- RQVSGDLTFRAATFGLILDE SLTHLTFGKDFT*AVEAKQV QQEAEKGQICWLEKAEQW AAIISAEGDSKAAELJANSLA* GDGIELRKLJF*AAFDIAYQI RSRNITYLPTGQSVLLQLPQI GRPLPCTSRGLDLGPQPRLILD SLSLLFTERIDGEIFMIGLK SLSLTLFTERIDGEIFMIGLK SLSLTLFTERIDGEIFMIGLK SLSLTLFTERIDGEIFMIGLK SLSLTLFTER	18623	48991	Α	18732	663	2089	AFTTRSTFSTNYRSLG\SVQAPS
RELAGGUAGIMGGIQNEKE' A/QALNDRLGLTWDRVRSL DRRTRKLGRAFREHFORKK PQVRUWSHYFENIEDLRAG RKYLDNAPPI-QDLTIAPS LD+P=FFKY*GQSLAMRQFLW NDIPLGSAKYUDDTQYHTDL AWRQRFEA*PQREELALSMKH PRRRKLKGLSSPRLPSSWG*P VRLPPHFQDLAGRSLADIPGP MNELGSKKNPRKLRQSTW QI*GRAPQLYTTTSLLEVGSL TTLUTQKLRRTSPGPWKIRPW MKKS*KAQLGRNSP*REVGR YGPYKMEASFRGSLLHPS* WQTRFGAEGTAPQAFRSYEG C*NIKRSKLEA*PRPYPPALI DIGEDF*SLVDPLDSKQLHAK QKTTTPPG*VGLGKVVS  18624 48992 A 18733 53 1100 NFRVEAGVRGQKETGAF LESINGFFGLALAVAGGVVN: LYNDAGHRAVIFDRFRGVC DIVVGKGTHFLIP:WVQETQ FDCRSRPRNIVPSQSTG*AKD QNVQHHTASLFRACRQSFS IFTSIGEDYGWSVCLPSUTTE KVSYGSLWMLGELITREBLL RQVSGDLTFERATFGLILDE SLTHLTFGKDFT*AVEAKQV QQEAEKGQICWLEKAEQQK AAIISABGDSKAAELJANSLA* GDGIJELRKLJF*AAFDIAJQI RSRNITYLPTGQSVLLQLPQ RSRNITYLPTGQSVLLQLPQ RSRNITYLPTGQSVLLQLPQ RSRRNITYLPTGQSVLLQLPQ RSRNITYLPTGQSVLLQLPQ RSRRNITYLPTGQSVLLQLPQ RSRRNITYLPTGQSVLLQLPQ RSRNITYLPTGQSVLLQLPQ RSRRNITYLPTGQSVLLQLPQ RSRRNITYLPTGQSVLLQLPQ RSRRNITYLPTGQSVLLQLPQ RSRRNITYLPTGQSVLLQLPQ RSRRNITYLPTGQSVLLQLPQ RSRRNITYLPTGQSVLLQLPQ RSRRNITYLPTGQSVLLQLPQ RSRRNITYLPTGQSVLLQLPQ RSRRNITYLPTGQSVLLQLPQ RSRRNITYLPTGQSVLLQLPQ RSRRNITYLPTGQSVLLQLPQ RSRRNITYLPTGQSVLLQLPQ RSRRNITYLPTGQSVLLQLPQ RSRRNITYLPTGQSVLLQLPQ RSRRNITYLPTGQSVLLQLPQ RSRRNITYLPTGQSVLLQLPQ RSRRNITYLPTGGSVLLQLPQ RSRRNITYLPTGQSVLLQLPQ RSRRNITYLPTGGSVLLQLPQ RSRRNITYLPTGGSVLLQLPQ RSRRNITYL							YGAGPGRAARPASYAGAGGSG
A/QALNDRIGGTTWDRVRSL DRRTRKLGRAKFREHFGRKK PQVRDWSHYFKINEDLRAC RKYLLDNAPHPFLQDLTIAPS LD*P*EFKY*GQALAMGPL* NDIPLGSAKVIDDTQYHTDL AWRQRFEAPQRELALSMK! PRRRKLKGLSSPRLPSSWG*P VRLPPHFQDLRQRSLADIPCP MNELGSKKNPRRKLRQSTWS QP*GRAPQLVTITSLLEVGSL TTLTQKLRKTSPGPWKIRPW MKKS*KAQLGRNSP*FEVGR GYGPYKMEASFRGSLLHP*S W/QTRPGAEGTAPQAPRSYE C*NIKRSKLEA*DRPPYPPALL D/GEDF*SLVDPLDSKQLHAK QKTTPPG*VGLGKVS  18624 48992 A 18733 53 1100 NFRVEAGVRQVQKETCAF LESINGKFGLALAVAGGVN LLYNVDAGHRAVIFDRFRGVC DIVVGKGTHFILIPWQETQ FDXCRSPRNNYPSQSTG*AKD QNVQHHTAASLFRACRQPSF IFTSIGEDYGWSVCLPSUITTE KVSVGSLWMGELITKREUL RQVSDDLTERAATFGILDD SLTHLTFGKBFT*AVEAKQV QQEAEKGQICWLEKAEQQK AAIISAEGDSKAAELJANSLA* GDGJELRKLIP*AAEDKJQLPQ GRPLPTSTRGLDLDQLPQLPQLP GRSRNITYLPTGQSVLLJEPQ GRPLPTSTRGLDLDQLPQLPQLIP GGPLPTSTRGLDLDQLPQLIP GRSRNITYLPTGQSVLLJEPQ GRPLPTSTRGLDLDQLQPQLIL SLSFLLFTERINGEIFMIGLK			l				SRISVSRSTSFRG\GMGSGGLGQ
DRRTRKLGRAFREHFIGRKK PQVRIDWSHYFKINEDLIRAC RKYLLDNAPHPFLQDLTIARS LD*P*EFKY*GQSLAMRQFLV NDIPIGSAKVIDDTQYHTDL AWRQREFAPQRELALSMKY PRRKLKGLSSPRLPSSWG*P VRLPPNFQDLRQRSLADIPGP MNELGSKKNPRKLRQSTWS QI*GRAPQLVTTSLLEVGSL TTLTQKLRRTSPGPWKIRPW MKKS*KAQLGRNSP*REVGR YGPYKMEASFKRGSLHP*S W\tilde{\text{WTRFAGFAGFAPQAPRSYEC}} U\tilde{\text{C*NKISKLEAP}} W\tilde{\text{WTRFAGFAGFAPQAPRSYEC}} U\tilde{\text{C*NKISKLEAP}} U\tilde{\text{C*NKISKLEAP}} U\tilde{\text{C*NKISKLEAP}} U\tilde{\text{C*NKISKLEAP}} U\tilde{\text{C*NKISKLEAP}} U\tilde{\text{C*NKISKLEAP}} U\tilde{\text{C*NKISKLEAP}} U\tilde{\text{VTPG*VGLGKVVS}} U\tilde{\text{VNYSAGFAGFAQVNN}} U\tilde{\text{VNYAGAGFAGFAQVNN}} U\tilde{\text{VNYAGAGFAGFACAQVNN}} U\tilde{\text{VNYAGAGFAGFACAQVNN}} U\tilde{\text{VNYAGAGFAGFACAQVSN}} U\tilde{\text{VNYAGAGFAGFACAQVNN}} U\text{VNYAGAGFAGFAGFAGFAGFAGFAGFAGFAGFAGFAGFAGFAG							RELAGG\LAG\MGGIQ\NEKETM
PQVRIDWSHYKKNIEDLIKAC RKYLLDNAPHPLQDLTIAPS LD*P*ERKY*GQSLAMRGFLV NDIPLGSAKVIDDIQYHTDL AWRQRFEAPGRELALSMK* PRRRLKGLS\$PRLPSSWG*P VRLPPHFQDLQRSLADIPGP MNELGSKKNPRKLRQSTWS QI*GRAPQLYTTISLLEVGSL TTUTQKLRRISPGPWKIRPW MKK**KAQLGNSP*PEVGR YGPYKMEASFRGSLLHP*S WQTRPGAEGTAPQAPRSYEC C*NIKRSKLEA*DRPPYPPALI DIGED**SLVDPLDSKQLHAK QKTTTPPG*VGLGKVVS NFRVEAQWKQQKETCAF* LESINGKFGLALAVAGGVN: LYNVDAGHRAVIFDRERGVG DIVVGKGTHFLIPWQETQ FDCKSRPRINVPSQSTG*AKD QNVQHHTAASLFRACRQPS* IFTSIGEDYGWSVCLPSUTTE KVSVGLWMLGELITRELU RQVSDDLTERAATFGLILDE SLTHLTFGKDFT*AVERGV QQEAEGGQCWLEKAEQGK AAIISAEGDSKAAELJANSLA* GDGLJELRKLJE*AAEDJAYQJ RSRNITYLPTGQSVLLQLPQJ RSRNITYLPTGGSPLADLATQLPQPPLLIN RSLSPLLTPTERDGSPMGLK							A/QALNDRLGLFTWDRVRSLG
RKYLLDNAPHPFLQDLTIAPS LD*F*EFKY*GSLAMRFLV NDIPI-GSAKVIDDIQYHTDL AWRQRFEAPQRELALSMK: PRRRILLGLSSPRLPSSWG*P VRLPPNFQDLRQRSLADIPGP MNELGSKKNPRKLRQSTWS QI*GRAPQLVTTSLLEVGSL TTLTQKLRKTSPGPWKIRPW MKK*S*KAQGRNSP*REVGR WQTRRGAEGTAPQAFRSYE C*NIKRSKLEA*PSPPYPPALI DIGEDF*SLVDPLDSKQLHAK QKTTTPPG*VGLGKVVS LESNGKFGLALAVAGGVVN: LYNVDAGHRAVIFDRFRGVC DIVVGKGTHFLIP-WQETQ FDCRSRPRNIVPSQSTG*AKD QNVQHHTAASLFRACRQPSF IFTSIGEDYGWSVCLPSUTTER KVSVGSLWMIGELITRELU- RQVSDBLTFRAATFGLILDE SLTHLTFGKDFT*AVEAKQV QQEAEKQICWLEKAEQU AAIISAEGDSKAAELJANSLA* GDGIELRKLJF*AAFDIAYQI GSRNITTYLPTGQSVLLQLPQI GSRPLTYLPTGQSVLLQLPQI GSRNITTYLPTGQSVLLQLPQI GSRNITTYLPTGQSVLLQLPQI GSRNITTYLPTGQSVLLQLPQI GSRPLTTSICEDIFIGGSIFMIGLK SLSFLLFTERIDGEIFMIGLK SLSFLTERIDGEIFMIGLK SLSFLTERIDGEIFMIGLK SLSFLTERIDGEIFMIGLK SLSFLTERIDGEIFMIGLK SLSFLTERIDGEIFMIGLK SLSF		1	1			1	DRRTRKLGRAKFREHFGRKKG
LD*P*EFKY**GQSLAMRQFLV NDIPLGSAKY\IDDITQYHTDL AWRQRFEAPQRRELALSMK PRRRLKLGLSSPRLPSSWG**P VRLPPNFQDLQRSLADIPGP MNELGSKK\PRRKLKGLSSPRLPSSWG**P VRLPPNFQDLQRSLADIPGP MNELGSKK\PRRKLRQSTWG QI**GRAPQLVTTTSLLEVGSL TTLJTQKLRRISPGPWKIRPW MKKS**KAQLGRNSP*REVCR YGPYKMEASFRGSLLPT**S W\rightarrow Trillevgrager W\rightarrow Trillevgrager W\rightarrow Trillevgrager W\rightarrow Trillevgrager W\rightarrow Trillevgrager W\rightarrow Trillevgrager W\rightarrow Trillevgrager W\rightarrow Trillevgrager W\rightarrow Trillevgrager W\rightarrow Trillevgrager W\rightarrow Trillevgrager U\rightarrow Trillev							PQ\VR\DWSHYFKI\IEDL\RAQIF
NDIPLGSAKVUDDTQYHTDL AWRQRFEAPQRRELALSMKI PRRRKLKGLSSPRLPSSWGPP VRLPPHFQDLRQRSLADIPGP MNELGSKKPRRKLRQTSWGP MNELGSKKPRRKLRQTSWGP MNELGSKKPRRKLRQTSWGP MNELGSKKPRRKLRQTSWGP MKKS*KAQLGRNSP*REVGR GPYKMBASFRGSLLHP*S WQTRGAGGTAPQAPSYGE C*NIKRSKLBA*DRPPYPPALL DGEDF*SLVDPLDSKQLHAK QKTTTPG*GCLGKV'S  18624 48992 A 18733 53 1100 NFRVEAGVRQVQKETCAF LESIGKFGLALAVAGGVVN. LYNVDAGHRAVIFDRFRGVC DIVVGKGTHFLIPIWQETQ FDCSRSPRNIVPSQSTG*AKD QNVQHHTAASLFRACRQPSF ITTSIGEDYGWSVCLSVITTE KVSVGSLWMGELITKREUL RQVSSDLTERAATFGLILDE SLTHLTFGKBFT*AVEAKQV QQEAEKGQICWLEKAEQQKI AAIISAEGDSKAAELJANSLA* GDGLIELKRLP*AAFDIAYQI RSRNITYLPTGQSVLLQLPQI GPPLPCTSRGLDLGPQPRILIN SLSFLLFTERGLDGPOPRILIN SLSFLLFTERGLDGPOPRILIN SLSFLLFTERGLDGPOPRILIN SLSFLLFTERGLDGPOPRILIN SLSFLLFTERINGEIFMIGLK			i				RKYLLDNAPHPFLQDLTIAPSLL
AWRQFEAPQRELALSMKI PRRKLKGLSSPKLPSSWG*P VRLPPNFQDLRQRSLADIPGP MNELGSKKNPRKLRQSTW QI*GRAPQLVTTSLLEVGSL TTLTQKLRRTSPGPWKIRPW MKKS*KAQLGRNSP*REVGR YGPYKMEASFKRGSLHP*S W\tilde{\text{WTRPAGAEGTAPQAPRSYEC}} C*\nikrsklea*\nipppypall D\tilde{\text{GEP*SLVDPLDSKQLHAK}} Q\tittpg\*vGLGKVS  18624 48992 A 18733 53 1100 NFRVEAGVRGVQQKETCAFF LESIKGFGLALAVAGGVN: LYNDAGHRAVIFDRFRGV. DIVVGKGTHFLIP\tilde{\text{WVOETQ}} FD\tilde{\text{CRSRPRNIVPQSTG*AKD}} Q\tilde{\text{NVOETQHAMAGTERFRGV}} FTSIGEDYGWSVCLPSITTE KVSVGSLWMLGELITRELU- RQVSGDL\tilde{\text{LTRE}} RQVSGDL\tilde{\text{LTRE}} Q\tilde{\text{QELITRE}} SLTHLTFGK\tilde{\text{DFT}}^+\tilde{\text{AKQV}} Q\tilde{\text{QAERGG}} AAIISABGDSKAAELJANSLA* G\tilde{\text{GGLIERKLIP}} G\tilde{\text{CGLIERKLIP}} G\tilde{\text{CGLIERKLIP}} G\tilde{\text{CGLIERKLIP}} SLSTLLTFGRSCDLGPQPRLILD SLSLFLLTFEINGEIFMGLK SLSLLLTFEINGEIFMIGLK				1			LD*F*EFKY*GQSLAMRQFLWR
PRRRKILKGLSSPRLPSSWG-P VRLPPNFQDLRQRSLADIPGP MNELGSKKNPRKKLRQSTWS QI*GRAPQLVTTTSLLEVGSL TTUTQKLRRISPGPWKIRPS MKKS*KAQLGRNSP;REVGR YGPYKMEASFRGSLLPTS* W/QTRPGAEGTAPQAPRSYEC C*NIKRSKLEA*DRPPYPPALI DIGEDF*SLVDPLDSKQLHAK QKTTTPPG*VGLGKVVS  I8624 48992 A 18733 53 1100 NFRVEAGVKQQKETCAFE LESNGKFGLALAVAGGVVN: LYNVDAGHRAVIFDRFRGVG DIVVAGKGTHFLIPWQETQ FDCKSRRRNIVPSQSTG*AKD QNVQHHTAGLFRACRQFS* IFTSIGGDYGWSVCLPSUTTE KVSVGSLWMLGELTTREELJ RQVSDDLTFRAATFGLILDE SLTHLTFGKDFT*AVEKQV QQEAEKGQICWLEKAEQQKS AAIISABGDSKAAELJANSLA* GDGIJELRKLJF*AAEDJAYQJ RSRNITYLPTGQSVLLQLPQJ RSRNITYLPTGQSVLLQLPQJ GPPLPCTSRGLDLGPQPRLILN SLSFLLFTERINGEIFMIGLK SISPLLFTERINGEIFMIGLK SLSFLFTERIN							NDIPLGSAKVIDDTOYHTDLO
VRLPPNFQDLRQRSLADIPCP MNELGSKKNPRRKLRQSTWS QI*GRAPQLVTITSILEVGSL TTLTQKLRRTSPGPWKIRPW MKKS*KAQIGRNSP*FEVGR W/QTRFQAEGTAPQAFRSYEC C*NIKRSKLEA*DRPPYPPALI DIGEDF*SLVDPLDSKQLHAK QKTTTPPG*SLVDPLDSKQLHAK QKTTTPPG*SLVDPLDSKQLHAK QKTTTPPG*SLVDPLDSKQLHAK QKTTPPG*VGLGKVVS LESNIGKFGLALAVAGGVVN: LYNVDAGHRAVIFDRFRGVC DIVVGKGTHFILIPWQETQ FDVCSRPRNIVPSQSTG*AKD QNVQHHTAASLFRACRQPSF IFTSIGEDYGWSVCLPSITTE KVSVGSLWMIGELITREFLU RQVSDDLTFERAATFGLILDE SLTHLTFGKJDFT*AVEAKQV QQEAEKQICWLEKAEQQK AAIISAEGDSKAAELJANSLA* GDGJELRKLJF*AAFDIAYQI RSRNITYLPTGQSVLLQLPQI GPPLPCTSRGLDLGPQPRILIN SLSFLLFTERICBIFMIGLK SLSFLLFTERINGBIFMIGLT SLSFLTERINGBIFMIGLT SLSFLTERINGBIFMIGLT SLSFLTERINGB		1					AWRORFEAPORRELALSMKKE
MNELGSKK)PRRKLRQSTW QI*GRAPQLVTTTSLLEVGSL TTL/TQKLRKTSPGPWKIRPW MKKS*KAQLGRNSP*REVCR YGPYKMEASFKGSLLHP*S WOTRGAEGTAPQAFRSYE C*NIKRSKLEA*PRPYPPALI DIGEDP*SLVDPLDSKQLHAK QKTTTPPG*VGLGKVVS  18624 48992 A 18733 53 1100 NFRVEAGVRGVQKETCAFK LESIKGFGLALAVAGGVVN: LYNDAGHRAW1FDRFRGV DIVVGKGTHFLIP:WVQETQ FDCRSRPRNIVPSQSTG*AKD QNVQHHTASLFRACRQSF* IFTSIGEDYGWSVCLPSUTTE KVSVGSLWMLGELIT/REGLL RQVSDDLTERAATFGLILDE SLTHLTFGKDFT*AVEAKQV QQEAEKGQICWLEKAEQQK AAIISAEGDSKAAELJANSLA* GDGLIELKRLF*AAFDIAYQI RSRNITYLPTGQSVLLQLPQI RSRNITYLPTGQSVLLQLPQI GPPLPCTSRGLDLGPQPRILIN SLSFLLFTERINGEIFMIGLK SLSFLTERINGEIFMIGLK SLSFLTERINGEIFMIGLK SLSFLTERINGEIFMIGLK SLSFLTERINGEIFMIGLK SLSFLTERINGEIFMIGLK SLSF		1 1	l				PRRRKLKGLSSPRLPSSWG*PVE
MNELGSKK)PRRKLRQSTW QI*GRAPQLVTTTSLLEVGSL TTL/TQKLRKTSPGPWKIRPW MKKS*KAQLGRNSP*REVCR YGPYKMEASFKGSLLHP*S WOTRGAEGTAPQAFRSYE C*NIKRSKLEA*PRPYPPALI DIGEDP*SLVDPLDSKQLHAK QKTTTPPG*VGLGKVVS  18624 48992 A 18733 53 1100 NFRVEAGVRGVQKETCAFK LESIKGFGLALAVAGGVVN: LYNDAGHRAW1FDRFRGV DIVVGKGTHFLIP:WVQETQ FDCRSRPRNIVPSQSTG*AKD QNVQHHTASLFRACRQSF* IFTSIGEDYGWSVCLPSUTTE KVSVGSLWMLGELIT/REGLL RQVSDDLTERAATFGLILDE SLTHLTFGKDFT*AVEAKQV QQEAEKGQICWLEKAEQQK AAIISAEGDSKAAELJANSLA* GDGLIELKRLF*AAFDIAYQI RSRNITYLPTGQSVLLQLPQI RSRNITYLPTGQSVLLQLPQI GPPLPCTSRGLDLGPQPRILIN SLSFLLFTERINGEIFMIGLK SLSFLTERINGEIFMIGLK SLSFLTERINGEIFMIGLK SLSFLTERINGEIFMIGLK SLSFLTERINGEIFMIGLK SLSFLTERINGEIFMIGLK SLSF	ŀ						VRLPPNFQDLRQRSLADIPGPN
TTL/TQKLRRTSPGPWKIRPW MKKS*KAQLGNRSP*REVGR YGPYKMEASFKRGSLHP*S W/GTRGAEGTAPQAFRSYE C*NIKRSKLEA*DRPPYPPALI D/GEDF*SLVDPLDSKQLHAK QKTTTPPG*SLVDPLDSKQLHAK QKTTTPPG*VGLGKVVS  18624 48992 A 18733 53 1100 NFRVEAGVRGVQQKETCAFR LESIKGFGLALAVAGGVVN. LYNDAGGHRAVIFDRFRGVC DIVVGKGTHFLIPLWQETQ FDV.CRSRPRNIVPSQSTG*AKD QNVQHHTAASLFRACROPSF IFTSIGEDYGWSVCLPSUTTER KVSVGSLWMLGELITKRELU RQVSDBLTFERATFGLILDE SLTHLTFGK/DFT*AVEAKQV QQEAEKGQICWLEKAEQQK AAIISAEGDSKAAELJANSLA* GDGJELRKLJF*AAFDIAYQI RSRNITYLPTGQSVLLQLPQI GPPLPCTSRGLDLGPQPRLILN SLSFLLFTERINGEIFMIGLK SLSFLTERINGEIFMIGLK SLSFLTERINGEIFMIGLK SLSFLTERINGEIFMIGLK SLSFLTERINGEIFMIGLK SLSFLTERINGE							MNELGSKKNPRRKLROSTWSO
MKKS*KAQLGRNSP*REVCR YGPYKMEASFKRGSLLHP*SC W/GTRPGAEGTAPQAPRSYPEC C*NIKRSKLEA*DRPPYPPALI D/GEDF*SLVDPDLDSKQLHAK QKTTTPPG*VGLGKVVS QKTTTPPG*VGLGKVVS INFRVEAGVRGVQQKETCAFF LESIKGFYGLAAVAGGVVN LYNVDAGHRAVIFDRFRGVC DIVVGKGTHFLLIP.WVQETQ FDLCRSRPRNVPSQSTG*AKD QNVQHHTAASLFRACRQPSF IFTSIGEDYGWSVCLPSHTTEL KVSVGSLWMLGELITKREUL RQVSSDDLTERAATFGLILDL SLTHLTFGKDFT*AVEAKQV QQEAEKQQICWLEKAEQQKF AAIISAEGDSKAAELIANSLA* GDGLIELRKLIP.*AAFDIAYQI RSRNITYLPTGQSVLLQLPQ GPPLPCTSRGLDLGPQPRLILN SLSFLLFTERGLDGPQPRLILN SLSFLLFTERGLDGPQPRLILN SLSFLLFTERGLDGPQPRLILN SLSFLLFTERGLDGPQPRLILN SLSFLLFTERINGEIFMIGLK							OI*GRAPOLVTTTSLLEVGSLLK
MKKS*KAQLGRNSP*REVCR YGPYKMEASFKRGSLLHP*SC W/GTRPGAEGTAPQAPRSYPEC C*NIKRSKLEA*DRPPYPPALI D/GEDF*SLVDPDLDSKQLHAK QKTTTPPG*VGLGKVVS QKTTTPPG*VGLGKVVS INFRVEAGVRGVQQKETCAFF LESIKGFYGLAAVAGGVVN LYNVDAGHRAVIFDRFRGVC DIVVGKGTHFLLIP.WVQETQ FDLCRSRPRNVPSQSTG*AKD QNVQHHTAASLFRACRQPSF IFTSIGEDYGWSVCLPSHTTEL KVSVGSLWMLGELITKREUL RQVSSDDLTERAATFGLILDL SLTHLTFGKDFT*AVEAKQV QQEAEKQQICWLEKAEQQKF AAIISAEGDSKAAELIANSLA* GDGLIELRKLIP.*AAFDIAYQI RSRNITYLPTGQSVLLQLPQ GPPLPCTSRGLDLGPQPRLILN SLSFLLFTERGLDGPQPRLILN SLSFLLFTERGLDGPQPRLILN SLSFLLFTERGLDGPQPRLILN SLSFLLFTERGLDGPQPRLILN SLSFLLFTERINGEIFMIGLK							TTL/TQKLRRTSPGPWKIRPWTS
WOTERGAEGTAPQAFRSYEG C*NIKRSKLEA*DRPPYPPALI DIGEDF*SLVDPLDSKQLHAK QKTTTPPG*VGLGKVVS  18624 48992 A 18733 53 1100 NFRVEAGVRGVQKETCAFR LESNGKFGLALAVAGGVVN. LYNVDAGHRAV1FDRFRGV DIVVGKGTHFLIPWVQETG FDCKSRPRNIVPSQSTG*AKD QNVQHHTAASLFRACRQFS* IFTSIGEDYGWSVCLPSUITTE KVSVGSLWMLGELITREGLU RQVSDDLTERAATFGILIDE SLTHLTFGKDFT*AVEAKCV QQEAEKGQICWLEKAEQQK AAIISAEGDSKAAELJANSLA* GDGLJELRKLJF*AAEDJAYQL RSRNITYLPTGQSVLLQLPQ GPPLPCTSRGLDLGPQPRLILN SLSFLLFTEBINGEIFMIGLK SLSFLLFTEBINGEIFMIGLK SLSFLLFTEBINGEIFMIGLK							MKKS*KAQLGRNSP*REVGRPP
C*NIKRSKLEA*DRIPYPPALI DIGED*SLVDPLDSKQLHAK QKTTTPPG*VGLGKVVS QKTTTPPG*VGLGKVVS NFRVEAGVRGVQQKETCAF LESIGKFIGLALAVAGGVVN LYNVDAGHRAVIFDRFRGVG DIVVIGKGTHFILIPIWVQETQ FDICRSPRRINVPGSGTG*ARD QNVQHHTAASLFRACRQPSF IFTSIGEDYGWSVCLPSITTEN KVSVGSLWMLGELITKREUL RQVSDDLTERAATFGLILDL SLTHLTFGKDFT*AVEAKQV QQEAEKGQICWLEKAEQQKI AAIISAEGDSKAAELJANSLA* GDGLIELRKLIP.*AAFDIAYQI RSRNITYLPTGQSVLLQLPQ GPPLPCTSRGLDLGPQPRILIN SLSFLLFTERGLDLGPQPRILIN SLSFLLFTERINGEIFMIGLK				1			YGPYKMEASFKRGSLLHP*SQS
DIGEDF*SLVDPLDSKQLHAK QKTTTPPG*VGLGKVVS  18624 48992 A 18733 53 11100 NFRVEAGVRGVQQKETCAFR LESINGRFGLALAVAGGVVN. LYNVDAGHRAVIFDRERGV. DIVVGKGTHFLIPLWQETQ FDLCRSRPRNIVPSQSTG*AKD QNVQHHTAASLFRACROPS* IFTSIGEDYGWSVCLPSHITTE KVSVGSLWMLGELITREUL) RQVSDDLTFRAATFGLILDE SLTHLTFGKDFT*AVEAKQV QQEAEKGQICWLEKAEQQK AAIISAEGDSKAAELJANSLA* GDGJELKKLJF*AAFDIAYQI RSRNITYLPTGQSVLLQLPQI GPPLPCTSRGLDLGPQPRLILN SLSFLLFTEBINGEIFMIGLK SLSFLLFTEBINGEIFMIGLK SLSFLLFTEBINGEIFMIGLK							W/QTRPGAEGTAPQAPRSYEGP
QKTTTPPG*VGLGKVVS  18624 48992 A 18733 53 1100 NFRVEAGVROVQQKETCAFR LESINGKFGLALAVAGGVVN LYNVDAGHRAVIFDRFRGVU DIVVGKGTHFLIP\WVQETQ FDLCRSRPRNVPSQSTG*AKD QNVQHHTAASLFRACRQPSF IFTSIGEDYGWSVCLPSUTTER KVSVGSLWMLGELITKRELV RQVSSDLATERAATFGLILDD SLTHLTFGKDFT"AVEAKQV QQEAEKQQICWLEKAEQQKV AAIISAEGDSKAAELIANSLA* GDGLIELRKILE*AAFDIAYQI RSRNITYLPTGQSVLLQLPQ GPPLPCTSRGLDLGPQPRLILN SLSFLLFTERGLDGPQPRLILN SLSFLLFTERINGEIFMIGLK							C*NIKRSKLEA*DRPPYPPALLE
18624 48992 A 18733 53 1100 NFRVEAGVROVQKETCAF LESIGKFIGLALAVAGGVVN LYNVDAGHRAVIFDRFRGVV DIVVIGKGTHFILIPIWVQETQ FDLCRSRPRNIVPSQSTG*AKD QNVQHHTAASLFRACRQPSF IFTISIGEDVGWSVCLPSUITER KVSVGSLWMLGELITKREUL RQVSDDLTFRAATFGILDD SLTHLTFGKBFT*AVEAKQV QQEAEKGQICWLEKAEQQKF AAIISAEGDSKAAELJANSLA* GDGJELRKLP*AAFDLAYQI RSRNITYLPTGGSVLLQLPQ GPPLPCTSRGLDLGPQPRILIN SLSFLLFTERGLDFIMGLK	l		1				D\GEDF*SLVDPLDSKQLHAKPI
LESIGKFIGLALAVAGGVVN. LYNVDAGHRAVIFDRFRGVU DIVVGKGTHFILPIWQETT FDCRSRPRNIVPSQSTG*AKD QNVQHHTAASLFRACRQPSF IFTSIGEDYGWSVCLPSUTTE* KVSVGSLWMLGELITKRELV RQVSDDL/TERAATFGLILDE SLTHLTFGKDFT*AVEARGV QQEAFKGQICWLEKAEQQKE AAIISAEGDSKAAELIANSLA* GDGLIELRKLE*AAFDIAYQI RSRNITYLPTGQSVLLQLPQI GPPLPCTSRGLDLGPQPRLILN SLSFLLPTERIDCEIFMIGLK					ļ		QKTTTPPG*VGLGKVVS
LYNVDAGHRAVIFDERGVG DIVVGKGTHFLIPWVQETQ FDCRSRPRNVPSQSTG*AKD QNVQHHTAASLERACRQPSF IFTSIGEDYGWSVCLPSHITEN KVSVGSLWMLGELITKREUL RQVSSDLYTERAATFCLILDL SLTHLTFGKDFT*AVEAKQV QQEAEKQQICWLEKAEQQKH AAIISAEGDSKAAELJANSLA* GDGLIELRKLIP*AAFDIAYQI RSRNITYLPTGQSVLLQLPQ GPPLPCTSRGLDLGPQPRLILN SLSFLLFTERGLIPMIGLK	18624	48992	Α	18733	53	1100	NFRVEAGVRGVQQKETCAFKV
DIVVGKGTHFLIPIWVQETQ FDLCRSRPRNIVPSQSTG*AKD QNVQHHTAASLFRACROPS* IFTSIGEDYGWSVCLPSUITTE KVSVGSLWMLGELITKRELU RQVSDDLTFRAATTGLILDE SLTHLTFGKDFT*AVEAKQV QQEAEKQICWLEKAEQQK AAIISAEGDSKAAELIANSLA* GDGJELKKLP*AAEDIAYQI RSRNITYLPTGQSVLLQLPQI GPPLPCTSRGLDLGPQPRLILN SLSFLLFTEBINGEIFMIGLK SLSFLLFTEBINGEIFMIGLK							LESI\GKF\GLALAVAGGVVNSA
FDICRSRPRNIVPSQSTG*AKD QNIVQHITAASLFRACRQPSF IFTSIGEDYGWSVCLPSUTTEV KVSVGSLWMLGELITKRELV RQVSDDL/TERAATFGILIDE SLTHLTFGKDFT*AVEAKQV QQEAFKQOJCWLEKAEQQKE AAIISAEGDSKAAELIANSLA* GDGLIELRKLE*AAFDIAYQI RSRNITYLPTGQSVLLQLPQ GPPLPCTSRGLDLGPQPRLILN SLSFLLFTERINCEIFMIGLK	ĺ		1	ļ			LYNVDAG\HRAVIFDRFRGVQ\
QNVOHITAASLERACROPSE IFTSIGEDYGWSVCLPSIITTEN KVSVGSLWMLGELITKREUL RQVSSDDLITERAATTGLILDE SLTHLTFGKBFT-AVEAKOV QQEAEKGQICWLEKAEQQKE AAIISAEGDSKAAELJANSLA' GDGLELKRLIP-AAFDLAYQI RSRNITYLPTGQSVLLQLPQI GPPLPCTSRGLDLGPQPRLILN SLSFLLFTERINGEIFMIGLK			1	1			DIVV\GKGTHF\LIP\WVQETQLS
IFTSIGEDYGWSVCLPSITTEV KVSVGSLWMLGELITKRELL RQVSDDLITERAATFGLILDE SLTHLTFGK:DFT*AVEAKQV QQEAEKQQ:CWLEKAEQQK: AAIISAEGDSKAAELIANSLA: GDGLIELRKL/E*AAEDIAYQI RSRNITYLPTGQSVLLQLPQi GPPLCTSRGLDLGPQPRLILN SLSFLLPTPEINCEIFMIGLK			l				FD\CRSRPRN\VPSQSTG*AKDL
KVSVGSLWMLGELITKRELL RQVSDDLTERAATFGLILDE SLTHLTEGKDFT-AVEAKQV QQEAEKGQICWLEKAEQQKI AAIISAEGDSKAAELIANSLA' GDGLIELRKLE'AAFDIAYQI RSRNITYLPTGQSVLLQLPQ GPPLPCTSRGLDLGPQPRLILIN SLSFLLFTPEINCEIFMIGLK							QNVQHHTAASLFRACRQPSFPR
RQVSDDL/TERAATFGLILDE SLTHLTFGK/DFT*AVEAKQV QQEAEKGQICWLEKAEQQK AAIISAEGDSKAAELIANSLA* GDGJELRKLJP*AAEDIAYQI RSRNITYLPTGQSVLLQLPQI GPPLPCTSRGLDLGPQPRLILN SLSFLLFTEBINGEIFMIGLK			1				IFTSIGEDYGWSVCLPS\ITTEV\L
SLTHLTFGK.DFT*AVEAKQV QQEAEKGQICWLEKAEQQKI AAIISAEGDSKAAELIANSLA; GDGLIELRKL/E*AAEDIAYQI RSRNITYLPTGQSVLLQLPQI GPPLCTSRGLDLGPQPRLILN SLSFLLPTPEINCEIFMIGLK			1				KVSVGSLWMLGELITKRE\LVS
QQAAEKQj(Wlekaeqqka AAIISAEGDSKAAELIANSLA* GDGLIELRKI,F*AAEDIAYQI RSRNITYL,PTGQSVLLQLPQ GPPLPCTSRGLDLGPQPRLILN SLSFLLPTETINCEIFMIGLK	1		1				RQV\SDDL\TERAATFGLILDDV
AAIISAEGDSKAAELIANSLA' GDGLIELKKLE*AAEDIA YQI RSRNITYLPTGQSVLLQU PQI GPPLPCTSRGLDLGPQPRLILI SLSFLLPTPEINCEIFMIGLK			1	1			SLTHLTFGK\DFT*AVEAKQVA
AAIISAEGDSKAAELIANSLA' GDGLIELKKLE*AAEDIA YQI RSRNITYLPTGQSVLLQU PQI GPPLPCTSRGLDLGPQPRLILI SLSFLLPTPEINCEIFMIGLK			1			1	QQEAEKGQICWLEKAEQQKK\
RSRNITYL PTGQSVLLQLPQ GPPLPCTSRGLDLGPQPRLILN SLSFLLPTPEINCEIFMIGLK			l		l		AAIISAEGDSKAAELIANSLATA
GPPLPCTSRGLDLGPQPRLILN SLSFLLPTPEINCEIFMIGLK							GDGLIELRKL/E*AAEDIAYQLS
GPPLPCTSRGLDLGPQPRLILN SLSFLLPTPEINCEIFMIGLK			l				RSRNITYLPTG\QSVLLQ\LPQLR
	l	1				l	GPPLPCTSRGLDLGPQPRLILNN
19725 48002 10 19724 1222 459			ŀ			l	SLSFLLPTPEINCEIFMIGLK
110023 140773 10 110734 1222 1436	18625	48993	С	18734	222	458	

SEQ ID NO:	SEQ ID NO; of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18626	48994	A	18735	2104	2758	QFCPSRQKGCLQKTFRHFVAGH GGDFLFRSPTHAFPECVPLFPLP PVTIVRRCPPFS*VLSSSPRNSQ NTIPRSPFLSPGTLSRSPAGSRDP ORPAGSNTRLGPTAPVSILAP VDIGFRSTDCWSLQPQVPVNPG SRPAPTNPRSRSTPVDPGSNTRL GPTAFVSRLAPVV*ALGPLTAG PYSPRCPVNPGSRPAPTNPRSR STPVDPGSNTRLGPTAPVSRLA PVDIGFRSTDCWSLQPQVPVNP GSRPAPTNPRSRSTPVDPGSNTRL PVDGSRTAPTNGFTAPVSRLA PVDIGFRSTDCWSLQPQVPVNP GSRPAPTNPRSRSTPVDPGTRTT PEGL
18627	48995	A	18736	2	280	AMGFIVAPSLGCF/VGSRFVHG EGLRWYAGLQKPSWHPPHWV LGPVWGTLYSAMGYGSYLVW KELGGFTGVSRASEVAPPEPPP GSSVLCFLHA
18628	48996	A	18737	331	972	TAAAAAMAPPWVPAMGFTLAP SLGCFVGSRFVHGEGLRWYAG LQKPSWHPPHWVLGPVWGTLY SAMGFVGVHWPGDKPGFLQGE AWPRTEDTGQLALNWA WPPIF FGARQMGGALVNLLLVS\GAA GHTTLGGRGAS\QWLAARLLYP VLGLA WPSTTTTQTTCVWRID\ NHGWHGGRRLARVSARPTMG LQLHQAGAITLVMWWPSRFHD HWAC
18629	48997	Α	18738	1	603	
18630	48998	A	18739	1	1782	
18631	48999	A	18740	237	876	CESFCWHIFFWDIFNLFVTAPF LVHVDYQGFESVAKKYDVMN DMMSLGIHRVWEGFSCSGKMH PLPGDIQLLDVAGGTGDIAFRH. NYVQSQHQRKQKRQLRAQQN LSWEEIAKEVQNEEDSLGGSRV VVCDINKEMLKVGKQKALAQQ YRAAHKSGVILDCLWFPPILHPI AQQICQL YLQNTSGIWSLEYL CYHLLVQATIFSYLDCCNSL

SEO ID	SEQ ID NO:	24-4	SEQ ID NO:	Nucleotide	Nucleotide to entire of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	coden for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
18632	49000	A	18741	112	995	VLGSLSQEKRAAETHFGFETVS EEEKGGKVYQVFESVAKKYDV MNDMMSLGIHRVWKDLLLWK MHPLPGTQLDVAGGTGDIAFF FLNYVSVPASEKTEEAVKGPTK FLIGKNLPKSTRMKKIPWAGTTR VVVCDINKEMLKVGKQKALAI KDTRAGLAWLL*DAGELPFDD DKFDIYTIAGIRWTHIDQALQ GSSFGCLKPGGRFLCLGFSQWE
						QSP\LSRLYDLYS\SRVIPVLGEV IAGDWKSYQYLVE\SIRRFPSQE \KFKD\MIEDAGFPQ\V*LTKV*H QGIVAIHSGFKL
18633	49001	Α	18742	117	403	
18634	49002	С	18743	62	370	
18635	49003	Α	18744	179	527	IQEPPVI**GLHMVHNFNTIFVSS YFKFESTFAISFLKVFNT/CFFSI* IKSLDEQCVVGKISKHWTGILR EAFTDADNFGIQFPLDLDVKMK AVMKVGICGKNLVKQGNFTMT HSN
18636	49004	A	18745	3	1242	AAPOAGLSPWAIAAAIQHLHLB TQCSSPYTOCLEPRITRATIYYSR WSYIIPLGSVP*SP*PFQEAS/AL TLPPACSFYGPLT*FQPKP*GSFS RQIPSSYLNCKDAFLPLCSNPP QCRPFTGVGLV DVLTGFETIN KYEIKNSFGORVYFAAEDTDCC TRNCCGPSRPFTLRIIDNMGQE VITLERPLRCSSCCCPCCLQEIKS LDEQCVVGKISKYWTGILREAF TDADNFGIQPFLDLDVKMKAV MIGACFLIBRNCSPAMEGSWM ENYFDEMTEIGFRRSVITNFSEL KEHVLTHCKEANKNLDKMLDG WLTRKNSVERTINSELMEVKTI NEKLTICKISKYWSGFVNDVFT NACNFGIHVPADLDVTVKAAM IGACFLIBRGHVTSLEHNI KACHTERSTENDER KEHVLTHCKEANKNLDKMLDG WLTRKNSVERTINBELMEVKTI NEKLTICKISKYWSGFVNDVFT NACNFGIHVPADLDVTVKAAM IGACFLFAFRLGSELHN
18637	49005	В	18746	277	2415	
18638	49006	Α	18747	102	196	

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN 09/540.217	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
18639	49007	Α	18748	897	1656	SNAGLRHVCRTSCQSGRARSCH
		1				VGLHTPWVS*VPWHPWGIRWR
		1				GDPOKSORSRKCCVPGGAP/OK
		1				GGDPEPQPSLSVSWNWLSGSCA
		1				GFRAVLPRKPQRKVWLFASSA
		1				GTAATEPPR**LAWKADSGGDP
		1				WOOPOOSARPHA*TWTWRGD
		1				GAPPGRVA/QGRGTAGGASAG
		l				VSSGRSRGSPOTGFOALOSCLE
		1				ASRRPPVVACNPHPAGALPAAC
		l				AGNRATLMTGSCLOMPIMYEE
		l				AOLRLEELCTKARLNCOWFL
18640	49008	A	18749	756	884	CLORLLPPGFRROPSKYRRNRG
	.,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	1				KSGKG*RPSPVATWOPDYNI
18641	49009	A	18750	1826	2772	RRVLEAMGPSRAAKVLSVCVR
		ĺ				SRIGPLICSORHPATSKTKPOGR
		l				PPGEOGTPRDNPRRNNRPARSA
		l				TPRGA/PQGAPPRPGEEPNAPQT
		l				IDKGPPSPPSRGHTRRLARSGNO
		l			ŀ	PPERHTPAAGGKTRYVROSVL
		l				HRARGGEPVRMPRLPRIAEA/P
		l				APDRVECF*VVQSPAREMHSCQ
		l				ADSMCPVW*GRIWRSAGSC*SR
		l				SEKILVWIPQSGLQAHACPSEA
		l			ŀ	HKMPGNPRDGGAGICKSSPGG
		l			1	KGERRKVEGGSTTRAGTSRDS
		l			ľ	VSKRHANTMGEQAQGEKHPRG
		l				TV*KTKRRGPKGOTRGTKAPEE
		ı				ETSREPPCTGPI
18642	49010	Α	18751	196	322	
18643	49011	С	18752	189	650	
18644	49012	A	18753	1	53	
18645	49013	Α	18754	31	449	
18646	49014	A	18755	1	389	GMPTSTIASCSQDGRVFIWTCD
	1	I	l	l		DASSNTWSPKLLHKFNDVVWH
		l		l		VSWSITANILAVSGGDNKVTEG
		l		l		QQNEQ*QDRWGLAPHPPAPGL
	1	I		l	į .	PLPGPTNQTTGKSPQLQQDYFP
		ı	ŀ		1	RRSYRCSHRLIICLNVIGNAL
18647	49015	Α	18756	1	1041	
18648	49016	В	18757	15	782	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hođ	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	endon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
18649	49017	A	18758		1425	EVKKINNAHTIGCNAVSWAPA
10012	17017	ľ`	10750	ľ	, , , ,	VVPGSLIDHPSGQKPNYIKRFAS
						GGCDNLIKLWKEEEDGQWKEE
						OKLEAHSDWVRDVAWAPSIG/
						LWPPSTIASCSQDGRVF\IWTL**
						CPQAITVVPLNCLHKFNDVVLG
				l		MLNWGPSOPTSLAVSGGDNKN
				l		GTNTVCPTGWLQDSNTLVHLV
				l		TYKMPRSLGLGFLWCOLLSPR
				l		KYREGTSPVSLWVGEVWFINP
						DWWGSIRVYHPSPSGSYRTHKP
				l		PLNNLSCDTSIRELLKGKKFLL
				l		FVSVYPVPSTVLGRKKVSVINT
				l		VDTSHEDMIHDAQMDYYGTRL
				1		ATCSSDRSVKIFDVRNGGOILIA
				1		DLRGWPRASRYQQGHQDLFIL
				1		RSDLPSQVFIRDKLMERRNRRT
				1		GRTEKARIWEVTDRTVRTWIGE AVAAAAADGVTFSVPVTPHTF
		l				
				l		RHSYAMHMLYAGIPLKVLQSL MGHKSISSTEVYTKVFALDVAA
				1	1	
18650	49018	В	18759	323	1583	RHRVQFAMPESDAVAMLKQLS
18651	49018	A	18760	3	419	PSASSSPARIPAATROGRRSPRIP
18031	49019	^	18700	ľ	*19	PAPSNEAPRLPADREFLEQOPPR
		l		İ		FPKPTIOASGADRAVDCGILKL
ł				1		OKS\PARLARPRWPRRPSKRFW
				l		SAAGSVEEQPKPPRRRAKSPEQ
						SPOLSVLPLVTITPOASGASFEK
				l		MKN
10650	40000		10761		205	WGRGGGRGLLYGRRHFVRRRR
18652	49020	A	18761	2	385	RGGRSPGESPALTVT*GAV\PSA
1				1		
1				1		AFRESAQPGPRSSEAHISTSPKR
1				i		TDGGRDS*PGLPRSSLTPSLPRP
1						ASFSTSPGRVSAPHRLPRHS/AG
10652	40001	<u>.                                    </u>	107/0	242	400	PGLSGSS*PQPYSDPT
18653	49021	Α	18762	242	422	

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X≡Unknown,
NO:	of peptide	hod	in USSN 09/540.217	location of first codon for peptide	eodon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/540,217	sequence	of peptide sequence	ucietion, (=possible nucleotide insertion)
18654	49022	Α	18763	2	992	AREKKQKTRRQNKNIPRQINKT
						QRICC*QSCLTMTQDFFWPLCQ
	İ					GHSRGAPCLLVPPGLSLTCAPA
						QPAARPGVSQLTCAIACTHIQW
	1				1	FPSSCPPSEKNGDTLTV\KTPSA
						SSSPARIPAATRQGRRSPRIPPAP
-	l					SNEASPAPGRPRVPGAA\PPRFP
			ļ			KPTIQASGADRAVDCGILKLQK
1		1			ļ	s\parlarprwprrpskrfwsa
ł						AGSVEEQPKPPKAP/PAKSPEQS
						PQLSVLPLATITPQAYGASFEK
			1		i	MKNLKTRRGGRSRWHFPFNVIF
					i	QAPSLKWGFQTSDASSAEVFH
1	l .	1				VDRSLASHKMGPGRRPRSPLW
						APPFCEAAAARRQEPGVCIMVE
18655	49023	A	18764	292	348	
18656	49024	Α	18765	2	466	LITVVKLLDTMVDTFLQKLVA
		1				AGSYQRFTDCYKCFYQLQPAM
						TQRIYDKFIAQLQTSIREEISDIK
		1				EEGNLEAVLNALDKIVEEGKVR
		1				KEPA/WQRDTLRRHVQKQEAE
		1				NQQLADAVLAGRRQVEELQLQ
				İ		VQAQQQAWQALHREQRELVA VLREPE
18657	49025	Α	18766	2	511	FNMAEASSANLGSGCEEKRHE
		1				GSSSESVPPGTTISRVKLLDTMV
						DTFLQKLVAAGS/YSTPSLGRK
		1				CWS\RLPSGGQSVKQAFSWAAC
						RLPQGRKEEISDIKEEGNLEAVL
	1					NALDKIVEEGKVRKEP\AWRPS
			i			GIPEKDLHSVMAPYFLQQRDTL
						RCHVQKQEAENQQLADA
18658	49026	Α	18767	224	748	NRPSVGRRAGYHRGGSYQRFT
		1				DCYKCFYQLQPA\MTQRIYD\K
		1				FIAQ\LQTSIREEILFDNQKQEGE
		1				PRKLSWNALG*KFVGTKGKVR
1		1				KEPAWRPSGIP\EKDLHSVMAP
l		1				YFLQQRDTLRRH\VQKQEAENQ
	1	1		1		QLADAVLAGRK\QVEELQLQV
						QAQQQAWQALHREQRELVAV LREPE
18659	49027	A	18768	i	421	LICE
10029	79027	1^	110700	1,	741	l

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
18660	49028	A	18769	666	1445	AGITTIEAAKRTIQVLHLQAND AQERA\ERSQREFREERRAREPG LRLK*SFLNRRIQ\LVEEEI.\DRA OERLGHLPCKKL*RS*KKLADE
						SERRY*RLFEN\RALKRLKEKIG TSREIPTQKKLKHICRKEAD\RK YEEV\ARKLGDHLKEDLEPTE\E RA\ELAESRC*EIDEQIRLIDQNL
19661	40020		19770		150	QCLSAAEDKYSQKEDKWEEE MKINTNKLREAETRAEFAERS VAKLKKTIDDLEDKLKCTKEEH LCTQRMLDQTLLDLNEM
18661		A	18770	2	158	SAAPAAVPPEADSTSAGMISKE PCSCALEPPEACSCASPSAVTAA GRPRSDSCKEESSTLSVKMKC DFNCNHVHSGLKLVKPDDIGBL USVSYNPAYLEGSCKDCIKDYER LSCIGSPIVSPRIVQLETESKRLH NKENOHVOGUTINSTNEELST SRLYEDSGYSSFSLQSGLSEHEE GSLYEDSGYSSFSLQSGLSEHEE GSLYEDSGYSSFSLQSGLSEHEE GSLYEDSGYSSFSLQSGLSEHEE GSLYEDSGYSSFSLQSGLSEHEE GSLYEDSGYSSFSLQSGLSEHEE GSLYEDSGYSSFSLQSGLSEHEE GSLYEDSGYSSFSLQSGLSEHEE GSLYEDSGYSSFSLQSGLSEHEE GSLYEDSGYSSFSLQSGLSEHEE GSLYEDSGYSSFSLQSGLSEHEE KNAKRPKYDEMILKEIIAGS FREGURT KNAKPPKYDEMILKEIIAGS FREGURT KNAKPPKYDEMILKEIIAGS LVSKASTTWKKILEDDKGAFO LVSKAIGNYTENNNKFSPHAST REYVMFRTPLASVQKSAQTSL KNDAGTKLSNGGDGKGSTYSR HNEFSEVAKTLKKNESLKACIR CNSPAKYDCYLQRATCKREGC GFDYCTKCLCNYHTTKDCSDG KLLKASCKIGPLFGTKKSKKNL

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	endon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
18662	49030	A	18771	4	1276	RKAASSYVSRMALPIIVKWGG
		1				QEYSVTTLSEDDTVLDLKQFLK
						TLTGVLPERQKLLGLKVKGKP
						AENDVKLGALKLKPNTKIMMN
		l				GTREESLEDVLGPPPDNDDVVN
		1				DFDIEDE/R*FEVENREENLLKIS
		1	İ	1		RRVKEYKVEILNPPREGKKLLV
		1				LDVDYTLFDHRSCAETGVELM
						RPYLHEFLTSAYEDYDIVIWSA
						TNMKWIEAKMKVKPLGVIWG
						KFSEFYSKKNTIMFDDIGRNFL
		l				MNPQNGLKIRPFMKAHLNRDK
						DKELLKLTQYLKEIAKLDDFLD
l						LNHKYWERPRVRCHIFHGKED
						RYDPCPMGACSCKTVCTTNLA
					l	LPALPLGSMKNGQPCRNVIGQK
		1				GYALTVINSGPQQGLFVRILLG
	1	1				LFIRDFFPAGCGARPFWNEGLM
		1				AYFQRRTLVGVMLVLSSSKSFK
18663	49031	С	18772	113	257	
18664	49032	Α	18773	143	330	HHGPVPFPRGLIS*HSLHCPCPT
						PGGKNVFFFCEYFLKLAGIETT
						NCSADKRGKKVCCLIPR
18665	49033	Α	18774	3	432 192	
18666	49034	C	18775	112	1015	SSRPVRPRPAARLSAMSSTOFN
18667	49035	Α	18776	3	1015	KGPSYGL\SAO\VKNRLL\SKYD
		1				POKE\AELRTW\IEGLTGLSIGPD
		1				FOKG\LKDG\TIL\CTLMNKLQP
						G\SVPKINRSMON\WHOLENLS
						NFIK\AMVSYGMNP\VDLFEAN
				Į		DLF\ESGNMT\QVQVSLLALGG
						KRPKTKGAAEGGLDIGVKYSE
						KOERNFDDATMKAGOCVIG\L
						OMGT\NKCASOSGMTAYGTRR
		1		İ		
		İ		l		HLYDPKNHILPPMDHSTISLQM
		1	1	1		GT\NKCASQVG\MTA\PGTRRHI
	1			1	1	YEYQAGNPTSCDNFSM\SLQ\M
	1					GYTQGAQTQSGQVF\GPGRPDI
	1					*TPSTCPQGTI\ADGAP\$GTGDC
19660	40026	-	10777	12	110	PDPGEVPEYPPYYQEEAGY
18668	49036	A	18777	74	110 289	-
18009	49037	IA_	18//8	1/4	209	L

SEQ ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	j	l		sequence		
18670	49038	Α	18779	138	2039	GAAMAAAGRLPSSWALFSPLL
						AGVALLGVGPVPARALHNVTA
	ŀ	1				ELFGAEAWGTLAAFGDLNSDK
						QTDLFV/LAGKK*LNRLFGRPE
	ŀ					CTRILNPK*RYLSRITVH**QV*S
					i	LGAYDGDSQMDVLLTYLPKNY
			ļ		İ	AK\MN*ELLSSGDKIKH*ILTI*P
						YSIGL/LQDEPLIMDFNGDLIPDI
						FGITNESNOPOILLGGD/CYHGI
					İ	QH*PLQVKCEFHI/PHAFIDLTE
						DFTADLFGATLNGTTSTFOFEI
						WENLDGNFSVSTILEKPONMM
					i	VVGQSAFADFDGDGHMGSFTC
						OGCGR*K/CAKRVPSYLVRSGM
						KOWVPVLQDFSNKGTLWGFVP
			ŀ			FVDEOOPTEIPIPITLHIGDYNM
						DGYPDALVILKNTSGSNOOAFL
					i	LENVPCNNASCEEARRMFKVY
						WGADRPKSN/SKGAMVATFFDI
						YEDGILDIVVLSKGYTKNDFAI
	į .					HTLKNNFEADAYFVKVIVLSGL
						S\SNDCPRKITPFGVNQPGTLYH
		1				VYNCRCKWVSEKWIRWPNSAQ
						SAHLALQLPYNVLGFRVGSANF
						LDHL\SLGIPRPSWRKIFYGKQE
						WTAIIPNSQLI\VIPYPHNVPPKL
				1		
			İ			GVPNCILYTKLILFWLTAIALIR
						CLCFQSLAINWHFTLGREKKAG WIEEKRTRKAHRFPFWMAMW
10/71	10020	<u>.                                    </u>	10700		966	WIEEKKIKKAHRFPFWMAMW
18671	49039	A	18780	1		DEDCEMBER OF STREET
18072	49040	A	18781	1	1035	RPPFPVPGVQKCPLPTRGGLHIG
				1		RWLRDRAGPPEAQDGTGGRSR
1	l	l				SRRRPPALPNSRPSPVASGREM
						VVLSVPAEVT\VILLDI\EGTTT\P
			ŀ			IAFVKG/DILFPYIERKMLK\EYL
		1				QTHW\EEEEFQ\QDVSLFEGNK
						A\EEDAHLDG\AVPIPGKHLGIG
1						V\DD\LQQMI\QAVVDNVCWQM
						SLDRKTTALK\QLQGH\MWRAA
			İ			FTAGRMK\AEFFADVVPA\VR\K
						WREAG\MKVYIYSSGSVEAQKL
1			1			LFGHSTEGDILELV\DGHF\DTKI
			1			GHKRRRVKVTRK\IADSIGCST\
		i I				NKHFVFWTDVTSRRASAGLRE
						AGCCTLAVV\VRPG\NAGINR*L
			1			RKTYYSLITSFOWNYYLPSST
Ц						, , , , , , , , , , , , , , , , , , , ,

SEQ ID	SEQ ID NO:	Me	SEQ ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
10.572	140044	ļ	10500	1,	1500	DUELL DVODDEUETT LOOPING
18673	49041	Α	18782	1	528	DNELLDYEDDEVETAAGGSMS
		1				EAPAKKDVKGSYFSIHSSGFRD
		1				FLLKPELLRAIVDCGFEH\PSEV\
		1				QHECIPQAILGMDFLCQAKSGM
					ŀ	GKTAVFVLATLQQLEPVTGQV
	ŀ	1				SVLVMCHTRELAFQTR*KTRPF
		l				WNVTVCPSGEDTRVGVKETLL
1000	100.10	l	10000	000	200	PPPLTAPTPWLPSFASPPLLNPH
18674	49042	Α	18783	207	309	PRINCIPLE PROPERTY PR
18675	49043	Α	18784	85	348	PPHSALLPFPTPFLPPSQLEIFVD
		l				DETKLTLHGLQQYYVKLKDNE
		l				KNRKLFDLLDVLEFNQVS*TSS
		ļ.,				RGMSIGALQL*QKPGY*VHFY
18676	49044	A	18785	I	930	CCCRHTRSPCLVMAENDVDNE
		l				LLDYEDDEVETAAGGDGAEAP
		1				AKKDVKGSYV\SIHSSGFRDFLL
		1				KPELLRAIVDCGFEHPSEVQHE
	Į.					CIPQAILGM\DVLCQAKSGSGER
						QAVF\VLATLQHLEPV\TGQGV
	İ					CAG*CCHTRELAFQISKEYERFS
	1	l				KYMPNVKVAVFF\GGLSIKKDE
						EVLKKNCPAYPSVGTPGRILA\L
						ARNKSLNLKHIKHFILDECDKM
						L\EQLDM\RRDVQE/IFFRMTPH
		1				EKQVM\MFSATLSKEIRPVCRK
		1				FMQDVNTLLPSLPPLPARCLLPF
		_				LALFLRLPCHSSAKKAACAQLG
18677	49045	A	18786	96	1618	LFTPCFHLFCENPSRSPFPSSPAG
		1				PVMAENDVDNE\LLDYER*MR
		1				WETAAGGDGAEAPAK\KDVKG
						SYVS/LSHSSGFRDFL\LKPELLR
}		ĺ				AI\VD\CGFEHPSEVQHECIPQAI
		l				LG\M\DVLCQGKSG\MGKTAVF
						VLATLQQLEPVTGQVSVLVMC
		l				HTRELAFQISKE\YERFSKYMPN
		l				VKVAVFF\GGLSIKKDEEVLK/R
		1				RNCPHI\VVG\TPGRILS/LWVRN
l		1				KSLNLKHIKHFILDECDKMLEQ
		l				LDMRRDVQEIFRMTPHEKQV\
	1	1				MMFQCYLGAKEIRPVCRKF\M
1	1	1		1	1	QDPMEIFR/VDDETKLTLHGLQ
		1			l	Q\YY\VKLKDN\EKN\RKLFDLL
1	1	1	l			DVLEFN\QVVIFVKSVQ\RCIAL
	1	1			1	APAY*WEQNFPA\IAI\HRGDAP
						RKERLS\R*SSSFKDFPTNEILIG
	1	1	l		l	YPTLFGRRHGTSEAGETIAF*FM
						NMP*GILKTLPCHR\VGPEQGRF
	1	1				GHPRGL\AITFVSDEE*LPRSCD
						DVQGSALRVKFSELPDEIGHLP
	1	1			1	PTLEQDTGRRLAHFGNVDRLFL
18678	49046	Α	18787	1	363	

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
18679	49047	Α	18788	78	714	GTTEGKRQEAVGYLCVLPLTTL
						PLVTRLPPQVADTMLPPMALPS
						VSWMLLSCLILLCQVQG\EETQ
		1				KELPSPRISCPKGSKAYGSPCYA
			l			LFLSPKSWN\DADLAC\QKRPSE
						KLVSVLSGAEGSFASLLA\RSIS
		1			1	NSYSYIWIGL\HDPKKG\SEPDG
						DG*EWSSTDVMNYFAWEKNPS
			l	1	1	TILNPGHCGSLSRSTGFLKWKD
					YNCDAK\LPYVCKFKD	
18680	49048	A	18789	52	186	QSEVHHGIISYTTGQGENLSEPI
						WKSWQRSQDL*QENHPEIYSLT
18681	49049	A	18790	666	2732	KQLIKMCYFILLLLILSSHIGKD
						KAIDKNGILVQYWQE*KLVEPF
						*KAIWPPCMETLNVDTPFPQPV
			l		ł	CLGIYPNE*KLSK/CFKP*APKV
					1	YFHGCL*Y*NHWEPTETIPPVK
						GWIK*ILF
18682	49050	A	18791	1 I2	340	
18683	49051	Α	18792	3	323	LSSLASMSFTTCSAFTNYWSPG
			l		i	SVQVPSYGTQPVSHAASVYAG
			l			LGGSGSRISVSH\SPMAGGLAG
						MGGIQNEKETMQSLRDRLASY
18684	49052	A	18793	1	994	LDRVRGLETENWKLESKIQEH APSYRA/RLVRSVASVYAGPGS
18084	49032	^	18/93	1	994	SGSRISMSRSTSFQGGLGSRSM
	l		İ			AA/GMAGGLAGMGGIQNEKET
						MQSLNDRLASYLDRVRSLEMG
						NWKLESKIWEHLEKKGPQVRD
			i			WGHYFKTIEEDLTQIFTSTVDN
		i	1			TCIILQIDNAHLAADDFRVKYE
						TEPATCOSVENDIHGLHKVIDD
			l			TSVTQLQLETEIEAL\KEALLFL\
						KKNHEEES/WRHTVOALEIDLD
						WMKNLEASLENSLK/EGVEAC
		l		1		YTLOMEOLNGILLHLESELAOT
1			1			WAEGQGQAQEYQALPNIKVKL
				1		EAEIATYRRLLEDGEDFNFGDA
	1			1		LDSSNSTQTIQKTPTC/RTVDGK
				1		VVSETNDTKVL
18685	49053	Α	18794	3	377	
18686	49054	В	18795	54	136	
18687	49055	Α	18796	149	419	

SEQ ID NO:	SEQ ID NO:	Met	SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	09/540,217	codon for peptide sequence	of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18688	49056	Α	18797	83	1402	AEKAGGKKGEAPSYRA/RLVRS
				1	1	VASVYAGPGSSGSRISMSRSTSF
					1	QGGLGSRSMAA/GMAGGLAG
						MGGIQNEKETMQSLNDRLASY
						LDRVRSLEMGNWKLESKIWEH
						LEKKGPQVRDWGHYFKTIEED
						LTQIFTSTVDNTCIILQIDNAHL
						AADDFRVKYETEPATCQSVEN
						DIHGLHKVIDDTSVTQLQLETEI
						EAL\KEALLFL\KKNHGEEIKGL
						SRRQIASSGVDPWRVDAPKSSG
		l			1	PSPKIMGRHPGPKYDEL\ARKR
		ļ.				TREE\LAKYSSQ\QIEEST/TQLV
						TNTSLL/GGLELAETNLHRS*TY
						KSRSLEDSTLDSIEKS*KAQAW
İ						KKQPLKGSWKAPLRPLPDWSK
						LQTGILACTFESRAGNKTRARG
		1				TSAPGPQEL*GPLLKHQKVKAG
						GLRSPTLPARLLEDAEAL*SLV
			1		l	DPLDSKQLPCNTIQKTTTPPG*V
18689	49057	С	18798	140	283	
18690	49058	Α	18799	2	783	VVQFARREKPSSSKVSQRHPCT
	1	l		l		EAVREVLHG\NQRKSPQRSWET
					ł	VELQISLKNYDPQEGQSAFSGT
		1				RQALSPLPRP\KFSCVCPGGTQQ
	1	1				H\CDEA\KARGISPPHGTFEGA*
		1				KNLNKE*KNWSKKAGPRKY*L
	1	1				RFFGPQKSLDQSKIPPNPSGPGF
		1				K*RAGK\FPFPWFTHN\ENMGG
		1				PKLDEGEVPPIQVFQMKERCLC
		1			1	L\AVAV\GHV\KMTD\DELVYNI
		1		l		HLGCQLSWVSLLKEKNW\QNV\
		1		1		RALYIKSTHGQSPKRLIFKAHFE
18691	49059	С	18800	239	555	

SEQ ID NO:		Met	SEQ ID NO:	Nucleotide location of first	Nucleotide location of last codon for last amino acid	
NO:	of peptide sequence	noa	09/540,217	endon for peptide	of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	acqueice.		07/340,217	sequence	or pepade sequence	determine possible nucleonide insertion)
18692	49060	A	18801	401	3014	TRASSTMSKSFQQSSLSRDSQG
						HGRDLSAAGIGLLAAATQSLSM
						PASLGRMNQGTARLASLMNLG
						MSSLLNQQGAHSALSSASTSSH
		Į				NSQSIFNIGSRGPLPLSSQHRGD
						ADQASNMLASFGLSARDSDELS
						RYPSDTITPENLRPILLQLKRRR
						TEEGPTLSYGRDGRSATREPPY
						RVPRDDWEEKRHFRRDSFDDR
		İ				GPSLNPVLDYDHGSRSQESGYY
	1					DRMDYEDDRLRDGERCRDDSF
						FGETSHNYHKFDSEYERMGRG
						PGPLQERSLFEKKRGAPPSSNIE
						DFHGLLPKGYPHLCSICDLPVH
					SNKEWSQHINGASHSRRCQLLL	
					EIYPEWNPDNDTGHTMGDPFM	
					LQQSTNPAPGILGPPPPSFHLGG	
					PAVGPRGNLGAGNGNLQGPRH	
						MQKGRVETSR\VV\HIMGFSTE
		1				GKTLRYQLLQLVEPFGVHFKFI
						*FLNKNLLRAFIEMATTE\DCFK
						AAV\DYYTTTPA\LVF\GKPVRV
		i				HLSQKYKRIKKPEGKPDQKFDQ
	1					KQELGRVIHLSNLPHSGYSDSA
						VLKLAEPYGKIKNYILMRMKS
		1				QAFIEMETREDAMAMVD\HCL
						KKALWFQGRCVKVDLSEKYK
						KLVLRIPNRGIDLLKKDKSRKR
		İ				SYSPDGKESPSDKKSKTDGSQE
		1				AERST\EGKEQEEKSGEDGEKD
						TKDDQTEQEPNMLLESEDELLV
						DEEEAAALL\ESGQFSGETSTDL
8693	49061	Α	18802	3	1013	NCRAAWRAKLEGCLSLRRNAC
						QCFLIWTQTPDREQSYSLDQLP
						REVLNQEEKSISIWDIYLHLEM
					GNGLSDQTSILSNLPSFQSFHIVI	
					\LGLDCAWKRQLSYTRLQFQLN	
					L*NT\VPYPKGFNTEKI*/RVTLG	
				İ	NSKTV\TFHF\WDVGGQEKLRP	
					LWKSYTRCTDGIVFVVDSVDV	
					ERMEEAKTELHKITRISANRGV	
					PVLIVAN\KQDLRNSLSLS\EIEK	
					LLAMGELSSSTPWHLQPTCAIIG	
					DGLKEGLEKL\HDMI\IKRRKML	
						RPTRKRKDEYQFPNIICVGVGF
						LWSDFDKNRRVSTAGVCLSAPF
				ŀ	İ	WMLLKLCFVEQFRCPTRVALW
						KMSKCSAS
8694	49062	A	18803	3	1103	
18695	49063	В	18804	34	734	
18696	49064	Α	18805	1	1741	

NO: of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
<u> </u>		09/540,217	leadon for pentide		
18697 49065	L			of peptide sequence	deletion, \=possible nucleotide insertion)
18697 49065	+-		sequence		
1,003	IA.	18806	6460	6635	RTSTERSHLKTRYQRTSCSSNR*
I I		10000	1		LNSSSSKTSFRCSLTTSLFWRHT
I I	1				IFNMLLINRRLL
18698 49066	A	18807	5567	5853	IGILEA*LLRNLPNDSIKALVDA
1,000	1.	10007	15507	1	*YKSLLSAVERCSFMVLFGEPM
	1				NKPPLAILRIQSGVNRPPVISIM
	1		1		ALIGPLVTPSASTYSGVTNADLS
	1		į.		SATK
18699 49067	A	18808	664	992	SCADIHGYHRGNSSNNDSNLIP
	1			· ·	KQTNRDCLNNGHQNHSCNG/D
	1		ŀ		*POPOR**QLTLONLMOHO*KO
	1				QYPLPQHQQQE*RTR
18700 49068	A	18809	3	1698	(11)
18701 49069	В	18810	227	883	
18702 49070	Α	18811	180	373	PDTLRSILPMLLEQLFCRTFGLL
					SP**RDTSLHLGHKTEQHT*LV
	1				MGSWFYLLASQQPRCCYAC
18703 49071	Α	18812	495	701	
18704 49072	Α	18813	138	418	AYRLLLCLVYSEGFYMHLEFQ
	1				NRLYHQLVF*GRLWHFW\KSIK
	1				RFSIY*FFWYRW*YICKLNKGR
	1				LQDVIGVINT*CHFLS*GLH*TIP
					GIHRL
18705 49073	С	18814	62	175	
18706 49074	Α	18815	644	828	
18707 49075 18708 49076	В	18816	84	1107	
18708 49076 18709 49077	A	18818	3	1399	
18710 49078	B	18819	1	1377	
18711 49079	A	18820	1	546	
18712 49080	A	18821	855	1099	VTLYSEYQHPSVREYGLYLTSH
10/12 45000	^	10021	833	1079	RIEPLECVHRTL*PVLLSMQPSV
	1		1		LEYYEOOGYEAEY*LOEECHH
	1		1		QRTSSL*DLLKQLLQ
18713 49081	A	18822	tr	1680	QK153E DEEKQEEQ
18714 49082	A	18823	1	3951	
18715 49083	Α	18824	2	6446	
18716 49084	A	18825	2497	21785	SSPYPFTKQSSTNNFVFDGNELF
	1				NSRDRLSORLFYILOSSVHLINR
	1				Q/LEGYVQHHLNLAEI*HHGLG
					KDAYIAAMYNNDDGATFQMEI
	1		İ		GGIHTNAALAAGDKLQCIWRY
1 1	1	l	1		LDVNGNAPAAENEFEVVSYEG
	1				FGTSNFSVKCKGMLPGKFIGCD
	1				AFYGKYLQTDGPIKQVDSVKW
		1	I		FTNLTVSGSGRKQLGQRKYPQ
	1		1		VVMGMGMTSGFDDGYNLTPE
					ROVKMAYGLGYRDWWTTYIG
		1			MSHYWKGLTAFQDKETGELI
18717 49085	Α	18826	31	479	

SEQ ID NO:	SEQ ID NO: of peptide		SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
18718	49086	A	18827	255	1002	SQFSLSQVLVDSAEEGSLAAAA
						ELAAQKREQRLRKFRELHLMR
1				i		NEARKLHHQEVVEEDKRLKLP
i i				ŀ		ANWEAKKARLEWELKEEEKK
						KECAARGEDYEKVKLLEISAED
1		l		ĺ		AERWERKKKRKNPDLGF\SDY
						AAAQLRQYHPV*PKQIKP\DME
						TY\ERLREKHG\EEFFPTSNSLLH
İ						G\THVAFHRGKFDRVVLRSGKN
		l				QFEKRD/KF*ARRRPYNDDADI
				ŀ		D\YINERNAQFNKKAERFY\GK
1						YTAEIKQNLERGTAV
18719	49087	С	18828	91	225	
18720	49088	Α	18829	3	212	
18721	49089	Α	18830	88	239	
18722	49090	Α	18831	865	1898	QQQQQQHRRYPRRRSPRAWC
				1		SHPRSPLLFLPSLAPWPDQLTEE
1						QIAEFKEAFSLFDKDG\DGTITT
		l		1		KEL\GTVM\RSLGQEPNKKLEL\
İ				1		QDMINESGMLMG\NGTHLTFPR
		l			ŀ	IF*LMMARKMKDTDSEEGN/LR
		l		ŀ		EAFRV\FAKDGNGYISAAELR\H
1		ļ				VMTNLGEKTTRF/KKVDEMIRE
	1					A\DIDGDGQVNYEEFVQMMTG
		1				KMEDLTFQLPFSPPLEESNWNL
						LLTFLQKKEKKKKVHLFHSCFL YSKTECQKYLLVHTHQNLHVL
1		1		i		VGGPCPLKDQATHQFYNINTCT
1						NLNDNGLLKRSILLMINTLFGL
					1	ASFFHACSFDDWSTSOGLWYL
1						KLENGKNQISKPIPNGVLVHFV
18723	49091	Α	18832	1	330	WVVLKNCVGVGLLIAT*MWFI
10/23	49091	l^	10032	l'	330	SNKYLVQRQSRDYDVEWGYAF
						DVHLNAFYPLLVILHFIOLFFIN
						PLPFLKNTVILLYPFAPLILLYGL
		l				SLALGWNFTHTLCSFYKYRVK
18724	49092	A	18833	1	534	VPSNSVNSLVOGNGVLNSRDA
10724	47072	ľ`	10055	ľ	334	ARH/TAGAKRYKYLRRLFRFRO
		1				MDFEFAAWOMLYLFTSPORVY
1	1				1	RNFHYRKOTKDOWARDDPAFL
				I	1	VLLSIWLCVSTIGFGFVLDMGF
					1	FETIKLLLWVVLIDCVGVGLLIA
1						TLM/WHCHFWKKOVILLYPFAP
		1	İ		1	LILLYGLSLALGWNFTHTLCSF
1		1				YKYRVK
18725	49093	c	18834	295	570	
10123	1.7073	<u> </u>	1.303,			

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequen <b>c</b> e	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
18726	49094	<del> </del> -	1,0026	418	1567	I SFTLKNCVLORVSSILPSNTAEV
18/20	49094	Α	18835	418	1367	DFPSWTTQSDWQQTRAQVLLQ
						ARARAALRLVLIILRHDGASPP
	l					MRTRLSPTATLATGSGASEAPV
						SGDRKPAATTSGGPRRKMLPST
		}		1		SVNSLVQGNGVLNSRDAARHT
l		ł		1		AGAKRYKYLR\RLFRFRQMDFE
		ì		l .		FAAWQ\MLYLL\TSP*RVYRNF
ŀ	1		l			H\YRKQTKDQWAR\DDPAFLGF
						PFKYSGFCVSTIGFG\FVLDMG\
						FFETIKLLLWVGLID\CVGVGLL
					į.	\IATL\MW\FISNKYLVKRQS\RD
		1				YDVEWGYAF\DVHLNAFYPLL
1						VILHFIQLFFINHVNLTDTF\IGY
						LVGNTL\WL\VAVGYYILR*LSL
						GYSVGLLFFSSIAHF*KNT\VILL
		1	1	I		YPFA/PL*FLPPTGFPLALGWNF
1						THTLCSFYKYRVK
18727	49095	A	18836	h	888	MPGLLLLRGSONLKQQAEILCG
10/2/	45075	ľ	10050	ľ	000	LGLALVISAVKPLSKKFMLPNP
	1		ı			TSMKPESDGIYSINLKRTWEKL
		1				LLAGHAIVVIENSADVSVISSRN
		ļ	1			TGQKAMLKFAAATGATPIAGH
1		ļ.	ł			FTPGTF/TNQIQAAYWEPRLLV
i						
1						VSDPRADHQSLTEASCVNPPAI
						ALCNTDSPLCH/VDIAITCNNKG
	1					APSVGQMW*MLAWEVLHMRG
	1			1		TISCN/SPWEVMSNLYFYRDPEE
l						TEKEEQAAAEKAVTKKEFQGK
			ļ	1		WTVSAPEFTVTQPEVADWSEG
		1		1		MQICNLGKAQQGQLSSDAEDD
			l			FWSLESLDGYSHTVTFR
18728	49096	Α	18837	74	848	REIFINVRSLLMACFVKEEDVL
						KFLAARNP/HVGGTNLDFQME
						QYIYIRKSDGIYIIRLKRTWEKL
		1		1		LLAARAIVAIENPADVSVISSRN
	1			l .		TGQRAVLKFAAATGATPIAGRF
1		1				TPGTFTNQIQAAFRE\PRLLVVT\
1		1				DPRADHOPLTEASYVNLPTIAL
	i	1	İ			CNTDSPLRYVDIAIPCNNKGAH
		1				SVGLMWWMLAREVLRMRGTI
1	1	1		1	1	SREHPWEVMPDLYFYRDPEEIE
1		1		1	1	KEEQAAAEKAVTKEEFQGEWT
		1				APAPETATOPEVADWSEG
18729	49097	A	18838	72	528	DEACGVCCYSPGASPMPP*GRT
18/29	49097	^ <u>`</u>	10030	l' <sup>2</sup>	320	
	1	1	1		1	RKEGRTAGKVRPKERPKTPVN\
	1	1	1		1	KSGGQGPKRKNWSKRQKFRDK
	1	1	1	1	1	L\NN\LVLFDKA\TYDKLCKEVP
1	1	1	1	1	1	N\YKLITPSLWSPERL\KIRGSLA
		1			1	KGKPFQEAP*VKGLI/RNLVSKH
1	1	1				RAPSNFTPGNYQGWEDAPSLL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18730	49098	В	18839	6	125	
18731	49099	В	18840	249	291	,
18732	49100	Α	18841	128	669	RPGHAQTI GSPSLALGMAGQF RSYVWDPLLILSQIVLMQTVYY GSLGLWLAIVVDGLLRISPSLD QMFDAEILGFS/TPFQGRLSMM SFILMALTCALGFAVISSGEEKQ CLDFTVTVHFFHLLGLLGSNSS PFSPSGG*TLVGLGPKPVVALH
	1					SLAVIGEYLCMRTELKEIPLNSA
18733	49101	A	18842		818	MAELTYMRFHTEPQGSGGLRLI RISGSKPKQMHYTWLEPLENGI CNGNTGNAQLLIPPGVIFHKYP SHYVTAMLKSLKWPPLQTELTS SGQALWGLVGGGSPHRQAST EKLFSEKVPKTAENFPCSELSC GENGGI-GYPCFHRLIPRVY AVRGODFHTAINGTIGGKSHPM GKKFEG FETSILKHTGPGDLIV ELSGLDGKPCGVLAKVEEGM NIVEAMEREFGSRINGKTSKKITI ANDCGTTPNKV
18734	49102	A	18843	4	10.1	MDWACDETKI I CCTWTI IOVD
18735	49103	A	18844		978	MRWACDETKLLSSTWTLIQYPEN AMMIRAWALLADCPEKTKAL RTTEDGIVDAANTEQPILQERIK VNGKVGNLGGGVVTIEKSKSK TVTSKGIPFNSM*I*GSASSFVER KRLLEF*KLLSSTWTLIQYPENA MIRAWALLADCPEKTKALRTI EDGIVDAANTEQELQERIK VNG KVGNLGGGVVTIEKSKSKSITIVT SKGHFQFYVNLRISFLICGKEK VGILEEIVLNLLIIFSSIDLITVKG TCSGCERGFFLEIYDEVEDSSYT NHLKDDDPKREGPGEQALST PPCCPLEKRPINDQTLIISWSGST NVIEEAGRHSVVQEGWGALGV LRTTLPSLPOTIGGAGFVGSHLI DKLMMDGIPETTVVDNFFTGR KRNVEHWIGHENFELINHUVVE PLYIEGRAERQLSHTVPOPVDL SDRIVNGFYELSL

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
18736	49104	Α	18845	167	1440	RDIWLSASAAAMVPVRKLV/AE
						GGOKTKOVLRFTLGCTHPIEDG
						IIDAANFEQFLQERIKVNGKVG
						NLGGGVVTIEKSKSKITVTSKG\
	İ					PFNSM*I*GSASSFVEKKRLLEF
						*KAENLSSKNWNKTRMPTFTTL
		l				TQVAPNPITGYTSKGKKISTLKR
		1				YLAFCLRCCHGAREKACGEGG
				l	İ	QKTKQVLRFTLGCTHPIEDGIID
				l		AANFEQFLQERIKVNGKVGNL
		1				GGGVVTIEKSKSKITVTSKGHF
		l		İ		QFYVNLRISFLICGKEKAVGILE
		l				EIVLNLLIIFSSIDILTVKGTCSSC
		l				ERGFFLEICDEVEDSSYDNHLK
		l		ŀ		DEDPKREECRKRDAYAPLKDQ
		l		ŀ		GNAEKRRHNVRKSWPLLSAKL
1						LKIRTNLTGTEEAELHANHIQQ
						VPIKCLSYKLTERKNGTQKHLH
						YALILHVKCDRRETSKFTKFYG
						THPLTALFVPRAWDGPPSALPE
	Ì					SELAVFLVAYEGNTLLHLFLSG
					1	AEQRGNSSLKERAGRARFSHQR
						KLNEQTIPPDNLTKSSVDLQSSF
						SAVHPNSQPTVWVDMPAHPLS
						QYLVPARKTVLPIWYGNSCPD
						VIFGSLSDSKLSEGKEFALPLKF
18737	49105	C	18846	713	831 303	
18738	49106	A	18847	97	233	RTVTCYHRNSRACHPQQITSCP
18/39	4910/	A	10048	احرا	233	*HRALPCLPLWSPKCPSRWPWF
				l		G
18740	49108	_	18849	229	359	MKWVYCSVTGMGKGQHRMP\
18/40	49108	Α	18849	229	339	SKG*GWVORYNRDGIPSPRVLE
				l		LF
		<u></u>		L	L	Lr

SEQ ID	Tomas en esta		SEQ ID NO:	In a sec	B	Amino acid sequence ( X=Unknown.
NO:	SEQ ID NO: of peptide		in USSN	location of first		*=Stop codon, /=possible nucleotide
NO:	sequence	nou	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	acquence		03/340,217	sequence	or pepade sequence	deterion, r-possible nucleonal insertion)
18741	49109	Α	18850	1	1185	MSTIDDPRLQGRRMCLMLRGT
						PEQKALVIGGEACMWGEYVDN
						TNLVPRLWLCPPSTQDLANEGI
		-				REMTILHRHIPDRGKGVMRSCS
	ŀ					FRTPRPFTLACGPEKSLMDPQS
İ						QSNSEGASSSLVVKLADTDRER
	ŀ					ALRRMQQMAGHLGAFHPAPLP
1	l	1				LGACGAYTTAILQHQAALLAA
						AQGPGLGPVAAVAAQMQHVA
	ļ.					AFSLVAAPLLPAAAANSPPGSG
						PGTLPGLPAPIGVNGFGPLTPQT
	ŀ					NGQP\APTRSTITGSPLI/SGWSQ
						SRPILRIMKYAEQRIPTLNEYCV
						VCDEQHVFQNGSMLKIQPDTII
						QVWREDIPVNYMKELELVTKA
	l l					GFRALLSAPWYLNRISYGPDW
						KDFYIVEPLSFEGTPEQKALVIG
						GEACMWGEYVDNTNLVPRLW
						AHRIQL
18742	49110	Α	18851	231	416	
18743	49111	В	18852	184	594	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first eodon for peptide sequence	Nucleotide location of last eodon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18744	49112	A	18853	247	2296	PVYLSIFMSCVGENGGSHIENW
						HSILRNGLVNASYTKLQDIKGQ FWNDDDSEGDNESEEFLYGVO
			i			GSCAADLYRHPQLDADIEAVK
1						EIYSENSVSIREYGTIDDVDIAL
1						HIN\ISFL\DEEVSTAW\KVLRTE
						P\IVLRLRFF\LSOYLDGPDPS\IE
	1			l		VFQPSNKEGFGLGLOLKKILGM
1	ŀ					FTSOOWKHL\SNDFLKTOOEKR
ŀ						HSWFK\ASG\TIKKFRAG\LOHSF
		l				SPIPKS\PSFPYS*O\DSMAGKGK
				l		LGV\PELRVGRLMNRSISCTMK
				l		NPKVEVFGYPPSPOAGLLCPOH
				l		VGLPPPARTSPLVSGHCKNIPTL
1			1			EYGFLVQIMKYAEQ\RIPTLNEY
						CVVCDEQHVFQNGSMLKPAVC
				l		TRELCVFSFYTLG\VMSGAAEE
		1		l		VATGAEVVDLLVAMCRAALES
						PRKSIIFEPYPSVVDPTDPKTLAF
				1		NP\KKKNYE\RLQKAL\DSVMSI\
				l		REMTQGS\YLEIKKQMDKVWIP
				l		L\AHPLLQWIISSN\RSHIVKLPL
						SRQLKFMHTSHQFLLLSSPPAK
				l		EARFRTAKKLYGSTFAFHGSHI
						E\NW\HSIL/RGNGLVQWHSYTK
				ĺ		LQLHGAAYGKGIYLSPISSISFG
				1		YSGMGKGQHRMPSKDELVQR
						YNRMNTIPQTRSIQS\RFLQSRN
						LNCI\ALC\EVITSKDLQK\HGEH LGCCPVFRPMSCTRFLPL*YED
				1		G\QVGDAQHYIPHGPQRVHERE
18745	49113	c	18854	122	486	GIQVODAQHTIFHOFQKVHEKE
18746	49113	A	18855	1	535	KNAAGNFISPT/ERLSPNAWKTI
18740	49114	ļ^	10033	l'	333	TDIVLNGTAFVTFLSITTIYAET
	1					GSGFVVPSASAKAGVEAMSKS
						LAAEWGKYGMRFNVIQPGPIK
						TKGAFSRLDPTGTFEKEMIGRIP
				l		CGRLGTVEELANLAAFLCSDY
1	1			l		ASWINGAVIKFDGGEEVLISGEF
	l			l		NDLRKVTKEQWDTIEELIRKTK
18747	49115	Α	18856	3	356	,
18748	49116	Α	18857	1	1581	

SEQ ID	SEQ ID NO:	Mct	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
18749	49117	Α	18858	2	1242	RRLGPSPRPIPRRPRORFOPREL
	i					CSFCPAPCGPTACGGFRPEFWRI
1						NMKLPAKVFFTLGSRLPCGLAP
						RRFFSYGTKILYONTEALOSKFF
1				İ		SPLQKAMLPPNSFQGKVAFITG
						GGTGLGK\GMTTLLSSLGAOCV
		1				IASRK\MDVLKATAEQISFSNW
		1	1	İ		EIKVHAIQCDVRDPDMVQNTV
		1				SELIKVAGHPNIVINNAAGNFIS
		1				PTERLSP*CWKNQ/ITNIV*NGT
		l				AFVTLEMGKHLIKAQKGAAFL\
		l				SITT\IYA\ETGSGFCRYPSASAQ
						SRVWEAHGASLLQLEWG*NM
						GLRIPIVDSNQGPIKTK\GALYPS
		1				GPPTGTFGEKKMIGQKFPCGSP
						WGLVEELRKSLPAF\LCSDYA\S
		l				W\INGAVIKFD\GGEEVLI\SGDF\
l		1				NDLRKVT\KEQWDTIEELIRKT
						KRFLRPLWPSSWLQKRE
18750	49118	Α	18859	8	432	NSKLPPVVTSQQMRFMY/DPQT
						DQHMKI\FPEQLPLDEFLQKTDP
		l				KDPANYILHAVLVHSGDNHGG
		[				HYVVYLNPKGDGKWCKFDDD
		l				VVSRCTKEEAIEHNYGGHDDD
		1				LSVRHCTNAYMLVYIRESKLSE
						VLQAVTDHDIPQQL
18751	49119	Α	18860	1	211	
18752	49120	Α	18861	1	242	
18753	49121	A	18862	3	733	LVHSRDNHGRHYVVYLNPKGD
						GKWCKFDDDVVS/QLVERL*EE
				l '		KRINAQKVDR\RQEVHLYMQA
						QVASEDQFCGHQGNDMYDEE
	1					KVKYTVFKVLKNSSLAEFVQN
						LSQIMEFPQDQIQL WPMQARSN
						GTKRPAMLDNEADGNKAMIEV
1						SDNENSWTIFLETVDLELAASG
		ŀ				VTLPKFDKAHDVMFFLKMYDP
1						KMRSLNYCGHIYTPISCEIRDLL
		ĺ				PVMCNRAGFIQDTSLILYEEVK
1055	40122	L.	10062	261		LNLTERIQD
18754	49122	Α	18863	261	659	KHLFYLFIT*EITLYPDKHGCVR
1		1	1			DLLEECKKAVELGEKASGKLR
1		1	l			LLEIVSYKIIGVHQEDELLECLS
			1			PATSRTFRIEEIPLDLLEECKKA
			1	1		VELGEKASGKLRLLEIVSYKIIG
10055	40122	<u> </u>	10064	107	407	VHQEDELLECLSPATSRTFR
18755	49123	Α	18864	107	407	CVFFADTSWRSEATFQFTVERF
1		1	l	1		SRLSESVLSPPCFVRNLPWKIM
						VMPRFYPDRPHQK\SVGFFLQR
1			l	l		NAESDSTEDSLNDATTNPHIVA
L	L	L	L	L		FHYWKPNLNSLV

SEO ID	SEQ ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence	ŀ	
			l			
18756	49124	Α	18865	2	3698	YVRVSLPPPPPAAGRPGAAVAD
						DAREEEEEAAPPPPPPPPPRLAA
			l			ARPPGSQPRPPAAGEAQAAAD
		İ			ŀ	MNHQQQQQQKAGEQQLSEPE
					ŀ	DMEMEAGDTDDPPRITONPVIN
						GNVALSDGHNTAEEDMEDDTS
		1				WRSEATFQFTVERFSRLSESVLS
						PPCFVRNLPWKIMVMPRFYPDR
		1				PHOK\SVGFFLO\CNAESDSTSW
	l	i				SCHAQAVLKIINYRDDEKSFSR
		1	ł			RISHLFFHKENDWGFSNFMAW
		1	ł			SEVTDPEKGFIDDD
10767	49125	-	18866	16	450	SEVIDFERGRIDDD
18757	49125	A	18867	16	26	OSGHSMDMRVPAOLLGLLLLR
18/38	49120	l <sup>A</sup>	1080/	ľ	20	
		1				LRGARCDIQMTQSPSSLSASVG
		1	i		1	DRVTITCRASLDISRWLAWFQL
		İ	ļ			KPG\EVPKLLIYAASTLQSGVPS
		l	ł		1	RFSGSGSGTDFTLTISSLQSEDIA
		l	}			MYYCQQYNNW/SSAPYTFGP\G
		ı	1			TKVEIKTKLWAA\PSVLHLPGPS
		l	ŀ		1	DEAVENLGTAFCLCALLEKTSN
			ł			PQSRPKSTSGRVD\NALPNGGK
		1				LPQGECSQKQD*TAWT
18759	49127	A	18868	3	694	
18760	49128	Α	18869	47	1712	FPTKMAAVGRVGSFGSSPPGLS
		1				STYTGGPLGNEIASGNGGAAAG
		i				DDEDGQNLWSCILSEVSTRSR\S
						KLPAG*NVLLLGEDGAGKTSLI
		l	l			RKIQGIEEYKKGRGLEYLYL\N
		l				VHE*MTGNDQTRCN\VWILDG
		l				DLYHKGLLKFSLDAVSLKDTL
1		l	1	l		VMLVVDMSKPWTALDSLOKW
		l				ASVVREHVDKLKIPPEEMKQM
		l				EQKLIREF\QEYVERGEDFPASP
1			ŀ			ORRNTASOEDKDDSVVLPLGA
					-	DTLTHNLGIPVLVVCTKCDAIS
i		1				VLEKEHDYRDEHFDFFOSHIRK
		ŀ				FCLRYGAALIYTSVKENKNIDL
	l	l				VYKYIVQKLYGFPYKIPAVVVE
	l	l	1			
	l	ı			1	KDAVFIPAGW\DNDKKIG\ILH\E
	l	1				NFQTFKRQEDNFWKDIITKPPV
1				1	1	RKFVHEKEIMAEDD\QVFLMKV
					l .	
						\QSLLSKSKPP/TTEAGRPVDA\S
						PKESQGGSPPNTKIESVSS*CCQ
						PKESQGGSPPNTKIESVSS*CCQ ACHPIPCWGQKKIDPNMESWE
						PKESQGGSPPNTKIESVSS*CCQ
						PKESQGGSPPNTKIESVSS*CCQ ACHPIPCWGQKKIDPNMESWE LTSGRAFLGKFSFNSFV*VKRL GSPRRPLVVSGG*PCRVGLGGG
						PKESQGGSPPNTKIESVSS*CCQ ACHPIPCWGQKKIDPNMESWE LTSGRAFLGKFSFNSFV*VKRL
						PKESQGGSPPNTKIESVSS*CCQ ACHPIPCWGQKKIDPNMESWE LTSGRAFLGKFSFNSFV*VKRL GSPRRPLVVSGG*PCRVGLGGG

SEQ 10 NO: Met   SEQ 10 NO: Motor   SEQ 10 NO: Motor   SEQ 10 NO: Motor   Sequence   Sequence   Se	FLPT GRL LAV NYL /MT A\AN (NCP C\CM PA\G TGF ()WET
18761   49129   A   18870   3   885   LVCLVRELLGPRRFFLKV	FLPT GRL LAV NYL /MT A\AN (NCP C\CM PA\G TGF (WET
18761   49129   A   18870   3   885	GRL LAV NYL /MT A\AN CNCP C\CM PA\G TGF (WET
FPGVPAPVLTATLPFFHP    YQVEVAPVLTATLPFFHP    YQVEVAPVLTATLPFFHP    YQVEVAPVLTATLPFFHP    YQVEVAPVLTATLPFFHP    YQVEVAPVLTATLPFFHP    RRKINDWAVINTOKKST*P     DSSTYTSLFPR*LENIWC   GMTS*PADSQVQRARYY   WKIQSMGYEIPVDMLCK   IFLQVYHTEMLKMKASLR   IFNWVIDEEQGFSRYIRCU   YYCG*VEYTASGS*TKLE.   LEKKKCKKFDWT*TR   ANTLPCLTVPIQLDFKTPQ   GVVTVENPKPIRLTEAEI   VAPSKRD   18762   49130   A 18871   I 471     18763   49131   A 18872   I 1524     18764   49132   A 18873   2 719   RPQRAGPVRRAGVMALL   EGMAVEGFVLEVLVLWLM   AIIYTRLHLNKKATDKQP   POVSLLEPLVLWLM   AIIYTRLHLNKKATDKQP   POVSLLEPLVSVAPMKF   QM**P*CSTY*YEVLLCVC   DPAIDVCKKLLGKYPNVC   DPAIDVCKKLLGKYPNVC   GGKKVGINPKINNLMPG*   KYDLIWICDSGIRGTHEM   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDIG   EGSYDPNVRDIG   EGSYDPNVRDIG   EGSYDPNVRDIG   EGSYDPNVRDIG   EGSYDPNVRDIG   EGSYDPNVRDIG   EGSTYPTRENDIG   EGSTYP	GRL LAV NYL /MT A\AN CNCP C\CM PA\G TGF (WET
FPGVPAPVLTATLPFFHP    YQVEVAPVLTATLPFFHP    YQVEVAPVLTATLPFFHP    YQVEVAPVLTATLPFFHP    YQVEVAPVLTATLPFFHP    YQVEVAPVLTATLPFFHP    RRKINDWAVINTOKKST*P     DSSTYTSLFPR*LENIWC   GMTS*PADSQVQRARYY   WKIQSMGYEIPVDMLCK   IFLQVYHTEMLKMKASLR   IFNWVIDEEQGFSRYIRCU   YYCG*VEYTASGS*TKLE.   LEKKKCKKFDWT*TR   ANTLPCLTVPIQLDFKTPQ   GVVTVENPKPIRLTEAEI   VAPSKRD   18762   49130   A 18871   I 471     18763   49131   A 18872   I 1524     18764   49132   A 18873   2 719   RPQRAGPVRRAGVMALL   EGMAVEGFVLEVLVLWLM   AIIYTRLHLNKKATDKQP   POVSLLEPLVLWLM   AIIYTRLHLNKKATDKQP   POVSLLEPLVSVAPMKF   QM**P*CSTY*YEVLLCVC   DPAIDVCKKLLGKYPNVC   DPAIDVCKKLLGKYPNVC   GGKKVGINPKINNLMPG*   KYDLIWICDSGIRGTHEM   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDPIXRNDIG   EGSYDPNVRDIG   EGSYDPNVRDIG   EGSYDPNVRDIG   EGSYDPNVRDIG   EGSYDPNVRDIG   EGSYDPNVRDIG   EGSYDPNVRDIG   EGSTYPTRENDIG   EGSTYP	GRL LAV NYL /MT A\AN CNCP C\CM PA\G TGF (WET
YQVEYAFKANI*PGGPLPS   RGK\DWAVINTQKKST*P   DSSTYTSLFPR*LKNIW\C   GMTS*PADSQV\QRARY\Y   WK\DGM\C GMTS*PADSQV\QRARY\Y   WK\DGM\C GMTS*PADSQV\QRARY\Y   WK\DGM\C GMTS*PADSQV\QRARY\Y   WK\DGM\C GMTS*PADSQV\QRARY\Y   WK\DGM\C GMTS*PADSQV\QRARY\Y   YYC\G*\F\F\F\F\F\F\F\F\F\F\F\F\F\F\F\F\F\F\	LAV NYL /MT A\AN (NCP C\CM PA\G TGF (WET
RGKIDWAVINTORKST*P	NYL /MT A\AN (NCP C\CM PA\G TGF (WET EIEV
DSSTYTSLFRR*LKNIWC   GMTS*PADSQVQRARYYE   WKIQSMGYEIPYDMLCK   IFLQVYHTEMLKMKASLE   IFNWVIDEEQGPSRYIRCI   YYCGV*KPTASGS*TKLR:   LEKKKCKKFDWTF*TR   ANTLPCLTVPIQLDFKTFQ   GVVTVENPKFIRILTEAEI   VAPSKRD   18762   49130   A   18871   1   471     18763   49131   A   18872   1   1524     18764   49132   A   18873   2   719   RPQRAGPVRRAGVMALLI   EGMAVFGFVLFULVLM   AIIYTELHINKRATDKOPP   POVSLLEPLKGVDPNLIND   FFELDYPKPFSVAPMK   QM**P*CSTY*YEVLUCY   DPAIDVCKKLLGKLYWVC   DPAIDVCKKLLGKLYWVC   GGKKVGRPKINNLMFG*   KYDLIWICDGGIRGTMEN   EQSYDPNVRDPIYRNNOL	/MT A\AN CNCP C\CM PA\G TGF (WET EIEV
GMTS*PADSQVQRARYE   WKIQSMGYEIPVDMLCK   IFLQVYHTEMLKMKASLR   IFNWIDEEQGFSKYIRCU   YYCGV*RFISGS*FKLR:   LEKKCKKFDWTF*TR   ANTLPCLTYPQLDFKTFQ   GVYTVENPKRRILTEAEI   VAPSKRD   18762   49130   A   18871   1       471     18763   49131   A   18872   1     1524     18764   49132   A   18873   2     719     RPQRAGPVRRAGVMALL   EGMAVEGFVLFULWLM   AIIYTELHLINKKATDKQP   PGVSLKPLKGVDPNLIN   FFELDYPKPLFSVAPMK   QM**P*CSTY*YEVLLCV   DPAIDVCKKLIGKYPNVD   GGKKVGNPKINNLIMFG   KYDLIWICDSGIRGTIMEM   EQSYDPNVRDPIYRNNOL	A\AN (NCP C\CM PA\G TGF (WET EIEV
GMTS*PADSQVQRARYE   WKIQSMGYEIPVDMLCK   IFLQVYHTEMLKMKASLR   IFNWIDEEQGFSKYIRCU   YYCGV*RFISGS*FKLR:   LEKKCKKFDWTF*TR   ANTLPCLTYPQLDFKTFQ   GVYTVENPKRRILTEAEI   VAPSKRD   18762   49130   A   18871   1       471     18763   49131   A   18872   1     1524     18764   49132   A   18873   2     719     RPQRAGPVRRAGVMALL   EGMAVEGFVLFULWLM   AIIYTELHLINKKATDKQP   PGVSLKPLKGVDPNLIN   FFELDYPKPLFSVAPMK   QM**P*CSTY*YEVLLCV   DPAIDVCKKLIGKYPNVD   GGKKVGNPKINNLIMFG   KYDLIWICDSGIRGTIMEM   EQSYDPNVRDPIYRNNOL	A\AN (NCP C\CM PA\G TGF (WET EIEV
WKIQSMGYEIPVDMLCK   IFLQYHTEMLKMKASLR   IFNW1DEEQGFSKYIRCU   YYCGV*KFTASGS*TKLR:   LEKKKCKKKFDWTF*TR   ANTLPCLTVPIQLDFKTFQ   GVVTVENPKFRILTEAEI     VAPSKRD	CNCP C\CM PA\G TGF WET EIEV
IFLQVYHTEMLKMKASLE	C\CM PA\G TGF WET EIEV
IFNWIDEEGGFSKYIRCE	PA\G TGF (WET EIEV
YYCGV*RFTASGS*TLKIE   LEKKKCKKFDWFF*TR   ANTLPCLTVPQLDFKTFQ   GVVTVENPKFRILTEAEI     18762   49130   A   18871   I             18763   49131   A   18872   I               18764   49132   A   18873   2                       18764   49132   A   18873   2                         18764	TGF WET EIEV
LEKKKCKKEPUNTF=TRR	WET EIEV
ANTLPCLTYPIQLDFKTFQ   GVVTVENPKPRILTEAEI   VAPSKRAD	EIEV
GVYTVENPKFRILTEAEI     18762   49130   A   18871   I   471     18763   49131   A   18872   I   1524     18764   49132   A   18873   2   719   RPQRAGPVRRAGVMALLI     EGMAVFGFVLELVLWLM     AIIYTRLHINKRATDKQPP     POVSLLKPLKGVDPPLINT     FFELDYPKPLFFSVAPMK     QM**P*CSTY*PEVLLGKYPNVD     GGKKVGNPKINNLMFG*     KYDLIWICDGSIRGTME     EQSYDPNVRDPIYRNNOD     EQSYDPNVRDPIYRNNOD     EQSYDPNVRDPIYRNNOD     EQSYDPNVRDPIYRNNOD     EQSYDPNVRDPIYRNNOD     EQSYDPNVRDPIYRNNOD     EQSYDPNVRDPIYRNNOD     EQSYDPNVRDPIYRNNOD     EQSYDPNVRDPIYRNOD     EQSYDPNVRDPI	
VAPSKRRD   VAPSKRRD	JAQL
18762   49130   A   18871   I   471	
18763   49131   A   18872   I   1524	
18764 49132 A 18873 2 719 RPQRAGPVRRAGVMALL ECMAVFGPVLFLVLWLM AINTREHLINKKATDKQP PGVSLLKPLKSVDPNLIN FFELDYPKPLFFSVAPMKF QM***PCSTY**PVLLCVC DPAIDVCKKLLGKYPNVL IGGKKVGNPKINNLMPG KYDLIWICDSGIRGTMEM EQSYDPNVRDPYRNNGD	
EGMAVFGFVLFLVLWLM AHTYTRLHLNKKATDKQP PGVSLLKPLKGVDPNLINI FFELDYPKPLFFSVAPMK QM**P*CSTY*YEVLLCV DPAIDVCKKLLGKYPNVD IGGKKVGNPKINNLMPG KYDLIWICDSGIRGTMEM EQSYDPNVRDPTYRNNGD	M A I
AIIYTELHINKKATDKOP PGVSLLKPLKGVDPNLINI FFELDYPKPLFFSVAPMKF QM**P*CSTY*YEVLLCVC DPAIDVCKKLLGKYPNVD IGGKKVGNPKINNLMPG KYDLIWICDSGIRGTIMEM EQSYDPNVRDPIYRNNOL	
PGVSLKPLKGVDPNLIN FFELDYPKPLFFSVAPMKF QM**P*CSTYP*EVLLCVC DPAIDVCKKLLGKYPNVC IGGKKVGNPKINNLMPG KYDLIWICDSGIRGTMEM EQSYDPNVRDPYKNNOD	
FFELDYPKPLFFSVAPMK QM*P*CSTY*YEVLLCV DPAIDVCKKLLGKYPNVD IGGKKVGNPKINILMFG KYDLIWICDSGIRGTMEM EQSYDPNVRDPIYKNNGD	
QM**P*CSTY*YEVLLCVC DPAIDVCKKLLGKYPNVD IGGKKVGINPKINNLMPG' KYDLIWICDSGIRGTMEM EQSYDPNVRDPIYRNNGD	
DPAIDVCKKLLGKYPNVE IGGKKVGNPKINNLMPÖ KYDLIWICDSGIRGTMEM EQSYDPNVRDPIYRNNGD	
IGGKKYGINPKINNLIMPC KYDLIWICDSGIRGTIMEM EQSYDPNVRDPIYRNNCID	
KYDLIWICDSGIRGTMEM EQSYDPNVRDPIYRNNGD	
EQSYDPNVRDPIYRNNGD	EVA
	MSL
	١DG
	LINA
18765 49133 A 18874 200 370	
18766 49134 B 18875 323 448	
18767 49135 A 18876 2 421 FVGPGPGDPPPSETHKLVV	
GGVGKSALTIQFIQ/ILDTA	GQE
EFGAMREQYMRAGHGFL	VFA
INDRQSFNEVGKLFTQILR	/KD
RDDFPVVLVGNKADLESC	RQV
PRSEASAFGASHHVAYFE	SAK
LRLNVDEAFE	
18768 49136 A 18877 2 236	
18769 49137 A 18878 I 763 MTPHSALRARGKGGGTGG	GSE
GSSSGGDMSSGAASGTGR	GRPR
GGGPGPGDPPPSETHKLV	
GGVGKSALTIOFIQSYFVS	
PTIEDSYTKICSVDGIPARL	
PAG\QEEFGAMREQYMRA	
GFLLVFAINDROEFSTRWG	DILD
HADFCGFKDRD\DFP\VVL	DILD G/HT
	DILD G/HT KLF
KAD\LESQRQVPRSEASAF	DILD G/HT KLF VGN
HHVAYF\EPSAKMRF\NVE	DILD G/HT KLF /GN GAS\
RSWCGVVREIPRNKELPPS	DILD G/HT KLF VGN GAS\ EGF*
CPPGRMGGGCPCVLL	DILD G/HT KLF VGN GAS\ EGF*

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18770	49138	A	18879	2	403	RFLARRTNSTFNQVVLKRLFMS RTNRPPLSLSRMIRKMKLPGRE NKTAVVGTITDDVRVQEVPK LKVCALRVTSRARSRILRAGGK ILTFDEVYRHFGKAPGTPHSHT KPYVRSKGRKFERARGRRASR GYKN
18771	49139	A	18880	1	1006	IRLIR*PEPSRNOYLLTREOJAVI F/LLSRLLQFFPRPARSRAFLSRK PKPGGKKPMALIVEFIGELPTG VHARPPSHVETLCNTESSQIEW HNLRTDRKGNAKSALA LIGTDT LAGDNCQLLISGADEGEHPGG SQWLRDEPFICDAPLAEVKSD ELEPLPVSLTNLNPQIIRARTVY SGRAGGIQTPISSLDLNALGNLP AAKGVDAEGSALEMIRTL NIEFRLLDSDGATSAILEAHRSL AGDTSLREHLLPVGCCANAASS TNHPFVTKKRQQCFVFRQRLA NGRNDSGWQITHAFWFFHIGH SRIMKYLYGGTARLKEHQPKLR
18772	49140	A	18881	1	716	VCCEFCRAERRHHGEWTIRHN KUDRKGSGARDPKEPGFLL*RC CVKLYRFSGPEEPNSNIQPRLW LKRLFMSRTNRPPSVPFSRDES GKMKASLA RAGKQDRPVVVGG PLT*LMLR VSGRVPKTERYVAL RRCPSFGPQAAFLQGGGKIPS LEPQAWPLGPLKGLLALVPGS SGSLGKGAREGGTRQFSAKAP KETPQKPHQNPYNRSKGRKFE RARGPTGPARGVYKLTLGSYSL
18773	49141	A	18882	3	168	TOTAL CHARLES
18774	49142	A	18883	23	2669	
18775	49143	Ā	18884	279	396	
18776	49144	c	18885	960	1250	
18777	49145	A	18886	52	925	EVLEPRLOVESNOG-FOGLSSVM ALGLKCFRMVHPTFRNYLAASI RYVSEVTLKTVHEROHGHROY MAYSAVPVRHFATKKAKAKA KGQSQTRVNINAALVEDIINLEE VNEEMKSVIEALQG-FQ-GLSI* GPHQDPIDKIAVVTA*REALL+T RFSQISMKSPQLNFG*IWASFPE CTAAAIKAIRESGMNLNPEVLEG CTHAQAIKAIRESGMNLNPEVLEG GOTEHQOGPKTLLREGFRTQLN EQAGRNPKD/NSLQEDTIRLTEK QISQMADDTVAELYRHLAVKT KELLG

SEQ ID	SEQ ID NO:		SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amine acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
18778	49146	Α	18887	2	389	DSGSHCHAPPTTARRAFPIPFGS
1						KSNMATLKDQLIYNLLKEEHTF
						QNKITAVRVGADGMACAITIL
İ		1		ľ		M/KDYNVTANSKLVIITGGARQ
		1				QQGESRLNLVQRNVNIFKFIIPN
						VAKYSPNCKLLIRSNPVDI
18779	49147	В	18888	217	423	
18780	49148	A	18889	27	1217	ARRPTRPPDLIATRPRRPARRCI
		1				SRFPFGSKSNYWQPLKDQLIYN
		l		l		LLKEEQTP\QNKITVVGVGAVG
				l		MACAISILMKDLADE\LALVDV
						EDKLKG\EMMDLQHGKPFSFR
						NTKVLSSGKRL*M*LANSKAGS
	i			]		FITGWGHRQQEGKKAVLILVQ AVNVNIFKFIIP\NVVKYSP\NCK
1				1		LLIVSNPVDILTYVAWKUSGFP
		t				KNRVIG\SGCNL\DSA\RFR\YLM
1		l		1		G\ERLGSSPH*ACHGWGPWGEH
		i .				GRFPVLPVMGVGLNVAGVSLE
		1				DFWHPDFRTDKD*E\OWKE\VH
		1				K\QVVE\SAYEVIKLK\GYTSLG
1		1				LIGLSCKPD\LAE\SIMEESFRRV
		1				HPS/SSHHGLKGLYGNKRMNVS
1		1	}			LSVPCILGONGIS\DLVKG\TLTS
1		1				EGRGPVGSKSADNNSWGSTKK
18781	49149	Α	18890	1	264	
18782	49150	Α	18891	3	736	
18783	49151	Α	18892	81	1065	GKGPVAAFIDQSNIFLTDPKIFL
l				1		GQWREEPKMPLLLLGETEPLKL
				ł		ERDCRSPVDPWAAASPDLALA
	1			İ		CLCHCQDLSSGAFPNRGVLGG
				į.		VLFPTVEMVIKVFVATSSGSIAI
						RKKQQEVVGFLEANKIDFKELD
l		l				IAGDEDNRRWMRENVS*REKP
						Q\NGIPLPSQI\FNEE\QYCG\DFD
1				l		SFFSAKKENIIYSF\LGWAPLPD\$
						KGSEKAEEG\GETEAQKEGSED
				1		VGNLPEAQEKNEEEGETATEET VEEIAMEGAEGEAEEEEETAEGE
				l		
						EEPGEDEDFLGLFMLHFFHFSQ
1		1		I		KMEAMKQHSNVLSTNQTETEY
10704	401.52		10002	10	445	FGLKPAHPRVTEDIMLPDLIR
18784	49152	Α	18893	19	443	

SEQ ID NO:	SEQ ID NO: of peptide		SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
	sequence		69/540,217	codon for peptide sequence	of peptide sequenee	deletinn, \=possible nucleotide insertion)
18785	49153	Α	18894	1	622	QAAWILKARALTEMVYIDEIDV
						DQEGIAEMMLDENAIAQVPRP
						GTSLKLPGTNQTGGPSQAVRP\
						TSHSEKPITGFLRPSTQSGRPGT
						MEQAIRTPRTAYTARPITSSSGR
				İ		FVRLGTASMLTSPDGPFIN*SRL
1		ŀ				NLTKYSQKPKMAKALPEYIFHH
		l				ENDVKTALELAALSTEHSQYK
1		1	1			DWWWKVQIEKRYYRLGMYRE
		l				AEKQLISAMKQ
18786	49154	A	18895	1	1651	MKAEICKSRTVKDWHNHQKLG
						EGNKTDSPPQPSEGTNTANTLIL
			1			DFWPLEMIACCWETFPQRLTAE
						LFMNPTHRWHGYKNQSVGAL
						RAPLGQGPSRRGLPGRVGRRQL
		l				FTPRPPLSWSAGPSLAAPAAMS
		1				SEMEPLLLAWSYFRRRKFQLCA
		1				DLCTQMLEKSPYDQEPDPELPV
		1				HQAAWILKARALTEMVYIDEID
		1				VDQEGIAEMMLDENAIA/PSSTP
						ITQAGRPITGFLRPSTQSGRPGT
						MEQAIRTPRTAYTARPITSSSGR
		1				FVRLG\RLGMYREAEKQFKSAL
i		1				KQQEMVDTFLYLAKVYVSLDQ
					1	PVTALNLFKQGLDKFPGEVTLL
						CGIARIYEEMNNMSSAAEYYKE
						VLKQDNTHVEAIACIGSNHFYS
1	ì					DQPEIALRFYRRLLQMGIYNGQ
						LFNNLGLCCFYAQQYDMTLTS
						FERALSLAENEEEAADVWYNL
						GHVAVGIGDTNLAHQCLRLAV
		1				VNSNNHAEAYNNLAVLGDAEG
	1	ŀ			-	/RHVEQARALLQTASSISTPYV*
		ŀ			1	TAFLILQQSLIRFGDLQRSYVAA
						QKSEAAFPDHVDTQHLIKQLRQ
		_				HFAML
18787	49155	A	18896	2	295	
18788	49156	A	18897	1	4470	MLGLGLLRLRQGSHAVTRCRP
		1				LPVRREGRRDGSPWRSVVCRY
						CRCSRQTGASVTTVSLPSSSSSP
		1				GLDPRGPRQASVKKPAEANPV
		l		1		LRPLVRHGTPYRDSEEGKREGL
		1			l l	SRLRAVCRRAGPRGRGSFSPRD
1		1	1	1		ARASPRLHFLVAAVTTGAASRR
1		1				QRGARVRQPSPSSSRRAKRLRE
1						CERRSLHAPPAMDASYDGTEV
		1				TVVMEEIEEAYCYTSPGPPKKK
		1				KKYKIHGEKTKKPRSAYLLYY
				l		YDIYLKVQQELPHLPQS

NO.	SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
18789   49157   A   18898   89   810							
18789   49157   A   18898   89   810   QRRSGCVLRMTEWETAAIPAG GQRTPDIKALWGSGAPDIVAR SMMISLQIDYIAS*RRKLCPSYL HISCOGGYAKNI,SSKAQUEPY VERLTINSPMMHIRPQQPARK LMTVRIVQAHAFEITPCSQAE NPLQVILGEPPSINSGPREDSHIT HILGAAGTVRRQAVDIVSPLRR EPGPPWACTERTUKSGLAP TFKTIG*VAWADIELINACQG/PSNSYCL*FEGRVAFLEHVAKS NR     18790   49158   A   18899   1   365   DTHFKZDSHHRTSTAHLLISLSC GPSPPNLPLGVPISISGMCLOPRG EGRANPIPTVLKRDQEGLGYRS APQPRVTHFPAWDTRAVAGRE RPPRVATLSWREERREEEDR WEEDLRTYMNLEF     18791   49159   A   18900   203   427   49160   A   18901   95   482   ALQSPKLWGYPSGRKVFLNYF SSQQVSEAVVATGSPRAWLTC LILPJEGIIFSLYEAMSPLLTT TPATDPSDLWKDGQQPQPEE PESTLDGLAKALYFEALIGDES SAPDSQRSQTEPARERKR GPGWIFFSVCRSLRLWLTGSS SAPDSQRSQTEPARERKR VFCHLIPJEGIIFSLKFSQKA VPGPILLTFTPATDPSDLWKDGQQQPPEE SAPDSQRSQTFT WPEERKRKRKGILKWLTGSS LSLALPCLILPJEGIIFSLKFSQKA VPGPILLTTPATDPSDLWKDGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA	1	sequence		09/540,217		of peptide sequence	deletion, \=possible nucleotide insertion)
GQRTPDIKALWGSGAPDDVAR					sequence		
SMMISLQIDYIAS*RRKLCPSYL     HSCQGGYAAKNLSRKAQICPI     VERLITNSPMMHRPQQPAK     LMTVRIVQAHAFEIITECSQAE     NPLQVLGEPPSINGSPREDSH     HLGAAGTVRRQAUDVSPLRR     EPGPFWVACCTRRLVKGLAFP     TFKTIG*VAWADIELINACQQF     PSNSYCL*EEGRVAFLEHVAKS     NR	18789	49157	A	18898	89	810	ORRSGCVLRMTEWETAA\PAG
WISCOGGY AAKNI SRKAQICPP				İ			GORTPDIKALWGSGAPDDVAR
VERLITISSMMMHRRQQPARK			1				SMNISLO\DYIAS*RRKLCPSYLP
LMTVRIVQAMAFEIITCSQAE   NPLQVLGEPPSINSGPREDSH  HLGAAGTVRRQAVDVSPLRR   EPGPFWACCTRRLVKGLAPP   TFKTIG*VAWADELINACQQC   PSNSYCL*EEGRVAFLEHVAKS   NR   NR   NR   NR   NR   NR   NR   N							\HSCQGGYAAKNLSRKAQ\CPI\
LMTVRIVQAMAFEIITCSQAE   NPLQVLGEPPSINSGPREDSH  HLGAAGTVRRQAVDVSPLRR   EPGPFWACCTRRLVKGLAPP   TFKTIG*VAWADELINACQQC   PSNSYCL*EEGRVAFLEHVAKS   NR   NR   NR   NR   NR   NR   NR   N							VER\LTNSPMMMHRPQQPARK
HLGAAGTVRRQADDVSPLRR					l		LMTVRIVQA/HAFEIITPCSQAE
EFGPFWYACCTRILVKGLAPP					l		NPL\QVLGEPPSINSG\PREDSHT
EFGPFWYACCTRILVKGLAPP							HLGAAGTVRRQAVDV\SPLRRV
TFKTIG*VAWADBELINACQG/PSNSYCL*EGRVAFLEHVVAKSNR							EPGPFWVACCTRRLVKGLAFPG
PSNSYCL*EEGRVAFLEHVÄKS   NR							TFKTIG*VAWAD\ELI\NACOGA
NR							PSNSYCL*EEGRVAFLEHVAKS
GRSPPNLPLGVPISIGMGLOPRC							
EGRANPIPTVLKROQEGLGVR: APQPRVTHFPAWDTRAVAGRE RPPRVATLSWREERRREEKDR. WERDLRTYMNLEF     18791   49159   A   18900   203   427     18792   49160   A   18901   95   482   ALQSPKLWGYPSGRKYFLNYF SSQQVSEAVVATGSPRAWLTC   LIP.PGIIFSVLPKAMSRPLLTT TPATDPSDLWKDGQQQPQPEK PESTLOGLAKALFYEALIGES SAPDSQRSQTEPARERKR     18793   49161   A   18902   348   1660   GYTHLFJEKRKLRNGIGAGRIK GPGWIFFSVCRSLRLWLLTGSS   CLSLALPCLLIP.PGIIFSLKFSQKA VPGPLLIFTFPATDPSDLWKDG QQQQPQPEKPESTL\DGAAARAI YEALIGDESSAPDSQRSQT*T WPFERKRKKRGILKAPAAEAL AEGAASGRPVQGRSLEADDPM YRILTSAQEGDLP*ILMRLLEPP   EAGGAGGNINARDAFWWTPL MCAARAGQGAAVSYLLGPGA AWVGVCELSGRDAAQULAEEA GPPEVARMVRSHGETRSPENI SPTFSLQYCENCDTHPQDISNHI \ VTSTVHLLSSQGPQPPCILLCY PRISTRE*ILLGGVGSPGMGLG PRGEGRANPHPQLILK*GPGRG LGVKSTSTPEF*ILLGGVGSPGMGLG PRGEGRANPHPQLILK*GPGRG LGVKSTSTPEF*ILLGGVGSPGMGLG PRGEGRANPHPQLILK*GPGRG LGVKSTSTPEF*ILLGGVGSPGMGLG PRGEGRANPHPQLILK*GPGRG LGVKSTSTPEF*ILLGGVGSPGMGLG PRGEGRANPHPQLILK*GPGRG LGVKSTSTPEF*VTHFPSSGIPRA VAGRERPPRVAYTINWKEERF RREEKDRAWREDLRTYMNLEF	18790	49158	A	18899	1	365	DTHFK/DSHHRTSTAHLL\SLSO
EGRANPIPTVLKROQEGLGVR: APQPRVTHFPAWDTRAVAGRE RPPRVATLSWREERRREEKDR. WERDLRTYMNLEF     18791   49159   A   18900   203   427     18792   49160   A   18901   95   482   ALQSPKLWGYPSGRKYFLNYF SSQQVSEAVVATGSPRAWLTC   LIP.PGIIFSVLPKAMSRPLLTT TPATDPSDLWKDGQQQPQPEK PESTLOGLAKALFYEALIGES SAPDSQRSQTEPARERKR     18793   49161   A   18902   348   1660   GYTHLFJEKRKLRNGIGAGRIK GPGWIFFSVCRSLRLWLLTGSS   CLSLALPCLLIP.PGIIFSLKFSQKA VPGPLLIFTFPATDPSDLWKDG QQQQPQPEKPESTL\DGAAARAI YEALIGDESSAPDSQRSQT*T WPFERKRKKRGILKAPAAEAL AEGAASGRPVQGRSLEADDPM YRILTSAQEGDLP*ILMRLLEPP   EAGGAGGNINARDAFWWTPL MCAARAGQGAAVSYLLGPGA AWVGVCELSGRDAAQULAEEA GPPEVARMVRSHGETRSPENI SPTFSLQYCENCDTHPQDISNHI \ VTSTVHLLSSQGPQPPCILLCY PRISTRE*ILLGGVGSPGMGLG PRGEGRANPHPQLILK*GPGRG LGVKSTSTPEF*ILLGGVGSPGMGLG PRGEGRANPHPQLILK*GPGRG LGVKSTSTPEF*ILLGGVGSPGMGLG PRGEGRANPHPQLILK*GPGRG LGVKSTSTPEF*ILLGGVGSPGMGLG PRGEGRANPHPQLILK*GPGRG LGVKSTSTPEF*ILLGGVGSPGMGLG PRGEGRANPHPQLILK*GPGRG LGVKSTSTPEF*VTHFPSSGIPRA VAGRERPPRVAYTINWKEERF RREEKDRAWREDLRTYMNLEF						i	GPSPPNLPLGVPIS\GMGLGPRG
APORVITHERA WDITRA VAGRE RPRVATLS WREERREEKDR.			ŀ				
RPPRVATLSWREERRREEKDR.   RPPRVATLSWREERRREEKDR.   RPPRVATLSWREERRREEKDR.   REPRESENTED   REPRESENT	1						
WERDLRTYMNLEF					i		
18792 49160 A 18901 95 482 ALQSPKLWGYPSGRKYPLNYF SSQQVSEAVVATGSPRAWLTC LILPLPGIIFSVLPKAMSRPLLIT TPATDPSDLWKDGQQQPQPEK PESTLOGLAKKLYPEALIGES SAPDSQRSQTEPARERKR GPGWIFFSVCRSLRIWLLTGSS LSLALPCLILPLPGIIFLKFSQKA VPGPLIIFTPATDPSDLWKDG QQQPQPEKPESTLDGAARAR YEALIGDESSAPDSQRSQT-T WPERKRKKRGLLKAPAAEAL AEGASGRPVQGRSLEADDPM YRILTSAGEGDUP-IMRLLEPP EAGGAGGNINARDAFWWTPL MCAARAGQGAAVSYLLGPGIA AWVGVCELSGRDAAQULAEEA GPFEVARMVRSHGETRSPENI SPTPSLQYCENCDTHPQD\SNH \text{VSTVHLLSSQGPQPPGLILCY} PESTPRF*ILLIGGVGSPGMGLG PRGEGRANPPIQLIK*GPRGKG LGVKISTPSPEVTIFPSSGIPRA VAGRERPPRVAYLINWKEERF REEKCDRAWERDLRTYMNLEF							
SSQQVSEAVVATGSPRAWLTC LILPLPGIIFSVLPKAMSRPLLIT TPATDPSDLWKDGQQQPQPEK PESTLUDGLAAKLFYEALIGDES SAPDSQRSQTEPARERRR 18793 49161 A 18902 348 1660 GVTHLFLFGKRKLRNGIAGRIK GPGWIFFSVCRSLRLWLLTGSP LSLALPCLILPLPGIIFLKFSQKA VPGPLLITTTATDPSDLWKUD QQQPQPEKPSTLDGAAARAI YEALINGDESSAPDSQRSQT-T WPEEKRKKRGLKAPAAEAL AEGVASGRPVQGRSLEADDPM YRILTSAQEGDLPPLMRLLEPI EAGGAGNINARDAFWWTHL MCAARAGQGAAVSYLLGPGW AWVGVCELSGRDAAQLLAEEA GPPEVARMVRESHGETRSPENI SPTBLQVCENCDTHPQDNNH VTSTYPLLLSGVGSPPGPLGLGV PISTPRF-ILLLGGVGSPGMGLG PRGGEGANPIPOLLK-GPRGK LGVKISTPSPEVTHFPSFGIPRA VAGRRRPPRVATILNWKEERR RREEKDRAWROLDRITYMLEPI RAGRERPPRVATILNWKEERR RREEKDRAWROLDRITYMLEPI RAGRERPPRVATILNWKEERR RREEKDRAWROLDRITYMLEPI RAGRERPPRVATILNWKEERR RREEKDRAWROLDRITYMLEPI RAGRERPPRVATILNWKEERR REEKENDAWROLDRITYMLEPI RAGRERPPRVATILNWKEERR REEKENDAWROLDRITYMLEPI RAGRERPPRVATILNWKEERR REEKENDAWROLDRITYMLEPI RAGRERPPRVATILNWKEERR REEKENDAWROLDRITYMLEPI RAGRERPPRVATILNWKEERR REEKENDAWROLDRITYMLEPI RAGRERPPRVATILNWKEERR REEKENDAWROLDRITYMLEPI RAGRERPPRVATILNWKEERR REEKENDAWROLDRITYMLEPI RAGRERPPRVATILNWKEERR REEKENDAWROLDRITYMLEPI RAGRERPPRVATILNWKEERR REEKENDAWROLDRITYMLEPI RAGRERPPRVATILNWKEERR REEKENDAWROLDRITYMLEPI RAGRERPPRVATILNWKEERR REEKENDAWROLDRITYMLEPI RAGRERPPRVATILNWKEERR REEKENDAWROLDRITYMLEPI RAGRERPPRVATILNWKEERR REEKENDAWROLDRITYMLEPI RAGRERPPRVATILNWKEERR REEKENDAWROLDRITYMLEPI RAGRERPPRVATILNWKEERR REEKENDAWROLDRITYMLEPI RAGRERPPRVATILNWKEERR REEKENDAWROLDRITYMLEPI RAGRERPPRVATILNWKEERR REEKENDAWROLDRITYMLEPI RAGRERPPRVATILNWKEERR REEKENDAWROLDRITYMLEPI RAGRERPPRVATILNWKEERR REEKENDAWROLDRITYMLEPI RAGRERPRVATILNWKEERR REEKENDAWROLDRITYMLEPI RAGRERPRVATILNWKEERR REEKENDAWROLDRITYMLEPI RAGRERPRVATILNWKEERR REEKENDAWROLDRITYMLEPI RAGRERPRVATILNWKEERR REEKENDAWROLDRITYMLEPI RAGRERPRVATILNWKEERR REEKENDAWROLDRITYMLEPI RAGRERPRVATILNWKEERR REEKENDAWROLDRITYMLEPI RAGRERPRVATILNWKEERR REEKENDAWROLDRITYMLEPI RAGRERPRVATILNWKEERR REEKENDAWROLDRITYMLEPI RAGRERPRVATILNWKEERR REEKENDAWROLDRITYMLEPI	18791	49159	Α	18900	203	427	
LILPLPGIJESVLPKAMSRPLLIT TPATDPSDLWKDGQQQPQPEK PESTLUDGLAKLFYEALIGDES SAPDSQRSQTEPARERKR  18793 49161 A 18902 348 1660 GVTHLFLFGKRKLRNGIGARIK GPGWIFFSYCRSLRLWLLTGSP LSLALPCLILPLPGIJELKFSQKA VPGPLLITFTATDPSDLWKUD QQQPQPEKPESTLDGAARAI YEALIGDESSAPDSQRSQT*T WPEEKKKKKRGLLKAPAAEAL AEGASGRPVQGRSLEADDPM YRILTSAQEGDUP-ILMRLLEPP EAGGAGGNINARDAFWYTPL MCAARAGGAAVSYLLGPGA AWWGVCELSGRDAAQLAEEA GPFEVARMVRESHGETRSPENI SPTPSLQVCENCDTHFQDISMH \text{VISTYPLLSLSQQPQPPQLPLQV} PISTTPRF*ILLLGCVGSPGMGLG PRGEGANNPPQLIK**GPRGK LGVKLSTPSPEVTHFPSFGIPRA VAGRERPRVAVILNWKEERF RREEKORAWERDLRTYMNLE	18792	49160	Α	18901	95	482	ALQSPKLWGYFSGRKVFLNYFF
TRATOPSDLWKOGOQOPOPER PESTLIDGLAKLFYEALIGDES SAPDSQRSQTEPARENKR  18793 49161 A 18902 348 1660 GVTHLFLFGKRKLRNGIAGRIK GPGWFFSYCRSLRLWLLTGSP LSLALPCLLIP.PGIFLKFSQKA VPGPLLIPFPATIDPSDLWKDC QQQPQPEKPESTLDGAARARI YEALINGDESSAPDSQRSQT-T WPEEKRKKRGLKAPAAEAL AEGVASGRPVQGRSLEADDPM YRILTSAQEGDLIP-LMRLLEPI EAGGAGGNINARDAFWWTHL MCAARAGQGAAVSYLLGPGW AWVGVCELSGRDAAQULAEEA GPPEVARMVRESHGETRSPENI SPTFSLQVCENCDTHFQDISNHI VTSTVFILLSLSQGPQPPGLLEVG PEGFGRANPIPGLLK-GPRGK LGVKISTPSPEVTHFPSGFOIPRA VAGRREPPRVATILNKEERR RREEKDRAWERDLRTYMNLEF							SSQQVSEAVVATGSPRAWLTC
PESTLOGLAAKLFYEALIGDES SAPDSQRSQTEPARERKR  18793 49161 A 18902 348 1660 GYTHLFLFGKRKLRNGIAGRIK GRGWIFFSYCRSLRLWLITGSP LSLALPCLLIP PGIFLKFSQKA VPGPLLITFTPATDPSDLWKUD QQQPQPERPESTLUGAAARAI YEALIGDESSAPDSQRSQT*T WPEERKRKRGLLKAPAAEAL AEGASGRIVQGRSLEADDPM YRILTSAQEGDUP*LMRULEPP EAGGAGGNINARDAFWUTPL MCAARAGQGAAVSYLLGPGIA AWVGVCELSGRDAAQULAEEA GPFEVAMVRESHGETRSPENI SPITPSLQYCENCDTHFQDISNH VTSTVHLLSLSQGPQPPQLPLGV PISTTRE*ILLIGGVGSPGMGLG PRGGEGANPIPPQLILK*GPRGR LGVKISTPSPEVTHFPSFGIPRA VAGRERYRVANTINWKEERR RREEKORAWERDLRTYMNLEIF							LILPLPGIIFSVLPKAMSRPLLITF
SAPDSQRSQTEPAKERKR  18793 49161 A 18902 348 1660 GVTHLFLFGKRKLRNGIAGRIK GPGWIFFSYCRSLRLWLLTGSP LSLALPCLILPLPGIIFLKFSQKA VPGPLLIFFPATDPSDLWKUG QQQPQPEKPESTL\DGAAARAI YEALIGDESSAPDSQRSQT*T WPEERKRKKRGLLKAPAAEAL AEG\ASGRPVQGRSLEADDPM YRILTSA\GEGDUP*LMRLLEPPI BAGGAGGNINARDAFWWTPL MCAARAGGAAVSYLLGPGIA AWVGYCELSGRDAAQILAEEA GPFEVARMVRSHGETRSPENI SPTPSLQYCENCDTHFQD\SNH \text{VTSTVHLLSLSQGPQPPQLLCV} PESTPRF*ILLGGVGSPGMGLG PRGEGANNPPQLLK*GPRGK LG\VKLSTPSPEVTHFPSFGIPRA VAGRERPPRVAYLNWKEERF REEKCDRAWERDLRTYMNLEF							TPATDPSDLWKDGQQQPQPEK
18793 49161 A 18902 348 1660 GVTHLFLFGKRKLRNGIAGRIK GPGWIFFSYCRSLRLWLLTGSP LSLALPCLLIP_PGIIFLKFSQKA VPGPL_ITTTPATDPSDLWKUD QQQPQPEPEPSTLDGAAARAI YEALIGGESSAPDSGRSQT*T WPEEKKRKKGLKAPAAEAL AEGASGRIVQGRSLEADDPM YRILTSAQEGDLP*LMRLLEP! EAGGAGGNINARDAFWWTPL MCAARAGQAAVSYLLGPGW AWVGVELSGRDAAQLLAEEA GPFEVARMVRESHGETRSPENI SIFTBLQVCENCDTHPQDISNHI VTSTYVHLLSSQCPOPPOPLOLEV PESTPRF*ILLIGGVGSPGMGLG PRGEGRANPHPGLIK**GPRKG LGIVKISTPSPEVTHFPSFGIPRA VAGRREPPRVATILNWKEERR RREEKDRAWREDLRTYMNLEFI RREEKCDRAWREDLRTYMNLEFI RREE							PESTL\DGLAAKLFYEALIGDES
GPGWIFFSYCRSLRLWLLTGSP LSLALPCLILPLPGIIFLKFSQKA VPGPLLIFTFATDPSDLWKUD QQQPQPEKPESTLDGAAARAI YEALNGDESS APDSQRSQT*T WPEERKRKKKRGLLKAPAAEAI AEGASGRPVQGRSLEADDPM YRILTSAQEGDUP*LMRLLEPP EAGGAGGNINARDAFWYTPL MCAARAGQGA VSYLLGPGA AWVGVCELSGRDAAQULAEEA GPFEVARMVRESHGETRSPENI SPTPSLQVCENCDTHFQDISNHI \text{VSTYHLLSLSQGPQPPQLPLGV} PISTPRF*ILLIGGVGSPGMGLG PRGEGANNPHQLILK*GPRGK LGVKLSTPSPEVTHFPSFGIPRA VAGREFPRVAVITNWKEERF RREEKQDRAWERDLRTYMNLEF					1		SAPDSQRSQTEPARERKR
LSLALPCLILPR-GIFLKFSQKA VPGPLLIFTPATIDPSDLWKDC QQQPQPEKPESTLDGAARARI YEALINGDESSAPDSQRSQT-T WPEEKRKKKGLIKAPAAEAI AEOASGRPVQGRSLEADDPM YRILTSAQEGDLIP-LMRLLEPI EAGGAGGNINARDAFWWTPL MCAARAGQGAAVSYLLGPGW AWVGVCELSGRDAAQULAEEA GPPEVAMVRESHGETRSPENI SPTFSLQVCENCDTHFQDISNHI VTSTVFILLSLSQGPQPPGLPLGW PESTPRF-IILLGGVGSPGMGLG PRGEGRANPHPGLIK-GPRGK LGIVKISTPSPEVTHFPSGIPRA VAGRRFPPRVATILNKEERR RREEKDRAWREDLRTYMNLEI	18793	49161	Α	18902	348	1660	GVTHLFLFGKRKLRNGIAGRIK
VPCPLLITETPATDPSDLWKDC QQQPQPEKPESTLDGAAARAI YEJALIGDESSAPDSQRSQTT WPEEKKRKRGLLKAPAAEAI AEGASGRPVQGRSLEADDPM YKILTSAQEGDLP-LMRLLEPI EAGGAGGNINARDAFWYFL MCAARAGQCA AVSYLLGPCA AWVGVCELSGRDAAQILAEEA GPPEVARMVRESHGETRSPENI SPTPSLQYCENCDTHFQDISNIH VTSTVHLLSLSQGPQPPQLPLGV PHSTRET*ILLIGGVOSPOMGLG PREGEGRANPHPQLILK*GPRKG LGVKLSTPSPEVTHFPSFGIPRA VAGRERPPRVAVILNWKEJERF RREEKORAWERDLRTYMNLEI							GPGWIFFSYCRSLRLWLLTGSP
QQQPQPEKPESTLDGAAARAI YEALIGDESSAPDSQRSQT*T WPEEKKRKKKKALLKAPAAEAI AEGASGRPVQGRSLEADDPM YRILTSAQEGDUP-I_MRLLEPP EAGGAGGNINARDAFWWTPL MCAARAGGGAAVSYLLGPGIA AWVGVCELSGRDAAQILAEEA GPFEVARMVRESHGETRSPENI SPITSLQYCENCDTHFQDISNHI VISTVHLLSLSQOPQPPQLPLCV PISTPRF*ILLIGGVGSPGMGLG PRGEGANPHPQLILK*GPRGK LGVKISTPSPEVTHFPSIGIPRA VAGRERPPRVAYLNWKEERF RREEKDRAWERDLRTYMNLEI							LSLALPCLILPLPGIIFLKFSQKAI
YEALIGDESSAPDSQRSQT=T WPEERKRKKRGLLKAPAAEAL AEGASGRPVQGRSLEADDPW YRILTSAQEGDLP-LMRLLEP! EAGAGGNINARDAFWITEL MCAARAQGAAVSVLLGPGW AWVOYCELSGRDAAQLLAEEA GFPEVARMVRESHGETRSPENI SITTBLQVGENCDTHFQDISNHI VISTYPLLLSLQSGOPPOPLLEV PISTPRF=TILLLGGVGSPGMGLG PRGEGRANPHPGLILK-*GPRKG LGIVKISTTSPEVTHFPSFGIPRA VAGRERPPRVATILNWEÆER RREEKDRAWERDLRTYMNLEI							VPGPLLITFTPATDPSDLWK\DG
WPEERKRKRCILKÄPÄÄEAL AEGASGRPVQGRSLEADDPM YRILTSAQEEDULP*LMRULEPP EAGGAGGNINARDAFWYFLL MCAARAGQGA VSYLLGPGVA AWVGVCELSGRDAAQULAEEA GPFEVARMVRESHGETRSPENI SPITPSLQYCENCDTHFQDISNHI VTSTVHLLSLSQGPQPPQLPLGV PISTPRF*ILLIGGVGSPGMGLG PRGEGRANPHPGLILK*GPRGR LGVKISTPSPEVTHFPSFGIPRA VAGREPPRVAVITLNWKEERF RREEKORAWERDLRTYMNLEH							QQQPQ\PEKPESTL\DGAAARAF
AEGNASGRPVQGRSLEADDPM' YRILTSAQEGD\LPPLMYRLLEPI EAGGAGGNINARDAFWYTPLI MCAARAQGAAVSYLLGPGW AWWQVCELSGRDAAQLAEEA GPPEVAMVRESHGETRSPENI SPTPSLQVCENCDTHFQDISNHI VITSTVHLLSLSQGPQPPGLPLGW PISTPRF*ILLLGGVGSPGMGLG PRGEGRANPHPGLILK*GPRGK LGIVKISTPSPEVTHFPSFGIPRA VAGRRPPPRVAYITLNKÆERR RREEKDRAWREDLRTYMNLEI							YE\ALI\GDESSAPDSQRSQT*T
YRILTSAQEGDLP*LMRILEP! EAGGAGONIARDAFWWTPL MCAARAGQGAAVSYLLGPGW AWVGVCELSGRDAQULAEEA GFPEVARMVRESHGETRSPENI SFTPSLQVCENCDTHFQDISNHI VTSTVHLLSLSQGFQPPQLPLGV PISTPF*ILLLGGVGSPGMGLG PRGEGRANPHPQLILK*GPRKG LGVKLSTPSPEVTHFPSFGIPRA VAGRERPPRVAVILNWKEÆRF RREEKDRAWERDLRTYMNLEH							WPEERKRKKRGLLKAPAAEAL
EAGGAGNINARDAFWYTEL  MCAARAGGAAVSYLLGPGIA AWVGVCELSGRDAAQLIAEEA GPFEVARMVRESHGETRSPENI SPTPSLQVCENCOTHFODISNHI \(\text{VTSTVHLLSLSQGPQPPQLPLGV}\) PISTPRF*ILLLGCVGSPGMGLG PRGEGANPHPQLILK**GPRGC LGVKLSTPSPEVTHFPSFGIPRA VAGREPPRVAVITLNWKEERF RREEKORAWERDLRTYMNLEI							AEG\ASGRPVQGRSLEADDPMT
MCAARAGQGA AVSYLLGPG\\ AWVGVCELSGRDA AQ\\\ AWVGVCELSGRDA AQ\\\\ GPFEVARMVRESHGETRSPPI\\ SPTPSLQYCENCDTHFQD\\\ NTSTVFILLSLSQGPQPPQLPLGV\\ PISTPRF*ILLLGGVGSPGMGLG\\ PRGEGRANPHPQLILK*GPRKG\\ LG\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	ŀ						YRILTSAQEGD\LP*LM\RLLEPH
AWVGVCELSGRDAQ/LAEEA GFPEVARMYRESHGETRSPENI SFTPSLQVCENCDTHFQD\SNH \text{VSTVHLLSLSQGFQPPQ/LFGV} PISTFR*ILLLGVQSFQFWQL/GV PRGEGRANPHPQ/LLK*\GPRG L\GVK\LST\SPEVTHFPS\GIPRA VAGRERPP\RVA\TLNWKE\ERF RREEK\DRAWERDLRT\M\LST\SPE\							EAGGAGGNINARDAFWWTPL
GPPEVARMVRESHGETRSPENI SPTPSLQYCENCDTHFQD\SNHI \text{VTSTVHLLSLSQGPQPPQLPLGV} PRSTPRF*ILLLGGVGSPGMGLG PRGEGRANPHPQLILK*GPRGS LG\YKISTPSPEVTHFPSFGIPRA VAGRERPPRVAYILNKEERR RREEKDRAWERDLRTYMNLEI	ŀ						MCAARAGQGAAVSYLLGPG\A
SPTPSLQYCENCDTHFQD\SNHI \text{VISTLYBLLSLSQGPQPPQLPLGV} PISTPRF*ILLLGGVGSPGMGLG PRGEGRANPHPQLILK*GPRKG LG\text{VKISTPSPEVTHFPSFGIPRA} VAGRERPPRVA\TLNWKE\ERF RREEKORAWERDLRTYM\LEI							AWVGVCELSGRDAAQ\LAEEA
\tag{ref}\ta							GFPEVARMVRESHGETRSPENR
PISTPRF*ILLLGGVGSPGMGLG PRGEGRANPHPQLILL*GPRKG LGYKISTPSPEVTHFPSFGIPRA VAGRERPPRVAYTLNWKE/ERR RREEKDRAWERDLRTYMNLEI						ŀ	SPTPSLQYCENCDTHFQD\SNHR
PRGEGRANPHPQLILK*GPRKG LO;YKISTPSPEVTHFPSFGIPRA VAGRERPPRVAYILNWKE/ERF RREEKORAWERDLRTYMNLEI			l				\TSTVHLLSLSQGPQPPQLPLGV
LOVKISTPSPEVTHFPSFGIPRA VAGRERPPRVAYTINWKEÆRF RREEKDRAWERDLRTYMNLEI	l				l		PISTPRF*ILLLGGVGSPGMGLG
VAGRERPPIRVA\TLNWKE/ERF RREEKDRAWERDLRTYMNLEI							PRGEGRANPHPQLILK*GPRKG
RREEKDRAWERDLRTYMNLEI	l			1	1	1	LG\YKISTPSPEVTHFPSFGIPRA
					l		VAGRERPP\RVA\TLNWKE/ERR
T8794 49162 C 18903 135 299							RREEKDRAWERDLRTYMNLEF
[	18794	49162	C	18903	135	299	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	İ	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
18795	49163	A	18904	3	2074	ERSRPVALRAAVPRMNPSTPSY
10775	47103	ľ^	10501	,	2071	PTASLYVGDLHPDVTEAMLYE
						KFSPAGPILSIRICRDLITSGSSN
						YAYVNFQHTKDAEHALDTMNF
						DVIKGKPVRIMWSQRDPSLRKS
				ŀ		GVGNIFVKNI.DKSINNKALYDT
						VSAFGNTLSCKVVCDENGSKG
						YGFVHFETH\EA\AERAIEKMNG
						ML\LNDRKVFVGRFKSRKEREA
						ELGARAKEFTNVYIKNFGEDM
1						D\DGRLK\DLFGKF\GPALKCEK
1						LMTDESGKSKGFGFVS\FERHE
1						DAQKAVDEMNGKELNGKQIY
						VGRAQKKV\ERQTELKRKFEQ
				ŀ		MKQDRITRYQGVNL\YVKNLD
				ŀ		DG\IDDE\RLRKEFSPFGTIQLVP
						KVMDGGLVAAKGLGFVCFSSP
						E\EATKAVTEMNF\RIVATEPL\Y
	]					VALA\QRKEERQAHLTNQYYG
						RGM\ASVTEAVPNPV\IQPLPGQ
				i		APPFRFTFMGRFSHRFRNRA\AY
						YP\PSQIAQTKTKFLRWTGQGA
ľ						RT\HPF\QNMPGCYPAQLAPRPP
						I*GTM\RPASSQ\VPR\VMPTQR\
						VANTSNTDKWVPRSCSLQAAA
				1		AYVLIRPAPFPQYKYAAGVRNS
						\QQHL\NAQPQVTMQQPCCSMV
						PRVQGTLWTCLPMVGHLPPPSR
				1		SKSQMLGWNGLFPSYSKPMHP
		1		ŀ		YSLLVKSLG\MLLEIDNSEL\LH
1						ML\ESP\ESLPF*RVDEAVAGTTS
				ŀ		PPQAKRGLAQKAG*QVPTGVP
18796	49164	A	18905	1	988	MAEDGEEAEFHFAALYISGOW
1.07,50	42104	ľ`	10703	ľ	,	PRLRADTDLQRLGSSAMAPSRK
1						FFVGGN\WKMNGR\KRRLGELI
						GTLNAAKVPADTEVVCAPPTA
						YIDF\ARQK\LDPKIAVAAQNCY
						KI\TN\GAFTGEISPG\MIKDCGO
						PWVVLGHSERRHVF\GESDELI\
				ľ		GQKVA\HALAEGL\GVIRLHLG
				Ì		RS*DERGSLGIT\EKVVFE\QTKV
				1		IRR*T*KDWKQ/VVVLGLMSPV
1		l				WGLWLLARLATPQQA\QEVHR
				1		RSSRGWL\KSNVS\DAVASEPPV
1		l	1	l		TIYG\GSV\TGATLQRSLAKPSP
						DVDGLPLWGGASLQARNSWDI
	1					IQCHNNEPPSHLSLPLRCQAQG
						LKQTQKPK
L	L	Ц	L			End. der it

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
18797	49165	A	18906	46	468	TGPTHASAAILVPRSLHKMPGE
						ATETVPATEQELPQPQAETGSG
			1			TESDS/GKSPASDTYIVFGEAKIE
						DLSQQAQLAAAEKFKVQGEAV
						SNIQENTOTPTVQEESEEEEVDE
						TGVEVKDIELVMSQANVSRAK
						AVRALKNNS
18798	49166	A	18907	I	360	
18799	49167	A	18908	52	513	QLGPHGHRQGPGGPAVPHPRG
		1				LVPLPPALLPSGPRRGRTOAPR
1						HSGPAL*GHPASDTYIVFGEAKI
						EDLSQQAQLAAAEKFKVQGEA
						VSNIQD\NTQTPTVQEESEEEEV
l						DETGVEVKDIELVMSOANVSR
i i						AKAVRALKNNSNDIVNAIMEL
18800	49168	A	18909	1	422	RSLCOTGLRO/VTG/VTKVTIGN
10000	49100	ľ	10,00	ľ	1722	LENLFVI/TKPDVYKSPASDTYI
		ŀ				VFGEAKIEDLSOOAQLAAAEKF
l		ŀ				KVQGEAVSNIQENTQTPTVQEE
		1				SEEEEVDETGVEVKDIELVMSQ
1						ANVSRAKAVRALKNNSNDIVN
1						AIMVSVQAFVP
18801	49169	В	18910	427	529	AIMVSVQAFVF
18802	49170	Ā	18911	122	252	
18803	49171	A	18912	44	189	SKLDYKSSKRHRKPVSFNFITSF
						OIWD*FLFFF*LKCQLQPRVFSQ
						PN
18804	49172	A	18913	2	609	PFLPEAHLGNQKCQNCNSTSGI
Į.						CRVSVKVCPGPWVHAKLCAPT
						LMSRDVTLPDAPVKKPCGEGG
					i	AKKKKQVLKFTL\DCTHP\VED
		1				G\IMDAAQF*ASFCKERIKV\NG
		l				KAGNL\GGGVVDPSKGARGKIT
		ĺ				VT\SEVPFSKRVF*KYL/TPKKY
						LKKNNLR*PGLPRSLPNQPKEK
						LPNFRYFQINQGRRKEGGRRGF
l		1		l		KFPLSGKILL
18805	49173	A	18914	107	524	AGTHLPPFLPVAVRQPMALR\Y
		1		1		P\IAVGLKOGPTKVTOEP*ASPR
		1				HHVRRGRL\TKHTKFVRDMIRE
		i i	l			VCGFSP\YE\RRAMELLKVSKD
		1	l	l		K\RALKFIKK\RVGTHIRAKRKR
1				l		EELEQQYWPAIEEKLACQERLE
						PLPLPSPLK
18806	49174	A	18915	39	465	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleatide	Nucleatide location of last	Amino acid sequence ( X=Unknown.
NO:	of peptide		in USSN	location of first		*=Stop codon. /=possible nucleotide
,	sequence		09/540,217	codon for peptide	of peptide sequence	deletion. \=possible nucleotide insertion)
:				sequence		, ,
18807	49175	Α	18916	439	1586	TWGPPARRLPSGSHVPSA/ASSR
		1				LPSHPREEPQLPQPAPVTITATM
						SSEAETQQPPAAPP\GAPALSAA
						DTKPGTTGSGAGSGGPGGLTSA
						APAGG\DKKVIATKVLGT\VKW
	İ					FNVRNGYGFINRNDT\KEDVFV
						HQTAIKKNNPQKYLRSVGDGE
						TVEF\DVVEGEKGAE\AANVTG\
	i					PGGVPVQG\SKYAADRNHYRR
				i		YPRRRGPPRHYPQ\NYQNS\ESG
						EKNRGIGRVLPEGQAQQRRPY\
	l					RRRRFPPYYMRRPYG\RRPQY\S
						NPPVQGEVMEGADNQGA\GEQ
						GRPVRQNMYRGYRPRF\RRGP\
l		l				PRQKTA*ERAAMEEDK\ENQGV
1						WDPRFGSPPQ\RRYRRNF\NYR\
						RRRPQKTPKP\QDGQKRPKAAG
						SHPA*EFVPLPEAE\QGGAE
18808	49176	Α	18917	1	651	MTAFNSGKVDIVAINDPFIDLN
		l				YMVYMFLYDSTHGKFHGTVK
		1				AENGTLVINGNPIT\IFQDQDPS
		ł				KIKWAP/LAKVIHDNFGIIEGFM
		l				TTVHTITATQTINGPSG\NCHVM
						AAGLSRTSSLSLLA/LAKPVGK
		l				VIPELNGKLTGMAFHVPTANVS
						VADLTCRLEKPA/KYDDIKK\NT
ĺ	l		1			HSSTFDAGAAIVLKDHSVKLIS
		1				WYDNEFGYSNRVVHLMAHNA
18809	49177	Α	18918	2	5264	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
18810	49178	A	18919	3	1466	PRSAPRAASWLEDPREVRSVCL
				_		SAPPVROSAAIFFCVASRATSLR
						TPMGKVKVGVNGFGRIGHLVT
						RAAFNSGKVDIVAINDPFIDLN
l						YMVYMFQYDSTHGKFHGT\VK
l						AENGKLVINGNPITIFQE\RDPSK
		l				IKWG\DAGAEY\VVE\STGVFNO
		l			i	PWRKAGAHLOGG\AKRVI\ISAP
						SG*MPPMFVMG\VNHEEV*QTA
		l				FKIISN\ASCTNQLA*QPLAKG*F
		l				HDNFG*SWEGLMTTVPWPSLG
						NPRKTVD\GPSRG\NCGPWMGR
						GGFSRNIFLCLYWALPRAVGKG
						HP*A*TGKLTG\MAFPVSPTAN
				l		VVSGWTLTCRFRKNLPKY\DDI
ŀ				1		KEGW*KOAFGGAPSKGIPGLOL
	1		ŀ			SHOVV\SSDFNSDT\HSFHPFDA
		1	i			GA\GIA\LNDHFVKL\ISWYDNE
						FGYSNRVVDLIGPHGLOGSKTP
l						WTTEPQARSKKGKERPSLLGSP
						CHTOTPTTLNLPSSOLPCRPLEE
						GRGLWEPHLVMYPSNKVSLCS
						TKKKKKKKKP
18811	49179	A	18920	3	364	STVINIHSETSVPDHV/VLVPVO
						HPLLE\RCCLGFIAFAYSVKSRD
						RKMVGDVTGAQ/ALCLHRQVP
						EHLGPDSGHPHDHWIHPVTGIR
	i					LCDSLPYYVTDNTGKTGLLVA
				l		AHSLOPLHSTVOCW
18812	49180	A	18921	41	696	PDRRWSSLGHHESHCPNHSSLL
						STVASPPNYEDAQGR*SR/EVA
	1			1		VLGAPHNP\APPTSTV\IHIRQSR
				l		PPWPDHVVWSRVQHPLQ*TPA
	ĺ					C\LGFIAFAYSVKSRGQGRWLG
						DV\TGAQGLMPPPAKVPETIWG
	1			ł		PDFWGILNDHF\VHRHPQWLIFP
				ŀ		G\HGIDOGRHHWRPGALPI/VTC
	1		Ì		1	IPRILIPT\SIPRPAPRSPKSCISPYI
						LTRESTMAENKSARVSGKKKK
				L		

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	ĺ	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
l		1		sequence		
10010	140.40	<u> </u>	18922	127	1016	law w naw ronw
18813	49181	Α	18922	127	1016	SNLILRNLFCPHLALASSAFDKC
		l	1			QEEETVEKTELLAERRGLTENH
				1		PGNPITAGHHEPHCANLLSCQQ
l		1		1		RPRLPNYEMLKEEQEVAMLGA
						PQKPCLPECPPVIHYPQARPPWP
ŀ					•	DHVRLGPCFNNPLQ*TTCCPGL
l						SLGISAYFRGSFRGTGKMV\GD
		-		}		VEPGPQGLMPPTAQVAP*TSGA
						PDFLGSLHEPILAHQSSPPKCW
		1				VVPGPAIDQE\ASLRP\GA\LPVT
		ŀ		ŀ		C\IPRTL\SSIPSPLPPEARELLPFD
				ŀ		LYSTYSTFHSSPCPHSRVLHQPF
				l		ILTRFSTMAFNKVYMFLVKKK
						KKKKKKV
18814	49182	A	18923	115	652	VSESTDLVSIGRLVTRA\AFNSG
l				l		KVDIVAINDPFIDLNYMVYMF\
l						QYDSTHGKFHGTVKAENGKLV
		ŀ		ŀ		INGNPITIFQE\RDPSKIKWGDA
l		1				G\AE\YVVES/TLGVFTTMEK\A
						GGSFCRGGAKRVIHLLPPLA*C
l						PPCFVMGVN\HEKDDN\TLKIIS
				1		N\ASCTTN\CLAPLASTGAAKGC
18815	49183	A	18924	91	399	GQGHPEA
18816	49183	A	18925	26	304	
18817	49185	A	18926	18	203	
18818	49186	A	18927	23	355	
18819	49187	A	18928	1	211	RLLRVRGPPSPRPPGTPAGROA
				[		RHTAPVPARASPSTPPRKLKER
		l		ŀ		APALASPERGSHSAAEG*RAPO
						VPPK
18820	49188	A	18929	2	800	
18821	49189	Α	18930	1098	1560	VSCPFTVIIFCYNFCRGGFSTTA
						VMARAKSMFLMLKGKAGPDF
						GIRFTASSGWFT*FEDRYALHN
1						VNMNAESVGADVKAAE\DFGS
i						LIMEEIYLPTQFFNMEEPSLFWK
						QMPERTFVICPKGFFPDHCNKE
						RPWHFCKRKSLTDTRVATPCG
18822	49190	Α	18931	33	211	
18823	49191	Α	18932	110	624	CILSKMLRSPQELARLPGGQRQ
			1	1		LTRW*QRWPLWTIALVLVLWR
						VKSGP*S*RVPSPSP/PVEPWVT
l	1	1		l		LNMAGAPHGNPAFPPGGPPHP
1	1	l		l		<b>VPQPGYPGCQPLGPYPPPYPPPA</b>
	İ			l		PGIPPVNPLAPGMVGPAVIVDK
						КМОККМККАНККМНКНОКН
	L					HKYHKHDKHSSSSSSSSSSDSD

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18824	49192	A	18933	2	664	CEPLRISGRPTRPGERSKPRRRL ER*WGWRTHLINMWNPNAGOP GPNPYPPNIGCPGGSNPAHPPI NPFFPGCPCPPPGAUHGNPAFP TGGPPHPVPOPGYPGCOPLGP YPPPYPPAPGIPPVNPLAPGIM VGTKQLISRGEDCRRLLKAS* KRCHKA/HQKHIKVHKHAS* FLLFPPSFQAVISGLEYRALDP
18825	49193	Α	18934	3	409	SILKSHOFCSPIKLOMPCCTGGM OTQVVIDAG/ALAVPFSLLTNPK TNIQKEATWTMSNITASR/QDQI QQVVNHGLVPFLVSDLS/KDFE TQKEAVWA/GGTVEQIVYLVH CGIIEPLMNILIPAKDTK/IILVII.D AISNIFQAAEKLGETEKLSIMIEE CGGV
18826	49194	Α	18935	133	400	VLGPHGLGDHLGQFHSCQSRA EPPIAGEDIHAGLDEPDCLTKDF LRI*LQLSTQLHAGQEEEDQNV VPETTSEGYTFQVQDGAPGTFN
18827	49195 49196	A A	18936 18937	218		TOSALOPLIPPASPSPWKAQARF GAFSLCLITMSTNENANTPACP VVHRKRNGKDSTEMRKRRIE VNYELIKAKKIDOMIKKERL *AHFLIDATSPLQENKNOGAT LLNWSVDDIVKGINSSINVENQ LQATQAARIKLLSREKQPPIDNII RAGLIPKFYSFLGAFTDCSPIQF ESAWALTNIASOTTSQOTKAVV DGGAIPAFIFSGWASSHAHISEQ AVWALGNIAGDGSVFREDLIV YGAVDPLLALLASS**CQSLAC GYLRNLTWITLSNLCRIKNPA PRIDAVEQILPTLURLLHHDDP GSVRQDTVCWGYPPTLLDGSK WNGIGHGWV/VKQGVVPQLVK LLGASELPIVTPALKSP*GNNW HLGTIDEQTQVVD/IDAGALAVI PSILLTIPKTINQKEATWTMSN ITAGRQDQIQQVV*NIGLVPF PLSVFLSKADFKTQKEATWTMSN ITAGRQDQIQQVV*NIGLVPF PLSVFLSKADFKTQKEATWTMSN ITAGRQDQIQQVV*NIGLVPF PLSVFLSKADFKTQKEATWTMSN ITAGRQDQIQQVV*NIGLVPF PLSVFLSKADFKTQKEATWTMSN ITAGRQDQIQQVV*NIGLVPF PLSVFLSKADFKTQKEATWTMSN ITAGRQDQIQST*TELVYLVYLCGII EPLMNLFYCKRLPRIILLILDAN FILSFQPABRILVDLEKPSINLE: ECGGLRPKLKALPKPMKMESV YKASVKA*FEKVFPCRGKEGTI

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18829	49197	Α	18938	2	251	KVTNVKDGTTH\QTSLELFMYL NEVAGKHGVGRIDIVENRFIGM KSR/GMNVQGDYEPTDATGFIN INSLRLKEYHRFQSKVTVK
18830	49198	Α	18939	I	888	
18831	49199	A	18940		1155	MSSKOSMVLAYSGGLTISCTL. WLKEQGYDVTAYLANTGQKE DFEEARKKALKLGAKKVFIEDV SREFVEEFIWAAIQSSALYEDH YLGTSLTRFICHHKKVETVQR VGAKYEGPWRAPWRMPEFYN WFKGRSDLMEYAKQHGIPILVT PINLWSIDKNLMHISYKAGILE NPKNQVPPGLYTKIQDPAKAPH TPDILKIQFEKGVPYNTSVKD GTTHQTSLELFMYLNEVAGKH GVG/YIAIVENIFTRQRPSPECEI VRPCIAKSQEPAEGKVQVPVLK GQVYILGWESPLSLYMELMSV WQGDVEPIDDTGFINNSLRLR EYHCLQSLLEFAGCRLQTLFAW VSPAGAAEQQRLLPVPSSGNFII EGHLPDASWSSPV
18832	49200	A	18941		993	MSSKGSVVLAYSGGLDTSCILV WLKEQGYDVIAYLGQAVKGN QLPYSLVKRKTTPGAQYANR LSPRVGRFINAAGTTGFFTGKR GSLKVRNELQEVSTVPMPAST QLPADTQCKLAE/LSAPVKK*T LGLSKT*GTVMSSQSADSMFP AWYRN*LFTNFTVRRLGNSPV1 GSSLPRLPG/RGJYETPAGTILYT AHLDIEAFTMDFEVRIKIQGLC LKFAELVYTGAECKLLVASVPP WRGNGGVEEGGRDIKEVQEH GSDSAESSTHPPASRPGEGCLA CIFCGKWRHLNTPLSCERYPRH SKDHRPH
18833	49201	В	18942	324	1035	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nuclcotide	Nuclcotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
18834	49202	A	18943	29	1516	KQIPDAGNSRLQSQTLLSSKGS
						VVLAY\SGGLDTSCILVWLKEQ
			l			GYDVIAYLANIGQKEDFEEARK
						KALKLGAKKVFIEDVSREFVE\I
						FIW\PAIQVQAHLY\EDRYLPGH
	ľ					LSLPGPCI\ARKQVGNSPSGRGA
		1				KYVVPTGATGKG\NEQV\RFEL
						S\CYSL\APQIKVIAP\WR\MPEFY
			1			NR\FKGRNDL\MEYGKATLGFPI
						PVTPKNP\WSMDENLMHI\SYE
				i		AGILENPKNOAPPGLYTK\TOGE
					ŀ	SQKPPTPLDILGDSSFKKGVPVE
						GGPTFKDG\TTHOTFL\ELF\MY
					1	LNEVAG\KHGRRAVFDIV\ENRF
		l			1	\IGN*SPRGILRRTP\AGHHSFYH
		l				AHLDIRGLSPWDRGSCGKIKQG
		1			ŀ	PGAWKFAEL\VYTGFPAOAPE\
		1				CEFCPPTGIAKVPRKPSGKGKV
		1				QVVRSFKGPQVYI/LSGREIPHC
						LLLTMRELVKHGTCKGDYWRF
						IDGHRGSSKHQIPFKAEGNYHR
		1				LPRAKVTCQIDPVYNEELGPPQ
		İ		1		FSGSPOVTGANCCDNL
18835	49203	Α	18944	1	560	GRARTPANMALRVVRSVRALL
						CSLRALWAPAVPCLPRPWQLG
						AGAIWTLLTGPVLLWVCKFTE
				1		KHEWITTENGIGTVGINNFANE
		l	l			ALGDVVYCSLSEVGTKI*TKPS
					1	WSLVLLE\SVKAASEL\FSPLSG
						EVPDFNEALAE\NPG\LVTKSRY
						EDG\WLIKM\TLSNPFRT*MHL
				i		MSEEAYEKYIK\SIEE
18836	49204	Α	18945	3	108	
18837	49205	Α	18946	1	845	MAIPGIPYERRLLIMADPRDKA
				1		LQDYRKKLLEHKEIDGRLKELR
						EQLKELTKQYEKSENDLKALQS
		1				VGQIVGEVLKQLTEEKFIVKAT
		1				NG\PRYVVGCRRQVIELPLTNPE
		l				LFQRVGIIPPKGCLLYGPPGTGK
	1	1				TLLARAVASQLDCNFLKVVSSS
		1				IVDKYIGESARLIREMFNYARD
		1				HQPCIIFMDEIDAIDIDLPNEQA
		l				RLDILKIHAGPITKHGEIDYEAI
						VKLSDGFNGADLRNVCTEAGM
		1				FAIRADHDFVVQEDFMKAVRK
	I	1	1	1	1	VADSKKLESKLDYKPV

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codnn for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
18838	49206	Α	18947	3	1181	LLIMADPRDKALQDYRKKLLE
						HKEIDGRIKELREQLKELTKQY
		1				EKSENDLKALQSV\GQI\VGEVL
						KQLT\EEKFIVKATNGPRYVVG
		1	i			C\RRQL*QKVSLKPG\TRVAL\D
						MTTLTI\MEDILPR\EVDPLVYN
						MS\HEDPG\DVSYSEIGGLS\EQI
						RGI*GEVIGLPLYKPQSYFQRVG
						IIPPK\GCLLYG\PPGTGKNT/LLA
						RAVASQLDCNFLKVVSSSIVDK
		1				YIGESARLIREMFNYARDHQPCI
			l			IFM\DEIDAIGG\RRFSEGTSADR
	ŀ		1			EIQRTLMELLNQMDGFDTLHR
						VKMIMATNRPDTLGP\ALLRPG
			j			RLDRKIHIDLPNEQARLDIL\KIH
	i	1	1			AGPITK\HGEIDFESNC*SFRMG
	ŀ	1				FNGADL\RNVCT*SQACSPIRAD
						P*FC*YREDF\MKA\VRKVA
18839	49207	Α	18948	1	220	VNMRDRFGQIMIENLRRRQCEL
		i .				AGVETCKSLES\RIESLEFLDEM
						*/LLEQLM/RHYCLCWATKGGN
		L				ELGLKEITY
18840	49208	Α	18949	1	645	
18841	49209	Α	18950	10	1226	AAPAEPGRALPSSVAFSLWLAP
						SPAARRPRFHVPGGAQLPGTVH
						ARWPARQR\ESSI\TSCCSTSSCD
						ADDEGVRGTCEDASLCKRFAV
						SIG\YW\HDPYIQDL\VRLSKQR\
		l				KAPEINRGYFARVHGCSVQLIK\
		1				AFLR\KTECHCSNCSNLGGQGM
						GSPPFW\RLKDEDLSSQVNIFEV
		1				DFPMIVT\RKLHSIKWLAFPLSS
		l				PILELHSEDTLQMASDCIC\DGH ILDSKRYAVIGADLRDLSELEE
						KLKKCNMNTQL\PTP*IAECVL
						VYMTPE\QSANLLKWAA\NSFE
		1				RAMFI\YYQQVNMGDLFGQIMI
		1				ENLRGRPV/CDLAGVET\CKSLE
		1		i		SOKERLLS\NGWENKHRPVRT*
				ł		LEFVPPGLPSKLK*SRIESLEI\LD
		1				ENWELLEQLIP\HYCL\CWATQR
	1			1		RK*SLGLKEITY
18842	49210	A	18951	3	502	TEANTLN*RGLQNME/ARLAE/
10042	149210	^	10931	ľ	302	RKFM/NPFNMPNLYQKLESD/P
	1		1			RTRTLLSDPTYRELIEQLRNKPS
						DLGTKLQDPRIMTTLSVLLGVD
	1		I	1		LGSMDEEEEIATPPPPLPSSSMS
				l		LSPAPSCCLGCSPIVGFFFIWGS
		1		1		GHVMGRGGGSSSLRSQLSHVV
	1		I	I		YSASPSPIKQASWAWL
18843	49211	В	18952	1	1071	TOMOFOFIKQMOWAWL
10043	47211	lp.	10932	1	10/1	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18844	49212	В	18953	67	1026	
18845	49213	A	18954	2	1910	PVASSMFQKAARAVGNAERTD
						SIQRCSGPRCAMEQVNELKEKG
						IKALSVGNIDDALQ\CYSEAI*/R
	ľ					LDPHNHVLYSNR\SAAYAKKG
						DYQKAYEDGCKTVDLK\P\DW
						GKGYSRKAAALEFLYRFEEAK
		1				RTYEEGLKHEANNP\QLKEGLQ
		l				N\MEARLAK\RKFMNPFNMPNL
		l				YQKLESDPRTRTLLSDPTYRELI
		İ				EQLRNKPSDLGTKLQDPRIMTT
						LSDLLGVDLGSMDEEEEIATPA
	ŀ	İ				PPPPAKKETKPEPMEEDLPENK
						KQALKEKELGNDAYKKKDFDT
		l				ALKHYDKAKELDPTNMTYITN
						QAAV\WFEKGDYNKCRELCEK
						AIEVGRES\REDYRQIAKAY\ARI
	İ					GNSYFKEEKYKDS\IHF\YNKSL
						AEHRTPDVLKKCQQAEKILKEQ
		l				ERLAYINPDLALEEKNKGNECF\
						QKGDYPQ\AMKHYTEAI\KRNP
		ı				KDAKL\YSIRAACYTKLLEFQL
			ĺ			ALKDWEEWYQLEPTFIKGYTR
		1				KA\AALEA\MKDYTKAMDVYQ
		ĺ .				KALDLDFSCKEAADGYQRCIM
		l				AQYNRHDSPEDVKRR\AMADP
						EVQQFMS\DPA\MRFILKQMQK
		1				DP\QALSE/HL*RNPLLPREIQKL
		l				MDVGSDCKFGDDLFIPAFLCPS
		ı				CGKRSWDRGEQAARSGRESST
						ERKGEQGERRPSSPYIYT
18846	49214	A	18955	2	293	
18847	49215	В	18956	53	182	
18848	49216	A	18957	2	403	
18849	49217	A	18958	3	1646	
18850	49218	A	18959	3	408	
1885I	49219	A	18960	1	2458	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nuclcotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18852	49220	٨	18961	88	1511	LWPLGMASNSSCPTFGGGHL  KNGYPPPYAFFPPMLGGLSP  GALTTLQHQLPVSGYSTPSPATI  ETQSSSSEIVPSPSPPPPPLPRIYK  PCFVCQDKSSGYHYGVSACEG  CKGFFRSIQKNMVYTCHEDK  KOIINKVTRNRCQYCRLQKCFE  VGMSKESVRNDRNKKKKEVPK  PECSESYTLTPEVGELIEKVRKA  HQETFPALCQLGKYTTNNSSE  QRVSLDIDLWDKFSELSTKCII  TLIKIAACLUDILIRICTRYTPE  AGTPPPS WDGLTLNRIYDMHNA  GFGPLYTDLVFAFNANQLIPLE  MDD/ARETGLLSAICLICGDRQ  DLEQPDRYDMLGPELLEALKV  VYKRRPSRPHMFPKMLMKIT  DLRSISAKGAERVITLKMEIPGS  MPPLIQEMLENSEGLDTLSQQP  GGGGRDGGCLAPPPGISCSPSLS  PSSNRSSPATHSP

SEQ ID NO:	SEQ ID NO: of peptide	Met	SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X-Unknown, *=Stop codon, /=possible nucleotide
140.	sequence	liou	09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		.,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
18853	49221	A	18962	143	2159	LTHSSTWLGRSCNHDRRQMGS
		1		1		KVMSYVVAGRGTCAQETPIYT
		1		1		TIRYLEDKEOYGGSLGVDSVL
		1		l		RLFSGASVLFISGPPFSSYLSGV
		1	ļ		}	PGHPMEDSM\DM\DMSPL\RPO
						NYLFGCELK\ADKDYHFKVD\N
		l				DENE\HQLSLR\TVNLGGLVAK
						G*VAHLLKAEAIEFTEASPNLK
					l	VTTWAT\LKM\SVPAORVFPLG
		l			1	GLLKITPTRWVLKGLKVWVQC
						PVHISGTAL**LWEGRCQSPED
					1	E\EEDVNRVLFMKPKGRGLKH
						MFGDLVCSWKLAAIETQSSSSE
						EIVPSPPSPPPLPRIYKPCFVCOD
				i		KSSGYHYGVSACEGCKGFFRR
						IQKNMVYTCHRDKNCIINKVTI
						NRCQYCRLQKCFEVGMSKESV
					RNDRNKKKKEVPKPECSESYTI	
						TPEVGELIEKVRKAHOETFPAL
			ł			CQLGKYTTNNSSEQRVSLDIDL
			i			WDKFSELSTKCIIKTVEFAKQLI
					GFTTLTIADQITLLKAACLDILII	
						RICTRYTPEQDTMTFSDGLTLN
						RTQMHNAGFGPLTDLVFAFAN
				Į.		QLLPLEMDDAETGLLSAICLIC
		1	Ì	l		DRQDLEQPDRVDMLQEPLLEA
				1		LKVYVRKRRPSRPHMFPKMLM
				l		KITDLRSISAKGAERVITLKMEI
						PGSMPPLIQEMLENSEGLDTLS
						GQPGGGGRDGGGLAPPPGSCSI
				Ì		SLSPSSNRSSPATHSP
18854	49222	A	18963	748	1075	ILPTSLFFLFCFVFFVCF*DRVLL
						LSPG\WSAVARSWLYCNLSLRG
						FKGFSCLSLLSNWDYRCTPLRS
						ANFVFL/CRDRVSPCWPTSVSNS
						*PQ\VIHPPWPPKVLGITRV
18855	49223	A	18964	3	674	GRRRLLRDAEGPEETVRLWPA
						<b>ARAAMDAAE</b> VEFLAE <b>KEL</b> VTII
						PNFSLDKIYLIGGDLGPFNPG\LE
				1		VEVPLWL/ARLNLKQRQK\CRL
						LPPEWMDVEKLEKMRDHE\RK
		1				EETF\TPMPKPFTTWELT\KLL\L
		l				NHA\SDNIPKGRTEFRDPGSRVF
		l				WGHSY*AKFRVFG\DSF\VRQQ
		l	1			EAHAKLD*LGPWMGDQQPAVT
				1		FLTQA\LNPHVTNSRTNPPSPLE
	1	F.	1	I	1	STSVLRTS

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				bequence		
18856	49224	Α	18965	261	876	VAQKIDMPEYQGEPDEISIQKC
	1	İ			\	QEAVRQVQGPVLVEDTCLSFN
						ALGGLPGPYIKV/WFLEKLKP\E
	1				GLHQLLA\GF\EDKSA\YALCTF	
						CTQAPGDPS\QPV\RLVSGGRDL
		1				RGRIRWHPEGCO\DFGWD\PC\F
		1				QPDG\YEQTYAEMP*GGRRNA
						V\SH\RFRAPCWEPAREYFWOV
						WPSLTSASWKEGPSRPGDLGK
						GLAPKPSPHRGRAPP
18857	49225	A	18966	2	181	TAEKMAVLAPLIALVYSVPRLS
10037	47223	l^	10,00	ľ	101	RWLAQPYYLLSALLSAAFLLVR
						KFPPLCHGLPTOREDGNPCDFD
						WREVEILMFLSAILMMKNRRSS
						TK*AHPTRRR
18858	49226	A	18967	5331	5454	ETEA*RINDLL*LLEFFCNI*QN*
18838	49220	^	18907	3331	3434	P*IRPTVIRSSLKYNT
18859	49227	A	18968	5186	5308	ETEA*RINDLL*LLEFFCNI*ON*
18859	49227	A	18908	5180	3308	P*IRPTVIRSSLKYNT
18860	49228	A	18969	4570	4691	ETEA*RINDLL*LLEFFCNI*ON*
18860	49228	A	18969	4570	4691	
		<u> </u>			4800	P*IRPTVIRSSLKYNT
18861	49229	Α	18970	5666	5788	ETEA*RINDLL*LLEFFCNI*QN*
		_				P*IRPTVIRSSLKYNT
18862	49230	A	18971	5630	5752	ETEA*RINDLL*LLEFFCNI*QN*
	L	1	ļ			P*IRPTVIRSSLKYNT
18863	49231	A	18972	224	456	
18864	49232	A	18973	5543	5665	ETEA*RINDLL*LLEFFCNI*QN*
		-				P*IRPTVIRSSLKYNT
18865	49233	A	18974	4602	4725	ETEA*RINDLL*LLEFFCNI*QN*
		_				P*IRPTVIRSSLKYNT
18866	49234	Α	18975	3	313	
18867	49235	Α	18976	5480	5602	ETEA*RINDLL*LLEFFCNI*QN*
		_				P*IRPTVIRSSLKYNT
18868	49236	A	18977	269	394	
18869	49237	A	18978	5322	5445	ETEA*RINDLL*LLEFFCNI*QN*
		L				P*IRPTVIRSSLKYNT
18870	49238	A	18979	164	434	
18871	49239	A	18980	5364	5487	ETEA*RINDLL*LLEFFCNI*QN*
		_				P*IRPTVIRSSLKYNT
18872	49240	В	18981	18	1904	
18873	49241	A	18982	1296	1973	RILPGGQQNSSWNFSEDTVISIL
						NTINEVIAENLEAAKKLRETQGI
						EKLVLINKSGNRSEKEVRAAAL
						VLQTIWGYKELRKPLEKEGWK
		1		I	I	KSDFQVNLNNASRSQSSHSYDD
		1		1	1	STLPLI*PGPKNQIRNLIGKKFR*
1		1		1	1	AIWDQTQNH*IT/DYSTPNERGD
					1	HNRTLDRSGDLGDMEPLKGTT
		1		l	1	PLMQDEGQESLEEELDVLVLD
					1	DEGGOVSYPSMVCPSVTPKIVL
						EEGGS
					1	00000

SEQ ID	ISEO ID NO:	: [Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	j			scquence	1	
18874	49242	A	18983	5844	5967	ETEA*RINDLL*LLEFFCNI*QN*
10077	1,72,12	1.	10500	150	1	P*IRPTVIRSSLKYNT
18875	49243	A	18984	5781	5904	ETEA*RINDLL*LLEFFCNI*QN*
10075	175275	,,	10,04	3,01	13701	P*IRPTVIRSSLKYNT
18876	49244	В	18985	1	1477	
18877	49245	Α	18986	152	1539	
18878	49246	Α	18987	5571	5694	ETEA*RINDLL*LLEFFCNI*QN*
						P*IRPTVIRSSLKYNT
18879	49247	A	18988	4551	4674	ETEA*RINDLL*LLEFFCNI*QN*
	100.10	4	V 00 00		10.00	P*IRPTVIRSSLKYNT
18880	49248	A	18989	2	1043	GVRLRYSPIAVVMVGEAGRDL
		1				RRRRAVAVTAEKMAVLAPLI/S
		1		1		LSVYSVPR\LSRWLAQPYYLLS
	1	1		1		A\LLSAAF\LLVRKLPPLCHGLP
	1	1		1		TQ\REDGNP\CDFDWRE\VEILM
		1		1		FLSAIVMMKN\RRSITVEQHIGN
		1				IFMFK/SKVANTILFF\RLDIRMG
		1		1	1	LLYITLCIVFLMTCKPP/LSPYM
		1		į.	1	GPEYIKYFN\DKPFDEELERDNR
		1		l	1	VNW/ILLEFFGNWSNDWQSFAP
		1			1	IYADLSLKYNCTGLNFGKVDV
		1		l		GRYTDVSTRYKVSTSPLTK\QLF
		1			i	TL\ILFQGGQGGQCGRPQI*QGK
		ı		į		GR/ALFSWDLL*GT*KEGOENV
		1				REFNLNELYQRAKKLSKAGDNI
		1		ŀ		P\EEQPVASTPTTVSDG\ENKKD
18881	49249	A	18990	ī	1105	MESTGEDAVNIVEMVTEDLVY
10001	77277	1	10270	l'	1103	RLVVLKSLQVWLSPGDFMGSE
	1	1				GTECMLIGPWVAMGRPSESTLS
		1				SHSGPRSPHGTGSPAPRLQAVH
	1	1				VLKCPKSRGVQGGWGLASQCL
		1				
		1	ì	l		PEHRHTQLSCDSTQAWPQLCSA
				İ		QSLRHNRSGQGAGAVTSEPAG
		1				AGGLPRPPRTQGCLGAES/PAG
				1		QLHSQQRGGPEEGRLLSDVDHF
						DLSSSQQRGPEGP/QVAGGWCV
						SAAWSSTHLAGPQQRWDQEEA
						RQWEQIPLSLLMMGDPPGYSR
						APGDPGPQPQPRQLQLCLGSSH
1		1			1	PTNS*GAELPPVPGSAECAALT
1		1			1	VLPSLHLPQWWQVGRPGPT*V
Į.						DPRVGLPGQQAPEQRVYSLTHF
						EQLPVLQVPLLIYRYSSTYNGV
18882	49250	C	18991	105	393	
18883	49251	Α	18992	38	230	LYWQKRKGKLLNNLTQGIVAD
						PVR*KKFHFKCPSNCPKIHNTES
18884	49252	A	18993	487	747	AYAVSFMKYSAHVLGSLYEM
18885	49252	C	18993	179	649	
18886	49254	A	18995	3	3187	
18887	49255	A	18996	274	423	
1008/	49233	I	10220	214	423	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
18888	49256	Ā	18997	1333	2243	RCWRPRTLGFASPPTRPCSPTH
10000	1,7230			1555		APGCEMTPRDWHRVLSFASPLR
						IEEIFQGYDKTFGLKNKKGAKO
						OKFIKAVTHOVKFGO/SKSTSGS
						TE*SWKRKLKKDDKKKELOEL
ļ.						NELFKPVVAAOKI/RVKGADPK
		ĺ				SVV\CAFFKQGQCTKGDKCKFS
						HDLTLGEKM\EKRSVYIDARDE
l						ELEKETKSSLIOADTMDNWDE
	l			l		KKLEEVVNKKHGEAEKKKPKT
			1			OIVCKHFLEAIENNKYGWFWV
l	ì					CPGGGDICMYRHALPPGFVLK
		1				KDKKKEEKEDEISLEDLIERERS
			İ			ALGPNVTKITLESFLAWKKRKR
18889	49257	A	18998	1	322	
18890	49258	A	18999	1	822	MGKAKEEVFLADELVHAKTNR
		l				NKECDYSVTANSKIVVVTAGV
ŀ		ì				RQQEGESRLNLVQRNVNVFKFI
		l				IPQIVKYSPDCIIIVVSNPVDILT
İ						YVTWKLSGLPKHRVIGSGCNL
		l				DSARFRYLMAEKLGIHPSSCHG
						WILGEHGDSSDHPGRPRPHPVPI
					1	KPPETLPGRDTSSWTSRGAHWR
	1	1				RNTQAAGRREHIDRHQQAIDR
		1				WNNVGFGRGGQRRARLLSDLT
	1					PTGKPSSYSVSLLAPPSAESYFH
ŀ	i	ı				SIKPCIHSPS*CMQRPIEIKN/RD
						YSVTANSKIVVVTAGVRQQEG
		ĺ				ESRLNLVQRNVNVFKFIIPQIVK
						YSPDCIIIVVSNPVDILTYVTWK
l		l				LSGLPKHRVIGSGCNLDSARFR
		İ				YLMAEKLGIHPSSCHGWILGEH
		l				GDSSDHPGRPRPHPVPIKPPETL
		l				PGRDTSSWTSRGAHWRRNTQA
	1	l				AGRREHIDRHQQAIDRWNNVG
		l				FGRGGQRRARLLSDLTPTGKPS
	1	1	l		1	SYSVSLLAPPSAESYFHSIKPCIH
	1	1		l	1	SPSPREIQFFGYTKARNPRVQK

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nuclcotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
18891	49259	ÍΑ	19000	1	1337	MEKPKRLRWLWGPAPSSLLAE
		1				PAPEETHAADFVFSARLLQRSP
		l				EPSLSWGGRALAEEQKAEGSSC
		1		į.		GSAERLVAFAAKTRPYLSLCK
1		1				MATLKEKLIAPVAEEEATVPNN
1		1		l		KITVVGVGQVGMACAISILGKS
l		1				RAMEHTTAGAPYTPRQQTCQC
		ł				NMMSLADELALVDVLEDKLKG
		1				EMMDLQHGSLFLQTPKIVADK
ŀ						DYSVTANSKIVVVTAGVRQQE
				1		GESRLNLVQRNVNVFKFIIPQIV
		1				KYSPDCIIIVVSNPRDI\LTYGTW
						KLSGLPKHRVIGSGCNLDSARF
		ĺ				RYLMAEKLGIHPSSCHGWILGE
						HGDSSVAVWSGVNVAGVSLQE
1	i	l				LNPEMGTDNDSENWKEVHKM
1				l		VVESAYEVIKLKGYTNWAIGLS
		1		i		VADLIESMLKNLSRIHPVSTMV
		1		ŀ		KGMYGIENEVFLSLPCILNARG
		1		l		LTSVINQKLKDDEVAQLKKSA
1	1		l	1		
						DTLWDIQKDLKDL
18892	49260	С	19001	462	728	
18892 18893	49260 49261	C A	19001 19002	462 1	728 1033	MSGSFLMFLPKADMPAPMLVQ
						MSGSFLMFLPKADMPAPMLVQ PAERFDSWVWAGPEQLHSNQL
						MSGSFLMFLPKADMPAPMLVQ PAERFDSWVWAGPEQLHSNQL PGDADALLLGRNLTKGTRRLC
						MSGSFLMFLPKADMPAPMLVQ PAERFDSWVWAGPEQLHSNQL PGDADALLLGRNLTKGTRRLC TEEQVKIPQPEPGPPQKLCVLSA
						MSGSFLMFLPKADMPAPMLVQ PAERFDSWVWAGPEQLHSNQL PGDADALLLGRNLTKGTRRLC TEEQVKIPQPEFGPPQKLCVLSA AGGQACLVLTFPRWTVWEEPP
						MSGSFLMFLPKADMPAPMLVQ PAERFDSWVWAGPEQLHSNQL PGDADALLLGRNLTKGTRRLC TEEQVKIPQPEPGPPQKLCVLSA AGGQACLVLTPPRWTVWEEPP PPGLVGVKACARWWGKGEPD
						MSGSFLMFLPKADMPAPMLVQ PAERFDSWVWAGPEQLHSNQL PGDADALLLGRNLTKGTRRLC TEEQVKIPQPEPGPPQKLCVLSA AGGQACLVLTPPRWTVWEEPP PPGLVGVKACARWWGKGEPD RKAPAPPPPPPGTEKVDQTSE\E
						MSGSFLMFLPKADMPAPMLVQ PAERFDSWVWAGPEQLHSNQL PGDADALLLGRNITKGTRRLC TEEQVKIPQPEPGPPQKLCVLSA AGGQACLVLTPPRWTVWEEPP PPGLWGVKACARWWGKGEPD RKAPAPPPPPPGTEKVDQTSEVE RGTLIQRPPAPALPGWVRKTGR
						MSGSFLMFLPKADMPAPMLVQ PAERFDSWVWAGPEQLHSNQL PGDADALLLGRNLTKGTRRLC TEEQVKIPQPEGPPQACLCVLSA AGGQACLVLTPFRWTVWEEPP PGLVGVKACARWWCKGEPP RKAPAPPPPPPGTEKVDQTSEVE RGTLIQRPPAPALFGWVRKTGR PPPPATGRQVPPLLGASTQPE
						MSGSFLMFLPKADMPAPMLVQ PAERFDSWVWAGPEQLHSNQL PGDADALLLGRNLTKGTRRLC EEQVKIPPEGPEPQEKLCVLS AGGQACLVLTFPRWTVWEEPP PFOLGVFPGFFCTEVFOTSEE RGTLIQRPPAPALFGWVRKTGR P/PPPATGRLQVPLLGASTQPE
						MSGSFLMFLPKADMPAPMLVQ PAERFDSWVWAGPEQLHSNQL PGDADALLLGRNITKGTRRLC TEEQVKIPQPEPGPPQKLCVLSA AGGQACLVLTPPRWTVWEEPP PPGLWGVKACARWWGKGEPD RKAPAPPPPPGTEKVDQTSEUE RGTLIQRPPAPALPGWVRKTGR PPPPATGRLQQVPLLGASTQPE PPPGRGV/PPGVSPGLGEDVEN DGMSLSYLAE*PQATSQRAPPG
						MSGSFLMFLPKADMPAPMLVO PAERFDSWVWAGPEQLHSNQL PGDADALLLGRNLTKGTRRLC TEEQVKIPGPEGPPQKLCVLSA AGGQACLVLTPPRWTVWEEP PPGLVGVKACARWWGKGEPD RKAPAPPPPPTEKVNDQTISEE RGTLIQRPPAPALFGWVRKTGR PPPPATGRLQOYPLLGASTQPE PPPGRGV/PPGVSPGLGEDVEN DGMSLSYLAF*PQATSRAP*G ENTVALSGRLGRNSSSYTCRPA
						MSGSFLMFLPKADMPAPMLVQ PAERFDSWVWAGPEQLHSNQL PGDADALLLGRNLTKGTRRLC TEEQVKIPQPEFGEPPQKLCVLSA AGGQACLVLTFPRWTVWEPP PFGLVGVKACARWWGKGEPD RKAPAPPPPFOTEKVDOTSELE RGTLIQRPAPALPGWVRKTGR PPPPATGRLQOVPLLGASTQPE PFPGRGV/PPGSFLGEDVEN DGMSLSYLAE*PQATSQRAP*G ENTVALSGRLGRNSTYCRA GERNFHPRGGPSSTAALHLKK
						MSGSFLMFLPKADMPAPMLVO PAERFDSWVWAGPEQLHSNQL PGDADALLLGRNLTKGTRRLC TEEQVKIPQPEGPPORLCVLSA AGGQACLVLTPFRWTVWEEPP PPGLVGVKACARWWCKGEPP RKAPAPPPPPPGTEKVDQTSEVE RGTLIQRPPAPALFGWVRKTGR PPPPATGRUQVPLLGASTQPE /PPGRGV/PPGVSPGLGEDVEN DGMLSYLAE-PPQATSQRAPPG ENTVALSGRLGRNSSSYTCRPA GERNFHPRGGPSSTALHLER MPGTTPQCEGRRAVPRALPET*M
						MSGSFLMFLPKADMPAPMLVQ PAERFDSWVWAGPEQLHSNQL PGDADALLLGRNLTKGTRRLC TEEQVKIPQEPGEPOPKCLCVLSA AGGQACLVLTFPRWTVWEEPP PFOLGVKACARWWGKGEPD RKAPPAPPPPTGTEKVDOTISEE RGTLIQRPPAPALFGWVRKTGP PPPPATGRLQQVPLLGASTGP PPPAGFQVPPLGSTGP PPGRGV/PPGVSPGLGEDVEN DGMSLSYLALF*PQATSQRAP*G ERNTVALSGRNSSSYTCRPA GERNFHPRGGPSSTAALHLRK MPGTPQCEGRRAVPRALPET*M LQGPGTTR*TPPGPLAFSPPSSP
18893	49261	Α	19002	1	1033	MSGSFLMFLPKADMPAPMLVO PAERFDSWVWAGPEQLHSNQL PGDADALLLGRNLTKGTRRLC TEEQVKIPQPEGPPORLCVLSA AGGQACLVLTPFRWTVWEEPP PPGLVGVKACARWWCKGEPP RKAPAPPPPPPGTEKVDQTSEVE RGTLIQRPPAPALFGWVRKTGR PPPPATGRUQVPLLGASTQPE /PPGRGV/PPGVSPGLGEDVEN DGMLSYLAE-PPQATSQRAPPG ENTVALSGRLGRNSSSYTCRPA GERNFHPRGGPSSTALHLER MPGTTPQCEGRRAVPRALPET*M
18893	49262	A	19002	2	1033	MSGSFLMFLPKADMPAPMLVQ PAERFDSWVWAGPEQLHSNQL PGDADALLLGRNLTKGTRRLC TEEQVKIPPGEPGPPQKLCVLSA AGGQACLVLTPPRWTVWEEP PPGLVGVKACARWWGKGEPD RKAPAPPPPPTEKVPQTISELE RGTLIQRPPAPALFGWVRKTGR PPPPATGRLQVPLLGEDVEN DGMSLSYLAE*PQATSQRAP*G ENTVALSGLGRNSSSYTCRPA GERNFHPRGGPSSTALHLRK MPGTPQCESRAVPRALPET*M LQGPGTTR*TPPCPLAFSPPSSP TGPQKVKSLGNSSARTILPPKW
18893	49261	Α	19002	1	1033	MSGSFLMFLPKADMPAPMLVQ PAERPDSWVWAGPEQLHSNQL PGDADALLLGRNLTKGTRRLC TEEQVKIPPEPGEPPORLCVLSA AGGQACLVLTFPRWTVWEEPP PFOLGVKACARWWGKGEPD RKAPPAPPPPGTEKVDDYTSEE RGTLIQRPPAPALFOWVRKTGR P/PPATGRLQQVPLLGASTQPE FPGGRGV/PPGVSPGLGEDVEN DGMSLSYLAE*PQATSQRAP'G ENTVALSGRIGNSSSYTCRPA GERNFHPRGGPSSTAALHLRK MPGTPQCEGRRAVPRALEET*M LQGPGTTR*TPPPOPLAFSPPSSP TGPQKVKSLGNSSARTILPPKW PTRPAVAEDGGLKKCKISSYC
18893	49262	A	19002	2	1033	MSGSFLMFLPKADMPAPMLVQ PAERFDSWVWAGPEQLHSNQL PGDADALLLGRNLTKGTRRLC TEEQVKIPQPEGPPORLCVLSA AGGQACLVLTPFRWTVWEEPP PPGLVGVKACARWWCKGEPP PRCAGACRWWCKGEPP RKAPAPPPPPPGTEKVDQTSEVE RGTLIQRPPAPALFGWVRKTGR PPPPATGRLQVPLLCASTQPE /PPGRGV/PPGVSPGLGEDVEN DGMLSYLAE-PPQATSQRAPPG ENTVALSGRLGRNSSSYTCRPA GENNFHPRGGPSSTAALHLRK MPGTPQCEGRRAVPRALPET-M LQGPGTTR*T/PPGPLAFSPPSSP TGPQKVKSLGNSSATTLPPKW PTRPAAVAEDGGLKKCKISSYC RSQPPARLISGEEHFSSKKCLA
18893	49262	A	19002	2	1033	MSGSFLMFLPKADMPAPMLVQ PAERFDSWVWAGPEQLHSNQL PGDADALLLGRNLTKGTRELC TEEQVKIPGPEGPPOKLCVLSA AGGQACLVLTFPRWTVWEEP PPGLVGVKACARWWGKGEPD RKAPAPPPPPTEKVPQTISEE RGTLIQRPPAPALFGWVRKTGR RGPPPPATGRUQVPLLGASTQPE PPPGRGV/PPGVSPGLGEDVEN DGMSLSYLAF*PQATSQRAP*G ERNTHALSGRIGNSSSYTCRPA GERNFHPRGGPSTAALHLRK HQGPGTFT*T/PPGPLAFSPPSSP TGPQKVKSLGNSSARTLEPFWW PTRPAAVAEDGGLKKCKISSYC RSQPPARLISGEEHFSSKCLA WFYEYAGPDEVVGPEGMEKFC
18893	49262	A	19002	2	1033	MSGSFLMFLPKADMPAPMLVQ PAERPDSWVWAGPEQLHSNQL PGDADALLLGRNLTKGTRRLC TEEQVKIPGPEGPPQKLCVLSA AGGQACLVLTFPRWTVWEPP PPGLGVWACARWWGKGEPD RKAPAPPPPPTGTEVDDTSELE RGTLIQRPPAPALPGWVRKTGR P/PPATGRLQVPLLGASTQPE BYPPATGRLQVPLLGASTQPE ENTVALSGRLGRNSSSYTAGRA GERNFHPRGOFSTAALHLRK MPGTPQCEGRRAVPRALPET MQGPGTTR-TIPPOPLAESPST TGPQKVKSLGNSSSATTILPPKW PTPPAVAEDGGLKCKISSYC RSOPPARLISGEHFSSKKCLA WYYEYAGPDEVVGPEGMEKFG EDIGVEEPNICDCTEKLQNKFDF
18893	49262	A	19002	2	1033	MSGSFLMFLPKADMPAPMLVQ PAERFDSWVWAGPEQLHSNQL PGDADALLLGRNLTKGTRRLC TEEQVKIPQPEGPPGPKCKUCVLSA AGGQACLVLTPFRWTVWEEPP PGLVGVKACARWWGKGEPD RKAPAPPPPFGTEKVPQTSEUE RGTLIQRPPAPALFGWVRKTGR RGTLIQRPPAPALFGWVRKTGR PPPPATGRLQVPLLGSTQPE PPGRGV/PPCVSPGLGEDVEN DGMSLSYLAE*PQATSQRAP*G ENTVALSGLGRNSSSYTCRPA GERNFHPRGGPSSTAALHLRK MPGTPQCEGRAVPRALPET*M LQGPGTTR*TPPGPLAFSPPSSP TGPQKVKSLGNSSATLIPPKW PTRPAAVAEDGGLKKCKISSYC TSQPPARLISGEBHFSSKKCLA WFYEYAGPDEVVGPEGMEKFC EDIGVEPENICDCTEKLQNKFDF LRSQLNDISSSKNIYBYAFDFAR
18893	49262	A	19002	2	1033	MSGSFLMFLPKADMPAPMLVQ PAERPDSWVWAGPEQLHSNQL PGDADALLLGRNLTKGTRRLC TEEQVKIPGPEGPPQKLCVLSA AGGQACLVLTFPRWTVWEPP PPGLGVWRACARWWGKGEPD RKAPAPPPPPGTEKVDDTSELE RGTLIQRPPAPALPGWVRKTGR P/PPATGRLQVPLLGASTQPE BYPPATGRLQVPLLGASTQPE ENTVALSGRLGRNSSSYTAGRA GERNFHPRGOPSSTAALHLRK MPGTPQCEGRRAVPRALPET MQGPGTTR-TIPPGPLAESPSST TGPQKVKSLGNSSSATTILPPKW PTPPAVAEDGGLKCKISSYC RSOPPARLISGEHFSSKKCLA WYYEYAGPDEVVGPEGMEKFG EDIGVEEPNICDCTEKLQNKFDF

NOS.   of peptide requence   not	SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
18896   49264   A   19005   229   1028							
18896   49264   A   19005   229   1028   GASKRTGTPFPGFPAHPAREGR   KMPVKKRKSPCVAAAVAED   GGLKKCKISSYCRSQPPARLISG   EEHFSSKKCLAWFYEVAGPDE   VVGPEGMEKPCEDIGVEPENI   ML.VLAWKLEAESMGFFTKEEW   VKGMTSLQCKLHRKGYKPNF   DFFAAHS*IDISSFKNIVRYAFDE   ARDKOQNSLONDTAKSMLAL   LLGGGHPJFSNYFVQVPGGGS   KYRVMNKDQWYNVSEFSRTV   HADLSNYDEEDGAWPVLLDEF   VEWQKVRQTS   VEWQKVRQTS   LSQGGPWAPLQRAMKPPGGES   SNLFGFPEATPSKPNTMSSNF   GFTEEPONILKRTNPFGVYGGG   FIDESTPVOTROHILPPGGKTS   DIFGSPVTATSRLAHPNKPKDH   VFLM   18899   49267   A   19008   1   684   18900   3268   A   19009   3   81   18901   49269   A   19010   1   465   18900   3468   A   19010   344   18902   49270   A   19011   120   344   18903   49271   A   19012   3   1334   SPQLISSASRPAVRNSRHDATRP   VVFQMSGGSADYNSREHGGPE   GMDPLGGVIESNWEIVDNFD   VTMIKLESLLINGGVAYGFEKP   SPIQQKAIIPCIKGY*CGLLKLQ   SGTGKTATFSLISILQPVGRLSF   KETGSTSYWAPTRELIAQOIQK   VILALGDYMGATCHACIGGTN   VRNEMQKLQAEAPHIVVGTING   RVFDMLNRRYLSFK WILKMFYL   DEADEMLSRGFK DQIYEIFQKL   NTSIQVYASATHMTDVLEVTK   KFMRDPRIL VKKEELTLEGIKQ   FYINVEREEWKLDTLCDLY FILL   TITQAVIELNTRRKV DWLTEEM   HARDFTVSALHGDMOQKERD   MREFRESGSSRULTITULARGI   DVQQVSLVINVDLFTRRENYIH   RIGRGGRFGRRGVANNFVTEED   KRFLRDIETFYNITTVEEMJEM)   RIGRGGRFGRRGVANNFVTEED   KRFLRDIETFYNITTVEEMJEM   RIGRGGRFGRRGVANNFVTEED   KRFLRDIETFYNITTVEEMJEM   RIGRGGRFGRRGVANNFVTEED   KRFLRDIETFYNITTVEEMJEM   RIGRGGRFGRRGVANNFVTEED   KRFLRDIETFYNITTVEEMJEM   RIGRGGRFGRRGVANNFVTEED   KRFLRDIETFYNITTVEEMJEM   RIGRGGRFGRRGVANNFVTEED   KRFLRDIETFYNITTVEEMJEM   RIGRGGRFGRRGVANNFVTEED   KRFLRDIETFYNITTVEEMJEM   RIGRGGRFGRRGVANNFVTEED   KRFLRDIETFYNITTVEEMJEM   RIGRGGRFGRRGVANNFVTEED   KRFLRDIETFYNITTVEEMJEM   RIGRGGRFGRRGVANNFVTEED   KRFLRDIETFYNITTVEEMJEM   RIGRGGRFGRRGVANNFVTEED   KRFLRDIETFYNITTVEEMJEM   RIGRGGRFGRRGVANNFVTEED   KRFLRDIETFYNITTVEEMJEM   RIGRGGRFGRRGVANNFVTEED   KRFLRDIETFYNITTVEEMJEM   RIGRGGRFGRRGVANNFVTEED   KRFLRDIETFYNITTVEEMJEM   RIGRGGRFGRRGVANNFVTEED   KRFLRDIETFYNITTVEEMJEM   RIGRGGRFGRRGVANNFVTEED   KRFLRDIETFYNITTVEEMJEM   RIGRGGRFGRRGVANNFVTEED   KRFLR			ŀ	09/540,217		of peptide sequence	deletion, \=possible nucleotide insertion)
RMPYKKKRKSPOVAAAVAED   GGLKKCKISSYCRSQPPARLISG   EEHFSSKKCLAWFYEVAGPDE   VYGPEGMEKFCEDIGVEPENI   MLVLAWKLEAESMGFTKEEW   VKGMTSLQCXLHRKGYKPNF   DFFAAHS*IDISSKNINTRYAFDE   ARDKDQRISLDNDTAKSIMLAL   LLGEGHGPLFSIVFYQVPGGQS   KYRWINKDQWYNSEFSRTV   HADLSNYDEDGGAWPVLLDEF   VEWQKVRQTS   VEWQKVRQTS   VEWQKVRQTS   VEWQKVRQTS   VEWQKVRQTS   VEWQKVRQTS   VEWGKVRQTS		l			sequenee		
RMPYKKKRKSPOVAAAVAED   GGLKKCKISSYCRSQPPARLISG   EEHFSSKKCLAWFYEVAGPDE   VYGPEGMEKFCEDIGVEPENI   MLVLAWKLEAESMGFTKEEW   VKGMTSLQCXLHRKGYKPNF   DFFAAHS*IDISSKNINTRYAFDE   ARDKDQRISLDNDTAKSIMLAL   LLGEGHGPLFSIVFYQVPGGQS   KYRWINKDQWYNSEFSRTV   HADLSNYDEDGGAWPVLLDEF   VEWQKVRQTS   VEWQKVRQTS   VEWQKVRQTS   VEWQKVRQTS   VEWQKVRQTS   VEWQKVRQTS   VEWGKVRQTS	-		Ļ.		1	11000	la compagnation con la con-
GGLKKCKISSYCRSQPPARLISG   EEHPSSKKCLAWFYEYAGPDE	18896	49264	A	19005	229	1028	
BEHFSSKKCLAWFYEYAGPDE					ŀ		
WYGPGGMEKPCEDIGVEPENII   MLVLAWKLEAESMGFFTKEEW   VKGMTSLQCXHLRKGYKPNF   DFFAAHS*IDISSFKNIYRYAFDF   ARDKOQRISLONDTAKSMILAL   LLGEGHGPLFSIVFYQVPGGQS   KYRVMNKDQWYNVSEFSRTV   HADLSNYDEDGAWPVLLDEF   VEWQKVRQTS   WEWQKVRQTS   WEWQKVRQTS   SIN_ENGFPEATPSKPNRMSNIN   FGPTEEPPONILKRTNPPGVFGS   SIN_ENGFPEATPSKPNRMSNIN   FGPTEEPPONILKRTNPPGVFGS   FIDESTPVQTRQHLIPPOGKTS   DIFGSPVTATSRLAHPNKPKDH   VFLM   WEWGWARD			l		ļ		
MLVLAWKLEAESMGFFTKEEW VKGMTSLQCNLRRKGYKPNF			1				
VKGMTSLQCXLHRKGYKPNF			l				
DPFAAHS**   DISSEKNIYRYAFDE			1				
ARDKOQRSLDNDTAKSMLAL   LLGEGHGPLFSNFYQVPGGQS   KYRVMNKDQWYNVSEFSRTV   HADLSNYDEDGWYNVSEFSRTV   HADLSNYDEDGWAWPVLLDEF   VEWQKVRQTS   18898   49266   A   19007   3   418   GRAGSRKWLLTGSLASTSPSL   LSQQFWAPLQRAMKPPGGES   SNLPGFPEATPSSKPNKMSNN   FGPTEPONILKKTPPGV*GS   IFDESTPVQTRQHLNPPGGKTS   DIFGSPVTATSRLAHPNKPKDH   VFLM   18900   49268   A   19009   3   81     18901   49269   A   19010   1   465   46			1				
LLGGGHCPLFSNYFYQVPGGGS   RYRYMNKDQWYNVSEFSRTV   HADLSNYDEDGGAWPVLLDEF   VEWQKVRQTS			1		ì		
RESP							,
HADLSNYDEDGAWPVLLDEF	į .						
NEWQKVRQTS							
18897   49265							
18898			_				VEWQKVRQTS
LSGGGPWAPLQRAMKPPGGES   SNLPGFPEEATPSSRPNRMSNI   FGPTEEPONILKRTNPPGV*GSG   IFPESTPVQTRQHLNPPGQKTS   DIFGSPVTATSRLAHPNKPKDH   VFLM     1890			_				
SNLPGFPEATPSSRPNRMSNI   FGPTEPONILKTNPPGV*GSG   IFPDESTPVQTRGPLNRFNGPGV*GSG   IFPDESTPVQTRGPLNRFNGPGV*GSG   IFPDESTPVQTRGPLNRFNGPGV*GSG   IFPDESTPVQTRGPLNRFNGPGV*GSG   IFPDESTPVQTRGPLNRFNGPGV*GST   VFLM     1890	18898	49266	A	19007	3	418	
REPTERPONILKRTNPPGV*GSG   IFDESTPVQTRQHLNPPG\GRTS			1				
B899   49267   A   19008   1   684			1				
18899   49267   A   19008   1   684							
NFLM						10	
18899   49267						ŀ	
18900   49268							VFLM
1890  49269			_				
18902   49270							
18903 49271 A 19012 3 1334 SPQLISSASEPAVRNSREHDATEP VVFQMSGGSADYNSREHGGFE GMDPDGVIESNWNEIVDNF70 VTMNLKESLLRGINAYGFEKP SPIQQKAIIPERICKOY**CGLLKLQ SGTGKTATF/SLISILQPVGRLSF KETQSTSYWAPTERLAQOJQK VILALGDYMGATCHACIGGTN VRNEMQKLQAEAPHIVVGTPG RVFDMLNRRVLSPKWIKMFYL DEADEMLSRGFKDQIYEIFQKL NTSIQVYFASATMPTDVLEVTK KFMRDPRILVKKEELTLEGIKQ FYINVEREEWKLDTLCDLYETL TITQAVIELNTERKYDWLTEKM HARDFTVSALHGDMOQKERDV IMREFESGSSRVLTTDLLARGI DVQQVSLVINYDLPTNRENYIH RIGRGGGRGGAGVANFYTED KRFLRDIETFVINTVEEMEMNI							
VVFQIMSGGSADYNSREHGGPE GMDPDG VIESNWEI/UDNF/D VTMNLKESLINGGNAYGEFEP SPIQOKAIIPCIKGY*CGLIALQ SGTGKTATF/SLISILQPVGRLSF KETQSTSYWAPTRELIAQQIQK VILALGTYMGATCHACIGGTN VRNEMQKLQAEAPHIVVGTFE RVFDMLNRRYLSPK WIKMFVL DEADEMLSRGFKDQIYEIFQKL NTSIQVVFASATMPTDVLEVTK KFMRDPRII.VKKEELTLEGIKQ PYNVEREEWKLDTLCDLVETL TITQAVIFLNTRKVDWLTEKM HARDFTVSALHGDMQQKERDV IMREFRSGSSRVLTTDLLARGI DVQQVSLVINYDLFTNRENYIH RIGRGGRFGRKGVAINTVTEED KRFLRDIETFYNITTVEEMFMH RIGRGGRFGRKGVAINTVTEED KRFLRDIETFYNITTVEEMFMH RIGRGGRFGRKGVAINTVEED							COOLICO + CDD+11D1CD11D + TDD
GMDPGGVIESNWAEIVDNF/D VTIMILKESLLRGILYAYGFEKP SPIQOKAIJIPCIKGY*CGLLKLQ SGTGKTATF/SLISILQPVGRLSF KETGSTSYWAPTRELIAQOJQK VILALGDYMCATCHACIGGTN VRNEMQKLQAEAPHIV\VGTPG RVFDMLNRRVLSPKWIKMFYL\ DEADEMLSRGFKDQIYEIFQKL NTSIQVYEASTMPTDVLEVTK KFMRDPIRILVKEELTLEGIKQ FYINVEREEWKLDTLCDLYETL TITIQAVIELNTRRKVDWLTEKM HARDFTVSALHGDMOQKERDV IMREFRSGSSRVLITTDLLARGI DVQQVSLVINYDLFTNERNYIH RIGRGGRGFGRGVAINFVTEED KRFLRDIETFYNITTVEEMJMH RIGRGGRGFGRGVAINFVTEED KRFLRDIETFYNITTVEEMJMH	18903	49271	A	19012	3	1334	
VTMNLKESLLRGIVAYGFEKP SPIQOKAIIFCIKGY*CGILKLQ SGTGKTATF/SISILQPVGRLSF KETQSTSY WAPTRELIAQQIQK VILALGDYMGATCHACIGGTN VRNEMQKLQAEAPHIVVGTTBE RVFDMLNRRVLSPKWIKMFVL DEADEMLSRGKKDQIYEIPGKL NTSIQVVFASATMPTDVLEVTK KFMRDPRILVKKEELTLEGIKQ FYNVFREEWKLDTLCDLYETL TITQAVIFLNTRRKVDWLTEKM HARDFTVSALHGDIMQQKERDV IMREFRSGSSRVLTTDLLARGI DVQQVSLVINYDLFTIRENYIH RIGRGGRFGRKGVAINFVTEED KRFLRDIETFYNITVEEMJEN			1				
SPIQKA\IIPCIKGY*CGLLKLQ SGTGKTATFSLISILQPVGRLSF KETQSTSYWAPTRELJAQQIQK VILALGDYMGATCHACIGGTN VRNEMQKLQAEAPHIVVGTTGO RVFDMLNRRYLSPKWIKMFVL DEADEMLSRGFKDQIYEIFQKL NTSIQVYFASATMFTDVLEVTK KFMRDPRILVKKEELTLEGIKQ FYNVEREEWKLDTLCDLYETL TITTQAVIFLNTRRKVDWLTEKM HARDFTVSALHGDMQQKERDV IMREFRSGSSRVLITTDLLARGI DVQQVSLVINYDLFTIRENYIH RIGRGGRFGRKGVANNFVTEED KRFLRDIETFYNITTVEEMJMN KRFLRDIETFYNITTVEEMJMN						1	
SGTÖKTATF/SLISILQPVQRLSF KETQSTSYWAPTRELIAQOIQK VILALGDYMGATCHACIGGTN VRNEMQKLQAEAPHINVOTFG RVFDMLNRRVLSPKWIKMFVL DEADEMLSRGFKDQIYEIFQKL NTSIQVYFASATMPTDVLEVTK KFMRDPIRILVKKEELTLEGIKQ FYINVEREEWKLDTLCDLYETL TITQAVIELNTEKVDWLTEKM HARDFTVSALHGDMOQKERDV IMREFESGSSRVLITTDLLARGI DVQQVSLVINYDLPTNRENYIH RIGRGGRFGRKGVANFYTEED KRFLRDIETFVNITVEEMEMN			l			l	
KETQSTSYWAPTRELAQOIQK VILALGDYMGATCHACIGGTN VRNEMQKLQAEAPHIVVOTTPG RYFDMLANRYLSPKWIKMFVL DEADEMLSRGFKDQIYEIFQKL NTSIQVVFASATMPTDVLEVTK KFMRDPRILVKKEELTLEGIKQ FYINVEREEWKLDTLCDLYETL TITQAVIFLNTRKVDWLTEKM HARDFTVSALHGDMOQKERDV IMREFRSGSSRVLTITDLLARGI DVQQVSLVINVDLFTNRENYIH RIGRGGRFGRKGVAINFVTEED KRFLRDIETFYNITVEEMJENN			1				
VILALGDYMGATCHACIGGTN VRNEMQKLQAEAPHIV\UGTRG RVFDMLNRRVLSPRWIKMFVL DEADEMLSRGFKDQIYEIFQKL NTSIQVYFASATMFTDVLEVTK KFMRDPRILVKKEELTLEGIKQ FYINVEREEWKLDTLCDLYETL TITIQAVIELNTRRKVDWLTEKM HARDFTVSALHGDMOQKERDV IMREFRSGSRVLITTDLLARGI DVQQVSLVINVDLFTKRENYIH RIGRGGRGFGRKGVANNFVTEED KRFLRDIETFYNITTVEEMJEM			ŀ				
VRNEMQKLQAEAPHIVVGTFG RVFDMLNRRYLSFK WIKMFVL DEADEMLSRGFKDQIYEIFQKL NTSIQVVFASATMFTDVLEVTK KFMRDPIRILVKKEELTLEGIKQ FYINVEREEWKLDTLCDLYETL TITTQAVIFLNTRKVDWLTEKM HARDFTVSALHGDMDQKERDV IMREFRSGSSRVLITTDLLARGI DVQQVSLVINVDLFTKRENYIH RIGRGGRFGRKGVAINFVTEED KRFLRDIETFYNITVEEMJEN	I						
RVFDMLNRRVLSPK WIJKMFVL  DEADEMLSRGFK DIQIYEIFQKL  NTSIQVVFASATMPTDVLEVTK  KFMRDPRII.VKKEELTLEGIKQ  FYNVFREEWKLDTLCDLY ETL  TITQAVIFLNTRRKVDWLTEKM  HARDFTVSALHGDMOQKERDV  IMREFRSGSSRVLTTDLLARGI  DVQQVSLVINYDLFTNRENYIH  RIGRGGRFGRKGVAINYTEED  KRFLRDIETFYNTTVEEMJEN  KRFLRDIETFYNTTVEEMJEN	1				l		
DEADEMLSRGFK D\QIYEIFQKL NTSIQVVFASATMPTDVLEVTK KFMRDPIRLIVKKEELTLEGIQ FYINVEREEWKLDTLCDLYETL TITTQAVIFLNTRRKVDWLTEKM HARDFTVSALHOMDOQKERDV IMREFRSGSSRVLITTDLLARGI DVQQVSLVINVDLFTNRENYIH RIGRGGFGRKGVAINFVTEED KRFLRDIETFYNITVEEMFMD							
NTSIQVVFASATMFTDVLEVTK KFMRDPIRILVKKEELTLEGIKQ FYINVEREEWKLDTLCDLYETL TITTQAVIELNTERKVDWLTEKM HARDFTVSALHGDMDQKERDV IMREFRSGSSRVLITTDLLARGI DVQQVSLVINVDLFTKRENYIH RIGRGGRFGRKGVAINFVTEED KRFLRDIETFYNITVEEMJEN			l				
KFMRDPIRIL VKKEELTLEGIKQ FYINVEREEWKLDTLCDLYETL TITIQA VIELNTRRK VDWLTEKM HARDFTVSALHGDMOQKERDV IMREFRSGSSRVLITTDLLARGI DVQQVSLVINVDLFTNRENYIH RIGRGGRFGRKGVANDYTEED KRFLRDIETFVNITTVEEMJEND			l				
FYINVEREEWKLDTLCDLYETL TITQAVIFLNTERKYDWLTEKM HARDFTYSALHOMOOKERDY IMREFRSGSSRVLITTDLLARGI DVQQVSLVINYDLFTNRENYIH RIGRGGRFGRKGVAINFVTEED KRFLRDIETFYNITVEEMFMN	1		l				
TITQAVIELNTRKVDWLTEKM HARDFTVSALIGDMQKERDV IMREFRSGSSRVLITTDLLARGI DVQQVSLVINYDLFTNRENYIH RIGRGGRFGRKGVAINFVTEED KRFLRDIETFVNITVEEMJEM			l				
HARDFTVSALHGDMDQKERDV IMREFESGSSRVLITTDLLARGI DVQVSLVINYDLPTNRENYIH RIGRGGRFGRKGVAINFVTEED KRFLRDIETFYNTTVEEMPMN			1			1	
IMREFRSGSSRVLITTDLLARGI DVQQVSLVNYDLPTMRENYIH RIGRGFRGRKQVAINFVTEBD KRFLRDIETFYNTTVEEMPMN	1		1		l	1	TITQAVIFLNTRRKVDWLTEKM
DVQQVSLVINYDLFTIRENYIH RIGRGGRFGRKGVAINFVTEED KRFLRDIETFYINTTVEEMJEMD	1		1		l	1	HARDFTVSALHGDMDQKERDV
RIGRGGRFGRKGVAINFVTEED KRFLRDIETFYNTTVEEMPMN	1		1				IMREFRSGSSRVLITTDLLARGI
KRFLRDIETFY\NTTVEEMPMN	1				1	1	DVQQVSLVINYDLPTNRENYIH
			1		l	1	RIGRGGRFGRKGVAINFVTEED
18904   49272   A   19013   75   540					1	1	KRFLRDIETFY\NTTVEEMPMN
	18904	49272	Α	19013	75	540	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
18905	49273	A	19014	774	1529	RWGERILLTWRKRQLQVPPSAL
						EAGGSSGLEDVLPLLQQADELH
						RGDEQGKREGFQLLL/TQQAW
ĺ				l		CMEAGRTFLWRLARAYSDMCE
ĺ						LTEEVSEKKSYALDGKEEAEAA
ĺ						LEKGDEE/SLTCHLWYAGALW
ĺ				ì		SAG*AMRASRRRIQELALTFKE
ĺ						HCGQKPFALQP\KTPMAHFLLG
ĺ						RWCYQVSHLSWLEKKTATALL
ĺ						ESPLSATVEDALQSFLKCYREL
ĺ						GKNSEARWWMKLALELPDVT
ĺ						KEDLAIQKDLEELEVILRD
18906	49274	A	19015	97	452	GTERRTGKLPALLTPNLVQLRR
ĺ						LLFPGIQTI*VPAQGRGHLLQRP
ĺ						AAA/RPRTRSAPPAAAAAPPQV
ĺ						EARPP*LQPTRQEEAAELQTAR
l						AGLWELWAGPQSPRDLNSLESI
l		l				RITCSPTP
18907	49275	Α	19016	1299	1800	FWGGRSGTVGYGADMGKFKN
		1				NTTNNQS*K*YRNTSRNPDHKD
		ĺ				*FLKGMDPKFPKNMHFA*KHN
		ł				EKGLEKMQDNNMRAEAIKA/L
		l				PKPMEVQPRVPKSASRKLD/LA
		1				YTAHPKAGKHARAHIATGLRL
		l				CWPKAKAKDQTKAQASASAA
		l				APASVLAPAQASKGAQAPMKA
						LE
18908	49276	A	19017	410	1323	RQEGTLIGVFIPAAAAAAAVAA
		1				AAAAAAAAAAAAAAA
1		l				AAAAAAAAAVAAAVAAAA
		l				AV/GTSFSKPHKLMKEHKEKPS
		l				KDSREHKSAFKEPSRDHNKSSK
		l				ESSKKPKENKPLKEEKIVPKMA
		l				FKEPKPMSKEPKPDSNLLTITSG
		1				QDKKAPSKRPPISDSEELSAKK
		1			1	RKKSSSEALFKSFSSAPPLILTCS
						ADKKQIKDKSHVKMGKVKIES
		1		1		ETSEKKKSTLPPFDDIVDPNDSD
		l		1		VEENISSKSDSVPGQSPVTNIFF
		l		1		TSSSTPTILKSYQLDNSDQQGA
		1		l		QEASDKQIEGYFSGEVPAYRQG
	l			l		ELILVASRQ

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18909	49277	A	19018	91	890	GABRLPEGFGKRMYFREFVEY GRVAYVYSFGPHARK/MWVAIV DVF*SEQGLLVE*PCTQVR\RQA MPFRCMQL\N*FHPSRFPNSAQP ESMFRQA WQK\ADINTK\WGSP HDGAKKIEAQRKGKPKDDQIF D\RFK\MEGQKKMREQE*SKE* SYSSFKRAALLEKLSPKKKHLG TGYCCLLLLLAAAAAAAA AACCLLACCLX\PSKKRSPAAS KKAPAQK\VPAQK\ATG\QKAP APKAQKQQKAPAQKAPAPKAS GQESISGNINK
18910	49278	A	19019	280	1249	SENEGIMYAQPYTNTKEVKW QKYU,YERQPFSLDKLWWDRRF LGRSSGKNHAPENTQYYWGCG *FESSYVYQQLCSVCYFVYIRW YMDEGLLAPHWLYGTGLSK IGYVLFDLIDGGERKKSG\QTR WADL*ELP*SFITFTYGFSPUK HALFPYGNANAIVSSTILLYN MAIFASIVCWASRLPRSLHAFI MVAHFAIQHFCPGGPML\QKKLK ACTPRSIYYGVTLLFAFSAVG\ GLLSISAVGAVLLAHLLMSISC LCYPYLHFAGSLFKENIHMGP WDEAEIRKEDLFIGSLS
18911	49279	Α	19020	1	310	
18912	49280	Α	19021	2	411	
18913	49281	A	19022	374	1275	VLTRLIRKRERKAGSOKERCR CVLAKDFLAGGOTAAISKMAV APTE/RVKLLLQVQSASKQITAD KQYTGVVDCMVRIPKE/GOVLS LWHIGIGPWIKFAGSLASGGAP GATSLCFVYPLDFARTRLAAD VGKAGAEREFRGLG*PAGLRIY KSDGK/RGLYQGFNVSVGMI YRAAYFGIYDTAKGMILPDPQ NTHIVISWMIAQTVTAVARVDF PIPPDTIVKRRNE*MQSRAPKEL THHVHQAFFDCWAFGLLRDEG GKAFFKGIAWYPMFLRGHGVG AFCALSLYGWKSKEGTHKLIS
18914	49282	A	19023	461	705	TERKKKGILPGNGNGFMSLRRT IRVWRNTPNYLGTNAVSPIRQD *IGKKGVCQRKQAGPCPPSNIQ GILEWRKHRISETKP
18915	49283	A	19024	2	408	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence	i	
18916	49284	Α	19025	1	885	MTQHAGKRDSELPVIVQDTET
						VPSVMDGKEYQAGRFARGLRL
				ĺ		QCFRRRRRRRRRRRRREEEE
	İ	l				EEEEEEEEEEVEEEGMKKEE
		l				EGRRRKKKKKKKAEEEEKKK
		l				KEEEEKKRRRREEPPRPRNDDD
		1			i	ARRRKEEEEGRRRSM/LGKRD
	}					SELPVIVQDTETVPSVMDGKEY
		1				QAGRFARGLRLQCFRRRRRR
	1					RTRRRRKEEEEEEEEEEEE
						EVEEEGMKKEEEGRRRKKKKK
						KKAEEEEKKKKEEEEKKRRR
	1					REEPPRPRNDDDARRRKEEEE
	i					GRRRSMKKEEEEEEEEEEE
		1				EEEEEEEEKKKRRIGPASKMM
	1	1				GGFEELRRGLNVGPTMAIFFLQ
		1				SAALAPAILYFCPSLKSNISKCN
	1	1				FQFLMFCQLLGRVTIPFLVSQRS
	1	1				RIEVGRHSLSTLNAETAHELYL
						GRTEPDECGKTAGLGTGLDLK
18917	49285	Α	19026	1	378	
18918	49286	Α	19027	36	3415	ESAANAQVLAAPSPCSPFAFTL
						SKVNMSLKNEPRVNTSALQKIA
		1				ADMSNIIENLDTRELHFEGEEV
		-		ł	ļ	DYDVSPSDPKIQEVYIPFSAIYN
		ŀ			-	TQGFKEPNIQTYLSGCPIKAQVL
	Į.					EVERFTSTTRVPSINLYTIELTH
		ļ				GEFKWQVKRKFKHFQEFHREL
	Į.			1		LKYKAFIRIPIPTRRHTFRRQNV
		1				REEPREMPSLPRSSENMIREEQF
			1	l		LGRRKQLEDYLTKILKMPMYR
	1	1	l	l	l	NYHATTEFLDISQLSFIHDLGPK
		<u>L</u>				GIEGMIMKR
18919	49287	В	19028	37	147	
18920	49288	В	19029	10	264	

SEQ ID NO:	of peptide sequence		SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18921	49289	^	19030	3	1255	HASGGRANMAADRGAVOQO SOMMEVDRAVESSESDEEG KKHSSGIVADLSEQSLKDGEEP GEEDPEEHELPVDMETINLAD RADEDPALINHYRICKIEGFEVL ESS*RLSCLRQNI.RKCLIENLGR ELPESFRELDLYDNQIKKIENLE ALTELEILDISFALLRNIEGVDK LITRLKKLFLVNNKISKIENLISN HQURMLGAGDLNRIRGOFSK YPTTLYTNLESWFLOKKTKITN FQNPGCASPALTVLSMQSNRLT KIEGLQNLVNLRELYFSINGIE VIEGLENNNKLTMLDIASNRIK KIEKSHALTELQFEWDGTTIPL KSWSDLDELEGEPGALEDSVP WGGNPLARRITKYRRKIVMLAI LIPSVRQDRCPSVSYRLKSFLGSL
18922	49290	A	19031	138	564	MWSLSSEELPSHGYFNPPCCS YREVMVSES*ETPAGARGRPYY FSAPGTA PPAINVHPPPSLSAT PHPPQPOPPPHQHNAKARVAT IRTKRTSNGKIRSKEVRKSPPEK WVGFNRRPKASCPSPPGAARV DVGGETERREQAAAPGEMGK WARPGGEYFHS
18923	49291	A	19032	1404	1586	ENESRFSDRNQASAGLGYLSDS L*QWIVGNGHATDLWQNCSTS SSGNVHHCFSSSPNGSG
18924	49292	А	19033	187	701	AELAARMILLLLSIIVLHVAAL VLLFVSTIVSQWIVGNGHATDL WQNCSTSSSGNWHHCFSSSPNE WLQSCSRGTMDPVDSSFSILSL FLFFCQLFTLTKGGGRF YITGIFQ ILAGLCVMSAAAIYTVRHPEW NLNSGYS*RFA*NLAWVAFPL\ ALLSGVIYVILRKRE
18925	49293	A	19034	1	493	
18926	49294	A	19035	105	307	
18927	49295	Α	19036	32	302	
18928	49296	В	19037	119	641	
18929	49297	Α	19038	496	653	
18930	49298	С	19039	568	747	
18931	49299	Α	19040	522	656	ESSQSHGKNFYMGKRIKLSLY WNVWRMLNSKSETTNCPLIRH RLSKRVGAPFLPAVLVLTKITIY QT*KFQIRNHKLPSNKTSAI

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
		<u></u>				
18932	49300	Α	19041	hii	277	RHVVAVVLGDVGRSPRMQYH
						ALSLAMHGFSVTLLGFCNSKPH
						DELLQNNRIQIVGLTELQSLAV
						GPRVFQYGVKVVLQAMYLLW
						KLMWREPGAYIFLQNPPGLPSI
						AVCWFVGCLCGSKLVIDWHNY
				İ		GYSIMGLVHGPNHPLVLLAKW
						YEKFFGRLSHLNLCVTNAMRE
						DLADNWHIRAVTVYDKPASFF
						KETPLD\RTHRLFTKLTNMHSPF
						RARSEPEDPVTERSAFTERDAG
		i				SGLVTRLRERPALLVSST\SWTE
						DEDFSILLAALESRV*TTDS/SIG
				ŀ		HNLPSLVCVITGKGPPREYYSR
						LIHQKHFQHIQVCTPWLEAEDY
			1	i	Ì	PR/ILGSVDLGVCLHTSCSGLDL
1				İ		PMKVVDMFGCCLPVCAVNFK
i						WQEQNPNLSGDSFTDPPLRRKQ
			i			CRASCPQ*GPAPGLHELVKHEE
						NGLVFEDSEELAAQLQVLFSNF
				İ		PDPAGKLNQFRKNLRESQQLR
1				i		WD*SWGSATPNPMMSSCRTTE
18933	49301	В	19042	110	2294	
18934	49302	В	19043	81	1538	
18935	49303	Α	19044	21	1158	AVVAALPTSSSSRHSLTQKPGS
						RRLRIESLLPPSSCEIFLIFSYIFR
						LCEKPYHQTRSASNVTNKTDPR
				İ		SMNS\RVFIGNLNTLV\VKKSDV
						EAIFSK\YGKI\VGCSVHKGLCLS
						VQVMLMRRNAPGLL*QGE\DG
			l	1		RMI/ALGQVLDINLAAEPK\VN\
						REKSSVKRSAAEMYG/SQ*QNT
						LLRPLYFSSSFDLDYDFQRDYY
1						DRMYSYPARVPPPPPIARAVVP
l						SKRORVSGNTS\RSGPRGFNSKE
			İ			WNSGVSSKFWKR*KGDDLQ\AI
						KEELT\OINOK\VDSLLENLEKIE
						KATGANKQLEMK\ND\KSEEEQ
		ĺ	Ì			SSSSREGKMRTNVKDGV*GGV
1	l	İ				PDDSAEGGGPTWMNDDNVKS
		l		1		GGMTSWELI/KDDEKEAEE/GE
1	I	ı	I	l		DD\RD\SANGGG
1		ı				
18936	49304	В	19045	93	303	DDIRDISANGOO
18936	49304	В	19045	93	303	DDINDISANOO
18936 18937 18938	49304 49305 49306	B A	19045 19046	93 I 123	303 246 487	DDIADISANGO

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon,/=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
18939	49307	IA	19048	584	1664	SGLFLFLFFYSEIFLIFSYIFRLCE
10/3/	7,507	ľ.	17040	304	1004	KPYHQTRSASNVTNKTDPRSM
						NS\RVFIGNLNTLV\VKKSDVEA
				1	ŀ	IFSK\YGKIVG\CSCFIKGFAFPFK
						*C**EEMPRACCSGRRVGRIDLL
ł						GQVLDI*PGLAEPK\VNPREKPG
						VETILPAGDVRGO*ONTLLRPL
	:			1		YFSSSFDLDYDFORDYYDRMY
						SYPARVPPPPPIARAVVPSKROR
						VSGNTSRRGK\SGFNSKEWNSG
				1		VSSKFWKR*KGDDLQ\AIKEEL
		ı		1		T\QINQK\VDSLLENLEKIEKAT
		1		1		GANKOLEMK\NDK\SEEEOSSSS
		l		l		REGKMRTNVKDGV*GGVPDDS
		1				AEEGGPTWMNDDNVKSGGMT
				l		SWELI\KDD\EKEAEE\GEDDKR
		1				QGPMARNDS
18940	49308	A	19049	158	1001	KRLGSSAISMSKYKLIMLR\HGE
		1		1		GAWNKENRFCSWVDQ\KLNSE
				Į.		GMEEARNCGKOLKALNFEFDL
		1		l		VFTSVLNRAIPTARL\IL\EELGQ
		1				EWVPVESSWRLNERH\YGAL\I
		1		l		GLNREQ\MA\LNHGE\EQVRL\W
		1				RRSYNVTP\PPIEE\SHPY\YQEIY
ľ		1				NRPGGIKVCDVPL\DQLPRSES\
						LKDVL\ERFLPYW\NERIAPEV\L
	ł	1				RG\KTILISAHGK*AVGALLKHL
		1				GRYPSGLKTSINIYSFLLGVPILL
						\ELD\ENLRAVGPH\QFLGDQEAI
						QAAIKKVEDQGKVKQAKK
18941	49309	A	19050	1	521	SASWVGVAMASRVLSAYVSRL
		l				PARFAP*PRVRMLAVARH\LST
						ALCSEGTQTRLGTLQPALVLA\
		l				QVPW*ELHMLCRQYSDMP/PRL
						TLEGIQ\DRVRLA*LKTLSDKVD
		l				PREAFQ*ILHFMKDLGLDSLDP
		1		ł		KWKII\MALED\EFGFEIP\DI\DA
18042	40210	<b>!</b>	10051	ļ.——	617	EKLM\TPPRKLVDLHCQDKKD
18942	49310	A	19051	1	516	IRALTMIWRRALLAGTRLVWS
		1		1		RSGSAGWLDRAAG\LR\DCG\TA
l		1	1	1		ASGMESNTSSSLENLATAPVNQ
1		1		1		I/QETISDNCVVIFSKTSCSYCTM
		1				AKK\LFHDM\NVN\YKVVELDL
						LEYGN\QFQDASLQK*LVERTV
1			1	1		PRIFVNGTFIGGATDTHRLHKE
18943	49311	A	19052	825	1080	GKLLPLVHQCYLKK\SKRKEFQ
18943	49311	l <sup>A</sup>	19032	023	1000	KRKIHQNFHKLSLKKAIEKDYS ESGSSVNQYKRIRPTDNVVIKQ
l		1		I		Y\WPGAVAHTCNSSTSVGQGR
				l		WIT*GOEFETSLANVVKPHLY
18944	49312	A	19053	80	429	WII GOEFEISLANVVAPHLY
10744	77312	1^_	1,7033	100	74/	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
18945	49313	A	19054	3	752	FKNAVGNLAMEGGGGIPLETL
						KEESQSRHVLPASFEVNSLQKS
						NWGFLLTGLVGGTLVAVYAVA
		)				TPF\VTPALRKVCLPFVPATTK\
		i				QIENVVKMLRCRRRDPLWDIGS
						GGRDGIVHRRLRRKGFTAVGF
						MEFKPMG*FWVFPRY\RAWRE
ļ						GVHGSAKFYISDLWKVTFSQYS
						NVVIFGVPQMMLQLEKKLERE
	1					LEDDARVIACREPEPHWTPDHV
	l	İ				TGKGIDTVWAYDASTFRGREK
	l .	1				RPCTSMHFQLPIQA
18946	49314	A	19055	157	829	TWGKGDPKKPRGKMSSYAFFV
10, 10	.,,,,,	1.				OTCRGG\HKKKHPDASVNFSEF
		1				SKKCSERWKTMSA*R/EKGKFE
1						DMAKA\DKARY\EREMKTYIPP
		1	-		i	QRGRQKRKFKDSQLHPRRPPSG
		1				LLSSSCSEYRPKIK\GEHP\GL\SI
		1				GDVAKKLGRDVGINTAAD\DK
			1			OP\YEKK\AAKLKEKYEKDIA\A
1				1		YRA\KGKPDAAKKG\VVKAEKS
1				i		KKKKEEEEDEEDEEDEEEEEDE
ł					ľ	EDEEDEEEDDG
18947	49315	Α	19056	85	267	GHLSHAWCGTYKPWPSPKEQS
		1				RAWKKDGLLFPPPP/PLFPTGLK
		1	i			VRGRESF*SVELIRPQG
18948	49316	Α	19057	1	1158	
18949	49317	Α	19058	452	517	
18950	49318	Α	19059	93	1069	YEGVTTSRLPELPRGCLVLQEQ
		1				ELVQMSGMEATVTIPIWQNKP
		1				HGC/SLRSVVRRIGTNLPLKPCA
		1				RASFETLPNISDLCLKRCAPSSL
	1	1				PWL\AWLGFLAE*KGSQKARV\
1		1		1		RSDTRPLRHTWKPSPLIVMQRN
						ASVPNLRGSEERLLALKKPA/L
				ŀ		ASPKAALLSCRTS*ATLRTKICK
		1	ĺ			DSGKLMQLRLH*RQISYLQEVQ
		1		ı		MSLLPLPCFGSSFHSTTSFCH**/
1	1	1	1		1	PSPRRQRWRSLSFHQSPCFVLP
1	1	1	1		1	ALNVANQNTKLPAVRLKRMTA
	1	1			1	SLCPRPAALQDMMGILKGLFTG
1	1	1			1	MKQSQDLNRSLLKEEDPAVLIS
	1	1		1	1	EVLRRKFALKEEDISRKGN
		_				

SEO ID	SEQ ID NO:	Mar	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
		_		ļ		
18951	49319	Α	19060	162	1410	GQASCPPPALGQQTPASSYTVQ
						IQTYAPSSPHPRQGPGQGSSDPR
				1		GLRGAIPRGRQGQGV*QQGPRC
		l				RPPSSPVLPHIPQLSCCGHDGRD
				ì		PEEGLGILELTLLHHAHPWSPN
			ŀ			SW*KDS\PSPHGEFPAHSEPHSR
						DQTSPMATTKHEVQPLPQASLS
				l	1	QPSLGIGCLVDWLRQLRTTQGS
				ŀ		/PQDAAQDSTWERP*DAS/GKP
1						WLL*PGVPTPGPPCQAKERKPP
		1				FMGNCPL*SRVPWPSRLPEEL/P
		1				AMPLAPPVAGEAAGPASSHQSL
						SPSQDPTPLPGADRREKERGGE
		l	İ			EGSSWPQTPRLTTHTTSPPPEKQ
		l		i		QQIESPPIRLSSFKTGFHLASSGH
		l				SYAIKPNSKTKAEKVGQVRVPR
		l		l		SHTIREOROGKRPGEHHRRTER
1		1				DAKPOGEEDHQATVVSQKLGT
		1				DRRLIKKQRTSVLSATAES
18952	49320	Α	19061	1	340	GSVGSGTTLNQLGFWSSPGTSP
		1				LEPPCPWLDSHIFPVPFWKDVA
		ı		İ	l	FGEGVCLPPGAPQPRRICPRRG
						QQPEFQQEEPETIPERTPADPGV
		l		Ì		LPPAFPGICLPRRLRAPPDPGPA
1		l		I		A*AVPPVADA*GSVGSGTTLNQ
		l				LGFWSSPGTSPLEPPCPWLDSHI
		l				FPVPFWKDVAFGEGVCLPPGAP
		l	1			OPRRICPRRGOOPEFOOEEPETI
		1				PERTPADPGVLPPAFPGICLPRR
		l				LRAPPDPGPAA
18953	49321	A	19062	3	396	IPLASLHLALPGHORGPPPGRLP
						SCSSQGTVPPPRAGPYQAGCPG
						TAPAPAAPASAPWSAPOASATG
						GTAHAAGPGSGGARSLPPARA
						HPPARCWOGRPLRSLLL*PSSVP
						ETGGPEKARLVKALSPNTAP
18954	49322	A	19063	563	1269	LEESTGRITHFKATLHCTMSNN
10551	1,7,522	ľ.	1,,005			LAWGGTKWLQESRVFFHIRRLP
						SDASAGPGCVYRVVPDGGSQG
						RPQGAPP*AAQA/GTPRGRPP\P
		ŀ				GAPSALLPPPPSGTSVGPGGLO
						QRRPPTGQEDSPTEPGFWKPRL
						WRSHLATSLATRCTMQGEPAR
		1	1	1	1	AHPPGGRGPAASEERHORGPPP
	1	1		1	1	GGCFAALRYCATPRPDLSGRCP
1		1		i	1	GTAPAPAAPASAPWTRLRHOPL
1				I	I	,
		L_	L	L	L	AAQLMQPGQVWWGPAASW

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon,/=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, :possible nucleotide insertion)
				sequence		
	10000	<u> </u>	10064		11158	L IMELKAKARELREECRSLRSRCD
18955	49323	A	19064	1	1136	
		1				QLEERVSVMENEMNEMKREG
		1				KFREKRIKRNEQSLQEIWDYVK
						RPNLHLIGVPESDGENGTKLEN
ļ		1				TLQDIIQENFPNLARQANIQIQEI
						QRTPQRYSSRRATPRHIIVRITK
						VEMKEKMLRAAREKGRVPHK
					1	GKPIRLTADLSSETLQARREWG
			1			PIFNILKRIFSFPQRGGTGGRRM
						VKLTAELIEQAAQYTSAVRDRE
						LDLRGYKIPVIENLGATLDQFD
						AIDFSDNEIRKLDGFPLLRRLKT
						LLVN/NNRIC/RVLDFQKVK/LK
						ERQEAEKMFKGKRGAQLAKDI
						ARRSKTFNPGAGLPTDKKKGG
ŀ		1				PSPGDVEAIKNAIANASTLAEV
l						ERLKGLLQSGQIPGRERRLGPT
		L				DDGEEEMEEDTVTNGS
18956	49324	A	19065	2	431	RKLDGFPLLRRLKTLLVNNNRI
						CRIGEGLDQALPCLTELILTNNS
				1		LVELGDLDPLASLKSLTYLSILR
						NPVTNKKHYRLYVIYKVPQVR
					ł.	VLDFQKVKLKF\NPGAGLPTDK
	ŀ			ł		KKGGPSPGDVEAIKNAIANAST
						LAEVERLKGLL
18957	49325	A	19066	92	303	NCFLVFSPARSTVGEFASMSSE
						ECI*MHVVFLFPLTLCVVSLYER
l l						QEAEKMFKGKRGAQLAKDIAR
	l					RSKT
18958	49326	A	19067	208	293	LLLLWWFPLGPTDDGEEEMEE\
						DTVTNGS
18959	49327	Α	19068	22	904	ARNPWSTHASGWREATGFPQR
1		1				GGTAGCTMGKLTAE\LIEQAAQ
1		ı				YTNAVRDRELDLRGYKIPVIËN
l						LGATLDQFDAIDFSDNEIRKLD
						GFPLLRRLKTLLVDTTRI\CGIGE
ł		1				GLDQA\LPCLTELILTNNSLVEL
						GDLDPLASLKSVAY\LTYLRNP
l		1			1	VTHKKHYRLYAIYKAPHVRVL
İ		İ				DFQNVKLK\ERQKAEKMSKGK
						RGAQLAKDIA\RRS\KTF*FPGA
		1				GLPN*PKRKGGP/SLPGDVEAIQ
						ECP*QNAFNSGLKVERLKGVCC
		1				KSG\QIP\GRERRSG\PTDDGEEE
						M\EEDTSHQTGS
18960	49328	Α	19069	1	395	AINYNEKIYELRVMETKP\DKA
l '		1			1	VSIIECDMNVDFDAP/LGYKEPE
		1				RQVQHEESTEGEADHSGYAGE/
l		1				LGFRAFSGSGNRLDGKKKGVE
		ı				PSPSPIKPGDIKRGIPNYEFKLG\
1		ı			1	EAGGRFVAFSGEGQSLRKKGR
					<u> </u>	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18961	49329	Α	19070	1	1108	
18962	49330	A	19071	353	693	GSLFLVKRREPER/QVQHEELTE GEADHSGYAGELGFRAFSGSG NRLDGKKESFSPIKPGDIKRGIP NHEFKLGKTPFIRNACPLVKKF EEDEAGGRFVAFSGEGOSLSKK
18963	49331	Α	19072	2	1112	RICGAAAAAAAAGRAVGGVSSI. HCPERSGVCQVVSIMFSRNDH HPIPRVFQNRTSTQYIRCFSLSM LAGPNDR/SSIGEKEGKIMPPLG POTIKLSRL*HYRIPMLFKILTIK NSGPHIGRIIGGVAGSLWA**GA SAYLPHWDDGRTYSLGRAA WVQGGRSVNLSSGPLISNFQPQ SNDFLIDITIN/KAVPENALRNF ALS*PPGDVIAINYYEKILRNCV VMETQTPTRPVSHH*SVNH*TV LE*LLPPGATKEPKDQVQP*G VRTEGESRPHSGIVAWKSLGFP RFSRGSGINRLIDGKKGVEPSPY SPIKPGDIKRGIPMYEFKLGKIT FVSRNSRPLVKKVEEDEAGGR FVAFSGEGGSURKLGKRGV
18964	49332	Α	19073	1	415	SGGRNRSATGSWVGTMAGIT TIEAVKRKIQVLQQQADDAEER AERLQREVEGERRAREKRGMK VIENRALKDEEKMELQEIQLKE AKHIAEEADRKYEEVARKLVII EGDLERTEEPSLSWQESKCSLEL EEELKNVT
18965	49333	Α	19074	1	421	
18966	49334	Α	19075	3	388	
18967	49335	A	19076	1	1332	
18968	49336	Α	19077	49	483	
18969	49337	A	19078	227	1030	AVSWYGTMAGITTIEAVREKIQ VLQQQADADERAJERSQREFR EERRAREQAJEAEVASLNIRIQ ULVEEELDDRAQERLGHCCKKL K#S*KKLADESERRY*BLJENNR ALKRIKEKIGTSREIPTSKKPKH HCRKEADIRKYEEVARKLGDH LKEDLERTEJERAVELASRC*EI DEQIRLIDQNLQCLSAAEDKYS QK EDB WAEEEMKILITONLKEAE THAELAERSVAKLEKTIODLED KLKCTKEEHLCTQRMLDQTLL DLNEM
18970	49338	Α	19079	50	864	
18971	49339	Α	19080	1	1014	

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
ŀ				sequence		
18972	49340	Α	19081	1	1650	MGFHHVGQAALELLTSGFSQT
						QELQKFLFLLFLLVYVTTIVGN
			1			LLIMVTVTFDCRLHTPMYFLLR
		1				NLALIDLCYSTVTSPKMLVDFL
						HETKTISYQGCMAQIFFFHLLG
						GGTVFFLSVMAYDRYIAISQPL
						RYVTIMNTQLCVGLVVAAWV
l		i			1	GGFVHSIVQLALILPLPFCGPNIL
						DNFYCDVPQVLRLACTDTSLLE
		1				FLMISNSGLLVIIWFLLLLISYTV
		1				ILVMLRSHSGKARRKAASTCTT
		1				HIIVVSMIFIPCIYIYTWPFTPFL
		1				MDKAVSISYTVMTPMLNPMIY
		ŀ				TLRNQDMKAAMRRLGKCLKG
		1				PAVAVGPGPGPGDAEAAAEER
		1				RVKVSSLPYSVDALVSDKKPPK
		1				EASPVPAKSASSGATLRLLLLP
		1				GHGAREAHSPGPLIKPFETASV
		1				KWENS\QDGAAWMQEPC*\YSP
		1				PPRHK\HKTNPKPRTAFTTSQLL
		1				ALEGKLLQKQYLSIAEGADFSS
						SPNLTETQVKILFQNRRAKTKR
				l		LQESELEKLKMAAKPMLPSSFS
						LPFPISSPLQAASIYAASYPFHRP
10072	49341	-	19082	62	440	VLPIPPVGLYATPVGYGMYHLS
18973	49341	B	19082	1	902	METEALMPGLGVAVAGAQVTL
107/4	49342	l^	19065	1'	702	GFLALETQLPFTGHKRILRLFFS
						SPRDPPHVPSKGLKRKWGARR
	1	1	1			GRTFALREAEPORLPSLSRAFG
1	l					TLARPYARLVRPGNPVVPFPLA
		1				GSAEAARAAATCERQARTCPM
1						PGVTVKDVNQQEFVRALAAFL
						KKS*V\GKLKVPEWVDT\VKLA
				1		KHKELAP\YDENWFY\TRAAST
		1				AQAPCTIRGGAG\VGSMTKIYG
		1				GRQRN\GVMP\SHFS\RGSKS\VA
		1		1		RRVPPKPWRG*KMVEKGTKNC
		ı				GPQNLTPSRDKRDFGTEFAGQV
		1		l .		AAANKEALEQIHCFGLIKLAHS
18975	49343	Α	19084	I	673	AGPDAEASERVPEGPEAPGAGP
1						SRPLEPRPRASGRPGHGRCLGV
1		1		1	1	TVK\DV\NQQEVRHELWAAFLS
					1	KSLR/LRVS*TVPEWL\DTVQAG
1						QAQKSLLPYDE\NWFYHAELAS
		1	1	1	1	TA\RH\LYHPGSALGVGSMTKIY
	I	1	1	1		
						GGTSDETASMPKPLSARGFQEI
						GGTSDETASMPKPLSARGFQEI
						GGTSDETASMPKPLSARGFQEI WARRV\LQSPGRGLKMGGKRD

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	delction, \=possible nucleotide insertion)
		ŀ		sequence		
18976	49344	Ā	19085	li .	427	HPVRFFVHRGPH/VDFSLEVVS
		1				OWYELVVFTASMEIYGSAVAD
		1				KLDNSRSILKRRYYROHCTLEL
l						GSYIKDLSVVHSDLSSIVILDNS
		ı				PGAYRSHPDNAIPIKSWFSDPSD
						TALLNLLPMLDALRFTADVRSV
				1		LSRNLHOHRL
18977	49345	Α	19086	2	832	WNSAELGRGGPGAGGAGVIGM
						MRTQCLLGLRTFVAFAAKLWS
						FFIYLLRRQIRTVIQYQTVRYDI
					1	LPLSPVSRNRLAQVKRKILVLD
						LDETLIHSHHDGVLRPTVRPGT
		1				PPDFILKVVIDKHPVRFFVHKRP
						HVDFFL\EV\VSQWYELVVF\TA
						SM\EIYG\SAVGRLNWDNSRSIL
						*GGRY\YROHCTLELG\SYIKDP
ļ.		1				LLWFHSDLS\GIVIL\DNSPGAYR
	İ					SHPGYGGR\DNAIPIKSWVSVTP
		l			i	ANTAILNLLPMLDALRFTADVR
	1	l	1			SVLSRNLHQHRLW
18978	49346	c	19087	69	206	5 · Sera issi quine.
18979	49347	Α	19088	312	438	
18980	49348	A	19089	635	826	QWISLWKCYKPEESGGQYLIFL
	10,000	1			1	KKSIFNDEFHVKPN*AS*GKEK*
		1			1	TPLQTSNC*GILSPPGLP
18981	49349	С	19090	1	390	
18982	49350	Α	19091	336	551	ARPLGSLASAPFPAPM*NVYPT
						GP*\YNADCPNVTAPVCASNGH
						TFQNECFFCVEQREFHYRIKFE
						KYGKCD
18983	49351	Α	19092	76	309	KGRFVIALTFTT*HSNLEKSCSK
						ICKIK\NKSLVCKHQLAKSIQSPS
					1	**WNGMNN*FTTLFICCHNTEK
						TFIHCGKRP
18984	49352	Α	19093	181	447	NKYQTDNIKLSDNDLTIGHQTG
						NTTAHC/RYIMLFRSFQQMAITT
						ILS*YRKNIYPLWKETLKRMWQ
						RHREKVGSFEKVNDIKILFHHW
18985	49353	B	19094	I	160	NLHSOMLWNORIR*LTSV*LEL
1.0900	49334	l^	19093	ľ	100	LCKNPNRVATRDQLLCLSGHL
		1		į		
18987	49355	A	19096	2	456	GMGRILELGG YKNTITDYYEHLYAHKLENLEE
1 898 /	49333	Ι^	19090	ľ	430	MNKRRASTICTETIPKKLRRRD
l		1				SSLTHSMRARRLSVDVKPQDRS
l					1	
l					1	RGPSECTIFRAGVPEGTRGALW
1			1			LPHFQTESDPGSKPAITLLVIHP
l	1					DELQIYVRTKTC/T/RMFIAALFI
	L					IAKT*KQPRYPSCLITST

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
18988	49356	A	19097	138	1193	LCFFGQHAPIYCSLRHSLLSYTR
						PASLICCLPGSHRYLEFVLLLLK
			ļ			HHRLHEDLNHCPIGSRSGRDVR
			ì			SQTTQEQHVIAMPFPLRKLEPL
			1			HSGLYSHSCCSRYLAGWLALA
	l		<b>!</b>			TGGAARSPPAISILOPOEPSVTPS
			1			DTQRACGRSTEAFESKEQKASV
						RVETTVSFSCSIKVDGGLLEPKR
						ADTGWHGHHCRPASITPAGWV
ı			1			PARYLLYVFFSRQCVLSMVCGP
ı		į.				QYTRGEIPGAVLKEECLPSLLT
		ŀ				GRFDLSGRARRLSVDVKPQDRS
		1				RGPSECTIFRAGVPEGTRGVLW
		1				LPHFQTESDPGSKPAITLLVIHP
						DELQIYVRTKTC/T/RMFIAALFI
Ì		ŀ				IAKT*KQPRYPSANTLLL
18989	49357	Α	19098	3	247	
18990	49358	Α	19099	1	1048	MQLKPMEINPEVSARCTATRRA
		1				RGRGRGSRVADRFGFAFFAFA
		1				FQMLNKVLS\RLGVAGQWRFV
		1			1	DV\LGLEEESLGSVPAPA\CALP
		1				ACLFPLTAQ\HENF\RKKQIEE\L
	İ	1				KGQEVSPKVYFMKQTIGNSCG
	1	1	İ			TIGLIHAVAQ*SKTNLGFE\DGS
	1				1	VL\KQF\LSETKKNVPLKDRAKC
	ł	1				F\EKN\EAIQAA\HECRGTRKGQ
	ľ					CRVDDK\VNFHFYSG*PTVDGP
	1	1				PSMNLDG\RMPFPRGPMAPS\Q
İ	l					GDTLLEGRFPRSCRRISPRREQR
	ł	1				RSPASSARGFSCKGSLNALWGG
		1				TWLISPLSPQHENILPPHASLKC
		ĺ				FSTCETQAVLLFCQTRPSPQPHP
		_				RHLSTSRVHSCPLGHCGVSFRW
18991	49359	Α	19100	57	450	VGDCLTSRGMSWVQATLLAR/
		1				ALCRAWGGT/CRGALTGTSISQ
	l	1				VPRLAP\RGLHCSA/ASVSSEQS
	1	ĺ				LVPSPPEPRQR/PPGGERDKASF
				l	1	LQTVQKFADTSVVDSGHIDFIY
				l		LALRKMREYGVERDLAVYNQL
		<u>_</u>				LNIFP
18992	49360	В	19101	307	390	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
18993	49361	A	19102	431	1267	SGTRTTSTAARTSRTWRS*TPLL ACTPRPCGSAKLATATSRTCIRP *SPSATQTLTVTKVPLPKDSTG
						AADPPQPHIV/GAQGMYVSTPG IQSPDQQAALARHNPARPVFVE GPFSLWLRNKCVYYHILRADLL
						PPEEREVEETPEEWNLYYPMQL DLEYVRSGWDNYEFDINEGKE QHVTI/LCSSGEC*ILRRRQNV*R
						LLDW/LAGKALTSPTCAPKITC VPLALPTPYCSGQNLNSSCSMT SVSDHLSPVPTLLSTISKAHGTP
19004	49362	В	19103	40	691	PPNTKVVTKVTVRQ
18994 18995	49362	A	19103	49 89	95	VGDCLTSRGMSWVQATLLARG
						LCRAWGOTGGAAL/SGEPPSLR  LASLPROLICASAAHSSEQSL  VPSPPEPRQRAHQGSWCPLR/VP  VLGQGAGLGERGQGRAFL/LD  GCRNLRITSYKRKGPH/VDLFY  LALRKMREWGVERGJDLAVYN  PRQQECGIAVLEQMENHGVIFVHY  PRQQECGIAVLEQMENHGVMP  NKETEFLLIQIFGRKSYPMLKL  KILKUFPFRHWNVPFFVPRDLP  QDPVELAMFGLRHMEPDLSAR  VTIYQVPLPKDSTGASKIPPKPH  IVGI/QRSPDQARPFLARHINPSR  PVFIVEGPFSLWLRNKVCV/YY  HIRADALIPEGREWASAKACV  GAGEWAGTTLRVHGRGWRRE  TERALASDPACTPHLGEEVEET  TERALASDPACTPHLGEEVEET  TERALASDPACTPHLGEEVEET  TERALASDPACTPHLGEEVET  TERALASDPACTPHLGET  TERALASDPACTPHLGET  TERALASDPACTPHLGET  TERALASDPACTPHLGET  TERALASDPACTPHLGET  TERALASDPACTPHLGET  TERALASDPACTPHLGET  TERALASDPACTPHLGET  TERALASDPACTPHLGET  TERALASDPACTPHLGET  TERALASDPACTPHLGET  TERALASDPACTPHLGET  TERALASDPACTPHLGET  TERALASDPACTPHLGET  TERALASDPACTPHLGET  TERALASDPACTPHLGET  TERALASDPACTPHLGET  TERALASDPACTPHLGET  TERALASDPACTP

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
18996	49364	A	19105	li -	1199	EFGALRRTRLGSSFPRRRDSSA
						MESYDVIANOPVVIDNGSGVIK
				İ		AGFAGDQIPKYCFPNYVGRPKH
						VRVMAGALEGDIFIGPKAEEHR
						GLLSIRYPMEHGIVKDWNDME
		1				RIWQYVYSKDQLQTFSEEHPVL
						LTEAPLNPRKNRERAAEVFFET
						FNVPALFISMQAVLSLYATGRT
		1				TGVVLDSGDGVTHAVPIYEGFA
		1				MPHSIMRIDIAGRDVSRFLRLYL
						RKEGYDFHSSSEFEIVKAIKERA
	l	l				CYL\SINPQKDETLETEKAQYYL
						PDG\STIETGPSRFRAPELLFRPD
	1					LIGEESEGIHEVLVFAIQKSDMD
						LRRTLFSNIVLSGGSTLFKGFGD
						RLLC\*VKKLAPKDGRIRISAPQ
				ŀ		ERLYSTWIGGSILASLDTFKKM
						WVSKKEYEEDGARSIHRKTF
18997	49365	Α	19106	l	3288	MPSGGDQSPPPPPPPAAAASD
		1				EEEEDDGEAEDAAPPAESPTPQI
						QQRFDELCSRLNMDEAARAEA
						WDSYRSMSESYTL/EGSGLWLP
						RGLFGHPGHCTGLLLLLRSGCV
		ĺ				RSQPSDRACR*EK\CHSSHLIEFF
		1				NKMKKWEDMANLPPHFRERTE
						RLERNFTVSAVIFKKYEPIFQDI
						FKYPQEEQPRQQRGRKQRRQP
						CTVSEIFHFCWVLFIYAKGNFP
						MISDDLVNSYHLLLCALDLVY
		_				GNALQCSNRKELV
18998	49366	A	19107	56	3552	GPAAQGCAMPSGGDQSPPPPPP
						PPAAAASDEEEEDDGEAEDAAP
						\PAESPTPQIQQRFDELCSRLNM
						DEAARAEAWDSYRSMSESYTL
						EGNDLHWLACALYVACRKSVP
				1		TVSKGTVEGNYVSLTRILKCSE
	l			l		QSLIEFFNKMKKWEDMANLPP
				1		HFRERTERLERNFTVSAVIFKK
				1		YEPIFQDIFKYPQEEQPRQQRGR
						KQRRQPCTVS*NFSIFCWVLFIC
				1		AKGNFPH*LSDDLVNSYHLLLG
			L	L		ALDLVYGNALQCS

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hođ	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleutide insertion)
18999	49367	ĪΛ	19108	1	1193	GRRRFWWRKRIGGGGGGMA
			.,	ľ		MPAEAPWMASSFNGFLSLPPG
1		1				WLLLPPPSDRNPPLQPSSRPPLC
1						VRMWMNAFTPLISLFFWASLV
		1				SSGARRLHPIQPQPCREQAPMP
						APGAARSAVAASMSDCTVAGP
		1				CTGSHTPCHSTSDSQSP/CGGVG
						SSLVV*AERSCAQCRMSPRKGH
						CCCCCCCCCCC/SCCCYCHYC
		ļ.				CCYCCCCCCCCCCCCCCCC
l		1				CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
						CCCYCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
				İ		CC*HYCCCCCCCF/GCCCCRYC
l		l				CCCRYRRCYCFCCCCCCCCYCY
İ		l				CCC*RTAHAWPSMNKSQCVLP/
						CICKVPLGRLAVTTGCPGFG*G
		1	1			GCWEDCMFPAKGPSIRLEQWFS
1		1				TTAILLPSGPGDFWQYLGTLLV
		1				VTTREEVLLESGG
19000	49368	Α	19109	1	762	GTRDATAEENRVLLAMVNPTV
l		ł				FFDIAVDGEPLGRVSFEVRGLD
						TKK*LLI*SIKLC*QIGGSSIFITS
		ļ				D*KNSCLPLIVQQCLLFLRILP\L
	1	ļ				FADRVPKASQKIFVALS\TGEKG
						FWL*GVPCFHRLFP\GFYVSRGG
1	1	1				DFHTAINGTG\GKSILWGENLK
1		1				DENFI\LKHTG\PGI\LSMANAGP\
	1	1				NTNGSPVFLTSCTA\KT\EWLDG
1		ł				K\HVVFG\KVKEGMNIVEAMER
		1				SLGPRMGKT\SNKFTIADCGQL
1					1	RIKFDLVFYL
19001	49369	Α	19110	95	240	LHSEITVCL*GSEHHFFENGTYI
						PHRSCHDPLEARAEDFL
19002	49370	Α	19111	I	1644	
19003	49371	Α	19112	237	632	AIGFPSYSSMQLVNIFGLLNLFSI
						ISSSFRHQG*HS*ELP\YPLEPGA
						EDFLR*GP\LAGHGHTGSQPFFC
						RVSEA/CGSHLVNSSRAALKRW
1						AGV*RKIWPRGSPETPRNLKDL
				1		SVLEYENTPDTSGKKALED

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
		<u> </u>			lene i	
19004	49372	Α	19113	274	2704	GISVLHGCGYRFQPRGMAAPGF
						FSEKPVPGCDAGDLQTPALSSW
1						TQTFIISHEQGIKFLNQRWSCWS
			1	1		KERNHGHCRVRGHVTAAQCDL
	1		l			FGNGLKHNLDLHIHDRNDASK
				1		NVKKSTNYGKMSFYTYCECTP
1			l	1		TGEKLWDHNQHRKIIGYKPASS
						QDQKIYSGEKSYECAEFGKSFT
		1	1			WKSQFKVHLKVPTGEKLYVCI
			l	Ì		ECGRAFVQKPEFITHQKTHMRE
				1		KPYKCNECGKSFFQVSSLFRHH
1			i			RIHTGEKLYECSECGKGFPYNS
			i			DLSIHEKIHTGERHHECTDCGK
						AFTQKSTLKIHQKIHTGERSYIC
						IECGQAFIQKTQLIAHRRIHSGE
						KPYECNNCGKSFISKSQLQVHQ
						RVHTRVKPYICTEYGKVFSNNS
	1					NLITHEKIOSREKSSICTECGKA
1				1		FTYRSELIIHORIHTGEKPYECS
1						DCGRAFTQKSALTVHQRIHTGE
				1		KSYICMKCGLAFIRKAHLITHQI
						IHTGEKPYKCGHCGKLFTSKSQ
1		1	1			LHVHKRIHTG\EKPYMCNKCGK
					1	AFTNRSNLITHOKTHTG\EKI\FI
				1		CSKCGKAFTORSDLITHORIHT
	ļ	1	1	1		GEKPYECNTCGKAFTOKSNLNI
	1	1	l			HQKIHTGERQYECHECGKAFN
		1		1		QKSILIVHQKIHTGEKPYVCTEC
1	i .	i			1	GRAFIRKSNFITHQRIHTGEKPY
1				i	l .	ECSDCGKSFTSKSQMT\EH*A\V
	1					HSG*KPYV\CAECGKAFSGRSN
L	ļ	ļ				LSKHQKTHTGEKPYICSECGKT
19005	49373	Α	19114	3	180	DUI DESIDENCE DEL DEL DECENDO
19006	49374	Α	19115	95	433	PVLRTHPGPQSLPRVPGVPCGG
	1	1	1	1	I	LLEPLSRAEVSPRLGLRRDLLG
	1	1	1	1	I	GMAPSGSST\VF\LLALTIIASTW
	1	1	1			ALTPTHYLTKHDVERLKASLDR
L	I	<u> </u>			<u> </u>	PFTNLESAFYSIVGLSSLGAQVP
19007	49375	A	19116	196	706	ISISNETKOLLLAAVSEDSSVTQ
		1		1	1	YHAVAALSGFGLPLASQEALSA
	1	1			1	LTARLSKEETVLATVQALQTAS
		1	l l		1	HLSQQADLRSIVEEIEDLVARL\
		1			1	DELGGVYLQF\EEGL\ETTALFV
	1	1		1	1	AATYKL\MDHVGTEPSIKEDQV
1	1	1	l .	1		IQLMN\AIFSKKNFE\SLSEAFSV\
		1		1		ASAAAVLSHNRYH
	L		L	L		ASAAAVLSHNRYH

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nueleotide location of first codon for peptide sequence	eodon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
19008	49376	A	19117	275	2192	MVVSPQGSSTVFLLALTIIASTW ALTPTHYLTKHDVERLKASLDR PFTKRLGSPKYTTCVTT*H*LFP TV*KACTYIRSKSLPCLPQIAKT CSKTLCLPILS*ISISNETKDLLL AAVSEDSSVTQIYHAVAALSGF GQVREGVSG*NKTCHSLGFYSL PSRTVDSGSCISFLLLLDIQHISV LLWQDLVARLDELGGVYLQFE EGLETSTAVALPPSQQRKRNSCI LLWQDLVARLDELGGVYLQFE EGLETSTAVALPPSQQRKRNSCI KNECKSCLCCKK*FFFYPQLQV TNVLSQPLTQATVIKLLFVISMT FRT*VLAKPIVLLNVSISHFPHPPILATVF SIFL*LRVKISTDIFSACSQRYTD PL*RLTLYASFRVTYPAKAKGT FTADROSMLGPGRILKLSDERL YYSSI*TFVRLHNQKTGQEVVF VAEPDNKNYVKFELDTSEKKIE FDSANIY*VSPTSLPCFYRLSL FF*ADVINPGHPLEFPEKSWHG LCCFPFKF*CLFNLFLPIGWILLA MLGLMYVYKTLNMFQTLKS FUNRSSKCYFRQHLFREPEKSWHG LCCFPFKF*CLFNLFNLGKTLAM MLGLMYVYWTQLNMFQTLKS FUNRSACSCFILDVMTPLLA KILDRAMSCFILDVMTPLLA MLGLMYVYWTQLNMFQTLKS
19009	49377	Α	19118	3	413	LAILGSYTFLA'GN\RMLA\QQA PRKEAPSTE\SQ\ALTPIK\QEIO\ HLF\REPEK\R\PPTVV\SNTFTALI LS\PLLLLFALW\RIGA\N\SN\FT FGL\PST\\H\G\G\S\P\S\PT\ Y\Y*T\QA\PC\S\TLEV\P\P\P\L\G QC\B\FLA\G\Q\S\G\ML\G\R\G\S\P\T\\A\Q\E N\O\H\N O\H\N
19010	49378	A	19119	2	535	GRVDPKAKKEAPAPPISLEPKA *AFKGPRAVLKGVIISPQKA GRSRTSTPPFRAGRKTTADSRR PAPKIILRKSRVPGGNKLDIHYA UIKFPADH*SASAVKKIEDNINT LVFIVDVVLKANKHQIKQGCE RSLYDIDVGQQQHPWIRPDIGE KKAYCSTWLLDYDGFGMFAN QNWGSI

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			ŀ	sequence		
19011	49379	A	19120	159	801	I IGAAGRRRLPEGEGEDEASAWR
19011	49377	^	19120	139	801	RLARCLMPKKNRIAIYE\LLFKE
						G\VMVAKKDVHMP\KHPE\LAE
						VKNVPQPFMVMKGHAGLSSPR
					ļ	G\YVKGTSFA\WRHFLTGTLTO*
						GVSQYSPWITLHLAPGRFVPCP
						PLRPVARPRRMGRP\RPKKVLG
						GVEATWRGFHKRGEV\DRGYL
l					į	TRRSACCQLGA\DKKSRGWGL
						GSSNPNFQFRG\GF\GCGRGO\PP
19012	49380	-	19121	334	989	EPPAETLPVAARDPTGLSPTYLS
19012	49380	A	19121	334	989	
						SHKHEKFQQVRHFPVLLGYPIA
				1		SSGASPEVRQRRTTFFRFRPGES LCGDMKLLTHNLLSSHVPAGG
						SLPFSGGMVGRGPVLA*TP/LAL
			ŀ			QATEGR\ICPVEINPQLRGRVMI
						P*KWKWS\AF\LEAGPDKLAV*I
				ŀ		PGARKGPG*GDMRENEEFS*GP
				l		WHHLACWEVGSD*EGTL\QVP
		_	10100		177	GNLGRYFSPFKPRGSPNMLAE
19013 19014	49381 49382	C A	19122	61	191	
19014	49382	A	19123	1902	2187	
19015	49384	A	19124	55	340	GELVLKALSAFIRAFRCPAEGS
13010	47304	^	19123	33	340	DPVGRAADP\SPPAPRGISQGS
					ł	ACGSPFLPGPITESLPLPPGLGSG
				l		SELPSLYLVSGIYGGVRRGPPA
1						RLEA
19017	49385	Α	19126	1228	2447	TSOGSSPPAHIGRWSSNHKKGL
19017	47303	l^	19120	1220	2447	GSSFSOSCCKAEALVKNA WPPT
				1		OA*VSICCFEODLGRGOOKGKS
						GGKWOKTAESREAVTECPACY
						RAARCRAAGDRGLRAEGAAAG
						HTASPSAYRVRGERGHRDMHS
					1	ASARLSHPGETNLMLGLAEPSV
						TSH*SHPFROS*LP*OAGP**EM/
						PLPPSARDSSDLCSG\SPSHDLLP
1						LPNTVIFWGPSSPODWOPLPLSP
						FCVSQAAGSPCSPLLQGLEPGGI
						STSCPPGPAPYIDFGAVSGAGOS
						AAORGAHFPAAMAERPSAGTS
			l	l		GSSGISGAIAATVVSWVAEGEQ
		l	l	I		
				l		AVKCLAEGSTRQTGQPSRRAPS
			1	l		RGCPAPGAPPGRAAPPQAPPAA PAAGGGRGPPAAPRAPAPRPOP
				l		
			l	l		QGAPRPVSPCRGTGAAPPPTLV
		Ц_	L			WGLSSEAEG_

SEQ ID NO:	of peptide sequence	hod	SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19018	49386	Λ	19127	164	563	CEAALKGDSGGSPWPDERPKE GVKTENNDHINLKVDGAEMVT VV\QFKIK\RHT\PL***LKAYL* TDRGLSMRQIRFRI*PGNPIN*K QTHLHQLGNGRIEDYNLMCFQ QARPGGVYLKKGTCFFYSKNS VSF
19019	49387	В	19128	166	426	
19020	49388	С	19129	76	285	
19021	49389	A	19130	3	179	
19022	49390	Α	19131	93	172	
19023	4939I	A	19132	1	2742	
19024	49392	A	19133	1287	2571	ILRQW/LASPEEKTGRPALAS SAETLSWLRAQGREPEGPAS VGAEHRTRTAPGSDPRCGILPS GRSPPSPPARLELASVPATI*AN TPSPTRLPAWPPPCRGPDASPE VVRKGGKAGOPRGSSPØPWSG AEFIVEVGLIPTTRALLFPGSP TALPAVYHFLAACEGICPHSCA APSMIELWDFLIQQHQPEKAVA TTTHHIPGILRISALNKHRAWG TDDDVAASEMPLGAAGAEPW DVP*LLPAALKIPTGHTATTSW GAGP*SPQGSCKGISGVGSGAT ADLLAPTAGVGTSRTACGG QFMSEGAPGVMNNGSPDWSST QFMSEGAPGVMNNGSPDWSST QFMSEGAPGVMNNGSPDWSST QFMSEGAPGVMNNGSPDWSST QFMSEGAPGVMNNGSPDWSST QFMSEGAPGVMNTGSPDWSST GFMSEGAPGVMTGSPDWST GFMSEGAPGVMTGSPDWSST GFMSEGAPGVMTGSPDWST GFMSEGAPGVMTGSPDWST GFMSEGAPGVMTGSPDWST GFMSEGAPGVMTGSPDWST GFMSEGAPGVMTGSPDWST GFMSEGAPGVMTGSPDWST GFMSEGAPGVMTGSPDWST GFMSEGAPGVMTGSPDWST GFMSEGAPGVMTGSPDWST GFMSEGAPGVMTGSPDWST GFMSEGAPGVMTGSPDWST GFMSEGAPGVMTGSPDWST GFMSEGAPGVMTGSPDWTG GFMSEGAPGVMTG GFMSEGAPGVMTGSPDWST GFMSEGAPGVMTG GFMSEGAPGVMTG GFMSEGAPGVMTG GFMSEGAPGVMTG GFMSEGAPGVMTG GFMSEGAPGVMTG GFMSEGAPGVMTG GFMSEGAPG
19025	49393	A	19134	31	202	ILITYIIKLINQADFSTP*FMSHLI VSSRILCTEKWNFHFPPHF*D*Q QTFCTLQFL
19026	49394	Α	19135	410	867	LLTLSRTTPLMSLGFFGIPKMIN RPRQSSPIKLQNSSSLSNLLFFQ EDSSTLDSGLERSQGLDSTGGG EDICRYWTAS*SFICLSDPQKVQ IQSAPNRKAWCUTLVVVSHSS TPFSWQKVMKWIKKISFRVFAA GQGLLGGYSNPRYSFSF

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:		Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
19027	49395	IA	19136	1111	743	VITILTPMLADRTRRIERPPKKK
						GTTSLGQRKWLLTQDWPSVYP
						VA\HPFKPSAVP\LPV\RMGYPV
					1	KKGRAHGDRRGNLELLKISOFF
1						WILTSCSNLKSTCEALKDF\CTG
						VGQPHWDSGRKKMLKKHFSN
						WKFGQHLDLCFHQGPSGSGNP
						RARVVVLKSKAFLV*I*HDHAK
				į.		KTLITLVGERYCKTPDVLTIKO
		1				NRWPLRSQITIMPVYL
19028	49396	A	19137	305	2291	YLDAEKMGOKASOOLALKDSK
17020	47370	n	17137	303	2271	EVPVVCEVVSEAIVHAAQKLKE
						YLGFEYPPSKLCPAANTLNEIFL
						IHFITFCOEKGVDEWLTTTKMT
1						KHQAFLFGADWIWTFWGSNKO
l						IKLOLAVOTLOMSSPPPVESKP
i						CDLSNPESRVEESSWKKSRFDK
		1				LEEFCNLIGEDCLGLFIIFGMPG
l l			1			KPKDIRGVVLDSVKSQMVRSH
						LPGGKAVAQFVLETEDCVFIKE
		1		i		LLRNCLSKKDGLREGGASPGSL
		1				RLAAPGPPLTLNAACPLRLAVL
	1			1		AAMAAAALPAWLSLQSRARTL RAFSTAVYSATPVPTPSLRVDD
		1				
		1				LHLTEIVGMLDSVLTPEDSSGK
1						YRFISGEVLCRITGCFTGVRVEA
1						KDLFGGCCSNPNEVMVTWIKVI
1		1				VEKEVWLYLRYILKALPPRTEK
i			l			MAVDQDWPSVYPVAAPFKPSA
		1				VPLPVRMGYPVK*GVPMAKEG
1		1				NLELLKIPNFLHLTPVAIKKHCE
						ALKDFCTEWPAALDSDEKCEK
l		1				HFPIEIDSTDYVSSGPSVRNPRA
		1				RVVVLRVKLSSLNLDDHAKKK
		1				LIKLVGERYCKTTDVLTIKTDR
		1				CPLRRQNYDYAVYLLTVLYHE
						SWE\TEEWGKK*D*SRHGKSIY
		1				GENSSSERKYPGERFSR*KLLR
						KNMGN*LKKSS/CGTKEIEEYK
		1_				KSVVSLKNEEENENSISQYKES
19029	49397	Α	19138	3	233	
19030	49398	Α	19139	1	256	
19031	49399	С	19140	5	114	mine was a series of the serie
19032	49400	Α	19141	8	444	TTDKEQ*EL*LLLDTE*GSYTKE
1		1			1	CHTDSLSRY*TSSTSAEDRDDSL
		1			1	LRRSGSYRDL*E*IPYSCRLDKD
		1			1	DSTDCIKLYEQILAE\NDKLKAQ
					1	LHDTNMELTDLKLQLEKATQR
						QERFADRSLLEMEKRERTALQR
		_				RISEMEERLQM
19033	49401	Α_	19142	1	287	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
19034	49402	Α	19143	211	346	
19035	49403	Λ	19144	175	3381	EDPAAGEGMKMADAKHKRNE
						QLKRWIGSETDLEPPVVKRQKT
						KVKFDDGAVFLAACSSGDTDE
		1				VLKLLHRGADINYANVDG/LSH
		1				ALHQACIDDNVDMAKLLVDNG
		l				ANINQPVNDGWIPLHAAPSCGY
		1				LDIAEFLNGQGAHVGAVNSEG
		1				DTPLDIAEEEAMEELLQNEVNR
		1				QGVDIEAARKEEERIMLRDARQ
		1				WLNSGHINDVRHAKSGGTALH
		1				VAAAKGYTEVLKLLIQAG\YDV
						NIKDYDGWTPLHA\AAH\W
19036	49404	Α	19145	1	2406	
19037	49405	Α	19146	1154	1365	
19038	49406	Α	19147	I	293	MGVSVLDFSHSDKCEVASRFAS
		1				GMPEPTNIVLPKLEVADTLGGC
						TTIPESDLEERSVEQDSTELFTN
						HRHLTAETPR/PW*RLDGLHKQ
10000	40.40	١.	10110		1000	VSPLQGVSE
19039	49407	Α	19148	3	1290	VSQATDVEVGTDLVPSVTVKV TLONRVILQKAKLSVYVOPPLE
						LTCDOFTFEFMNRNPDGIPRVIO
						CKFRLPLKLICLPGOPSKTASHK
						ITIDTNKSPVSLLSLFPGFASOSD
						DDQVNVMGFHFLGGARITVLA
		1				SKTSQRYRIQSEQFEDLWLITNE
						LILRLOEYFEKOGVKDFACSFS
						GSIPLQEYFELIDHHFELRINGE
		1				KLEELLSERAVQFRAIQRRLLA
		i				RFKDKTPAPLOHLDTLLDGTYK
						QVIALADAVEENOGNLFOSFTR
						LKSATHLVILLIALWOKLSADO
						VAILEAAFLPLOEDTOELGWEE
		1				TVDAAISHLLKTCLSKSSKEQA
		1				LNLNSQLNIPKDTSQLKKHITLL
		1				CDRLSKGGRLCLSTDAAAPQT
						MVMPGGCTTIP\ESDL*ERSVEQ
		1		İ	1	DSTELFTNHRHLTVETPRPEVSP
19040	49408	Α	19149	48	642	WNSALREPRLNGADMAKSKN
		ı				HTTNNQ\SRKWP\RNGIKKP\RSP
		1	1	-		KIRILLKGVAPPSFL\RNM\RFAQ
				1		ESPNKKGP*RRLQANKLPRAMS
	1	l		1		ATLPRAIKA\LVKPQGGLSPKIP\
		l		l		KGVSSRKLDSTCLTFAQPQALG
		l	l	l		SVARCP*LPRGPRL\CPPKAKAK
			1	l		AKAKPRPKPRPRAKDQNQGPG
				i		LQPQASVPAQ\APKRTQAP\TKA
						SE

SEQ ID	SEQ ID NO: of peptide	Met	SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
NO:	scquence	nou	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide
				sequence		
19041	49409	Α	19150	1953	2447	WTPQYMDTEYKNGPWMMEK
		1				KVWLDP/NETNEIPNANFRQQIR
		l				KLIKDGLILRHRKPVTVHSRAQ
		1				CWKSTLARRKGRHLGIESKKID
		1				RHMYHSLYLKLKGNVFKHKRI
	i	l				LTEHSHKLKADKARKKPLADQ
	1	l				AEARGSKTKEARKLREEHLQT
19042	49410	A	19151	1	693	KKEEIIKTLSQEEKAKK MAVMEKLYWVNREESYASLR
19042	49410	l^	19151	11	693	VHLPICNATTMSMLSLOKRLAS
	1					SVLRCGKKKVWLDPKETSEIAN
	1	l		l		ANSHOWIRKLIKDGLIIHKPVTV
		l				HS/*ARYR/KNTLACOKGRHMG
	1	l				I*KATANARMPEKIMWMR/RM
	1	İ				RILCOLLRRYCDSKKIDHHMYH
	1	l				RRYHESKKVDRHMYHSLYLKV
1	1	l				KGNVFKNKRILMEHIHNLKAD
		l				KACKKLLADOAETRRSKIKEAR
		1				KHREEHLQAKKEEIIKTLV
19043	49411	Α	19152	34	280	EVIHAAIGEKKGSY/NA**PWVE
		l				EQLTRQPLIHHQPASLHSVY/RC
		l	l			RYHSLYLKVKGNVFKNKRILM
						EHIHKLKADKARKKLLA
19044	49412	Α	19153	2	625	HEAMSMLRLQKRLASSVLRCG
		l				KKKVWLDPNETNEIANANSRQ
		ł				QIRKLIKDGLIIRKP\VTVHSRLR
		1				CRKNT\LAR\*KGRHMGIGKRK
		l	İ			VPANA\RMP\EKVT\WMRENEG
		l			1	FCRRLASEDTRES\KKIDRPHVV
		ŀ				TALYL\EVKGNVFKNKRIL\ME HIHKLKA\DKARKKL\LAD\OAE
		l				ARRSKTKEATKRREERLP/ARPR
		l				KREII*TLSKEEETKK
19045	49413	С	19154	154	291	RREIT TESKELLTRK
19046	49414	Ā	19155	3	253	
19047	49415	A	19156	2	474	FKDKQNKPTGFALGSIEGRVAL
		l				HYINPPNP*V*LCQLADFTGLFL
		1		l		TKEDLHEPLSFSAKDNFTFKCH
	1	l		l		RSNGTNTSAPQDIYAVNGIAFH
						PVHGTLATVGSDGRFSFWDKD
		l				ARTKLKTSEQLDQPISACCFNH
l	1	l				NGNIF/AYASSYDWSKGHEFYN
l	1	1		l		PQKKK

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first		*-Stop codon, /-possible nucleotide
İ	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
19048	49416	Α	19157	97	1728	IRGFFRGSQGSFYRRLKEASGS
						WDFCPRSWPSSLRARSGSQTPE
					1	TLLLPAGVFRRSETPMFKMSLF
		l				GTTSRFGTSGTIMFGSAT\TDNH
						NPIEGY*K*HSFSLMDSIG\CSCL
		l				FSPPTLPGNFLIAGSW\ANDVRC
						W\EVQD\$GQTIPKAQQMHTGP
						VL\DVCWE/SDGGSKVFT\ASCG
						\KTAKMW\DLRQ*PRRLQIAQH\
				l		DAPV\KTIHWIKAPNYSCVMTG
					l	SWDKTLKFWDTRSSNPMMVL
						QLP\ERCYCADVIYPMAVVATA
				ĺ		\ERGLIVLIQL/ERIQPSEFRRIESP
						L\KHQH\RCVAIF\KDKQNKPTG
						F\ALESIQGRVAIHYINPPNPA\K
		l		l	ł	DTFTFK\CHRSNGTNTSAPQ\DI
1						YAVNGI\AF\HPVHGHPCNCGD
		l				LDGRFSF\WDI\DARTKLKNFRE
						QLDQP/LSSAC\CFNH\NGKHILP
l						YAS\SYDWVKGDH\EFYNP\QK
						KKFTFFPA*MQAEELKAPGNKE
				Į.		VVAGRTLGSAQSLFLLHSGLIS
				1		VRIWAPNLVGVVSPWTMEFQP
		l				PGENDVIVQQLESPRRPAGDLP
		l	1			VFSIPTGLVAEVFSGKPKGGLK
19049	49417	Α	19158	1	1254	
19050	49418	Α	19159	1	921	
19051	49419	Α	19160	1	1386	
19052	49420	Α	19161	49	731	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last eodon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19053	49421	A	19162	61	1533	PLKAKMGKEKTHINIVVIGHV DSGKSTTTGHLIYKCGGIDKRTI EKFEKEAAEMGKDSFKIFAWV LDKLKAERERGITIDISLWFFET SKYYYTIIDAPGHRDFIKNMITG VISQADCAVLIWAAGVGEFEAG ISKNGQTREHALLAYTLGIVE QLIVGVNKMDSTEPPYSQKRY EEMWLREVSTFIKKIWLQPPTQ HFVPISWFGIGDIMMLEFSAN MPWFKGWKYTFKDGNASGIT LLEALDCILPPTRPTDKPLRLIPL QGVHKLGGIGTNYSSAPMETNGF SNPGMYVTFAPYSSTYTTESKIL SKMHPYSFEVKLIPGDQCGPSM SKNYFCQGMFRRGKRLLGDQQ KMTPPNGKAAGLHWSRVIILW HFRPK*GAGPMPLYLDC:HTGS HLHAKFAELKEKIDRR:GGKKL EDGLKFLKSSGDAAIVDIYPGIPM CVESFSDYPPLGRFAVRDMR QTVAVGVJSKAVDKKGCWEL GKVTKVWPRKAPEG
19054	49423	A	19164	433	1015	EFOTRAKKEAPAPP*SLKPKRK AFKGPRKAVLKGVHISHQKEE DPARSPTFPGGPKTLRLRRQPK YPRKSRVPGETRLDHLCLSIND* PLTH*VLPMKKIEDNNTLVFV DVKANKHQIKQAVKKLLYDID VAKVNTTLWIRPDGEKKAYYR LAPDLPIAFGMFANKIWGFI GLISNLDMASRGAS**PTGPDTG NKICQFKLSTSGESPAVCKSSLV LRFVKQGPHEFQESTIGAAFLT QTVCLIDDTTEKFEIWDTAGQE RYHSLAPMYYRGAQA\AIVVY DITNEESFARAKNWVKELQRQ ASPNIVIALSGNKADLANKRAV DFQLEAQSYADDNSLLFMETSA NTSMNVNEIFMAIGKNISF
19056	49424	В	19165	1	2511	
19057	49425	Α	19166	2	360	L

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19058	49426	A	19167	125	211	FRPGSPRQPRAQPISAPDCTRA MVGRRAL\IVL\AHSERTSFNYA MKEAAAAA\LKKKGWEVVE\S
						DLYAMNF\NPIIS\RKDIT\GKLE GPLRTFQYPGRSLFLAYK\EGHL EP/EIICGLNKKKLEAADLV\IFQ
						FPLAVGLEVPAIL\KGWFEPSVH KESFA*HFTAGHVMDKGPFPG VKKAVAFPFTTGG\SGS\MYSC
						QGI\HG\DMNVILWP\IQSG\ILPF LGLPKSLDPQLT\YSIWPPLPAR RPEFSILE\GWKK\RLE\NIWDET\
						PLYFAP\SSLFDLNFQAGF\LMK KEVQDEEENKKF\GLSVG\H\HL GKSIPTD\NOIOS*KRECTVHYT
						RDSHKVAAGAAQLTESLVPAR VAPATTSPANQRPGLHQSHGR
19059	49427	Α	19168	2	331	WVDSQQK\RYVPVKGDHVIGIV TAKSGDIFKVDVGGSEPASLSY LSFEGATKRNRPNVQVGDLIYG
19060	49428	A	19169	145	350	QFVVANKDMEPEMVCIDSCGR ANGMGVIGQDGLLFKVTLGLIR OEFHLSSEPSIRLGRSLYHIHHI.
19000	47420	^	15109	143	330	FASKKVLD*QWLDQSL*VCSW EHMRRSQ*GIFSRLANRGFQNG DC

SEQ ID NO:	of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codnn for peptide scquence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19061	49429	A	19170	1	1863	MAVAIRLSADTQWEDSPGKSIL ELHMSCTKIPERCEADKESTS SWCTRKIRFRMDLEKECKVYLLS GGGSRMGSOKGDGYGR WSSS WCGLSSCHILAPPTOFEHIAPL SKARQHLLVSVSVLFCFSAPLD VQPLKVLDECQNORACHLLVN SWFVGPDLCGSSKYLLVSFKC QPKQMFTQQGGPVLSIGETGV STSSYTRSSSPYGPDHICEFHTN MCKIPDELKNKTVCEDQELKL HCHESKFLNIYSATYGRRTQER APVSSIANPVKGCFHLGKKQDC LSYSALQVLSSRCYGKQRCKII VNNHHFGSPCLPGVKKYLTVT YACATLSSMGPILAEVPPETAK VTLSTSLDSSSGRMEDGRLDTG HTEVPVTSGLFIRVLNKQNIS LGNCSSFGFGKLSHCWAGA AIALGTEYILVKGDQVTGIVTA KSGDIFRVDVGSEPVSLSYLL SGDIFRVDVGSEPVSLSYLS FEGATKRNRONGVGSGEVSLSYLS FEGATKRNRONGVGSGEVSLSYLS FEGATKRNRONGVGSGLIFVLTLGLN°G GMGVIGGDGLLFKVTLGLN°E SLLASQICEFISIGEVGKLLUPLEI SLLASQICEFISIGEVGKLLUPLEI SLASQICEFISIGEVGKLLUPLEI SLASQICEFISIGEVGKLLUPLEI SLASQICEFISIGEVGKLLUPLEI SLASQICEFISIGEVGKLLUPLEI SLASQICEFISIGEVGKLLUPLEI SLASQICEFISIGEVGKLLUPLEI SLASQICEFISIGEVGKLLUPLEI SLASQICEFISIGEVGKLLUPLEI SLASQICEFISIGEVGKLLUPLEI SLASQICEFISIGEVGCKLLUPLEI SLASQICEFISIGEVGGOKTHPSOTLL
						LA\NIL\EACEHMT\SDORKTDLP
19062	49430	В	19171	29	82	
19063	49431	A	19172	1	427	

SEQ ID	SEO ID NO	Mar	SEQ ID NO:	Nuelcotido	Nucleotide location of loca	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
NO:	sequence	nou	09/540.217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	sequence		057.540,217	sequence	or pepulae sequence	deretion, v-possible nucleotide insertion)
		1				
19064	49432	Α	19173	1	1548	MTMAAAAVVARGAGARAATA
		İ				AALRGGCGTAARGRPCAGPAR
į.						PLCTAPGTAPDMKRYLWERYR
l						EAKRSTEGTKKYTTSLNARHY
	1					YTHFTEENEDEINSSSSYASQKK
	1			ŀ		TFEINPRHPLIRDMLRRIKEDED
İ				l		DKTVLDLAVVLFETATLRSGYL
						LPDTKAYGDRIERMLRLSLNID
1						PDAKVEEEPEEPEETAEDTTE
1				ł		DTEPDEDEEMDVGTDEEEETG
						KESDDPMAYIHFTAEGEVTFKS
						ILFVPTSAPRGLFDEYGSKKSDY
						IKLYVRRVFITDDFHDMMPKYL
l	1	ļ	1			NFVKGVVIRKKLVRKTLDMIK
l		ļ				KIADDKYNDTFWKEFGTNIKLO
						VIEDHSNRTRLAKLSRFQSSHH
		1				PTDITSLDQYVERMKEKQDKIY
	i	l	1			FMAGSSRKEAESSPFVERLLKK
		1				GYEVIYLTEPVDEYCIQALPEFD
1		1				GKRFQNVAKEGVKFDESEKTK
		1				ESREAVEKEFEPLLNW\MKDKA
1	1	1				LKDKI*K/ALWVSSAALTESPVL
		ı				LLVAQPVRDWS\GQHWERIMK
		1			İ	AQAYQTGKDISTN\YYA
19065	49433	Λ	19174	37	266	WADRAAGGVRILTQGCVGGG
		1	1			GSCDRRGLETSPARTPVRALWY
		1				LG\LCCVLLTFGSV/READDEVD
1		1				VDGT\VEEDLG*KYEKDQVTDD
1						EVVQREEEAI\QLDGLNASQIRE
1		1				LIREKSENFPFIQAEVNRMIETLE
		1				IOFHCIKNKEIFLERLISNSSC\AL
						DRLSLISLTIDENALSGNEELTV
	i					KVIKCDKEKNLLHVQHTGVGM
	i	l	1			T/REELVKN/LGTIA/KSGTKRVF
						*TKRPEA\QEDGPSQPS*IDWPS
		_				LGVRF
19066	49434	Α	19175	233	664	RAPEQSSGVSAAEQERVPNAG
1	1	1				WPCSVAPTCPSPRSAEPARCT*
		l				GKEEGG/CEDSDRADSGSPFQE
1	1	l				PRYPSSGPFPIPQASFPCPCLLVL
1		1				GIRGHSTILQYRGQEHHVLFTG
1	1	1				RCLLVDPTLLVLVVSKKSPNAA
1	1	1		I		RDOPARYPRGPL
						r

SEO ID	SEQ ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop eodon, /=possible nueleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				scquence		
19067	49435	A	19176	1	672	MAEAGPKPQRTLMWAWESVL
					\	SORKPREAGRLSEGCVKATGTF
						GFGWQARPDQKEHRLDGRVID
		ļ.				PKDRHGLVKDTEPRLNEQSLCC
		Į.				GLNPEATEEKIREYLASLGRRR
						PVKKVLEKKFHTVSGS/KCGPQ
		l				VPPSWSETYRTRA*SGDQLGTP
						AAPNPRWPME*EQEIEAQRRSA
						HSGARAPWPPWPPRPDGPPGNI
						GPKFMVSLSCWNISSLRAGLLY
		1				AGCGCSP
19068	49436	Α	19177	3	684	RHASARKKYNPPSWFHRGLPPF
						EDQEDEMSVSEELE\PITLTPSSA
		1		1		LKPSDRMTMSSLGERACCRDY
1						QRLGLGTLSSSLSRAKSEPFRIS
						PVNRMYAICRSYPGLLIVPQSV
						QDNALQRVSRCYRQNRFPVVC
ĺ		1				WRSGRSKAVLLRSGGLHGKGV
	1					VGLFKAQNAPSPGQSQADSSSL
						EQEKYLQAVVSSMPRYADASG
ļ						RNTLSGFSSAHMGSHGKWGSV
}						RTSGRSSGLG
19069	49437	Α	19178	1	341	
19070	49438	Α	19179	1	3710	MVSGARAAAAAAAAAAAER
ĺ						TRGVPGHPDSTGRLPAHQQLQ
	1					RGLLFRQLGITNVLSLVCATLM
						EHEVLFLSRSYQQLTDACRSLL
						ALLFPLRYSFTYVPILPAQLLEA
1						LSTPTPFIIGVNAAFQAETQELL
l	1			ļ		DVIVADLDGETVTIPECVHIPPL
	1					LEPLQSQTHSVLRMVLDPELEL
				1		VDLAFPPPM/HDKELRLFHQLL
	1					QGYLWCLHV\VCIHPEPVIRFH
						KAAFLGQCGLVEDNFLMNVLE
		_				GMAFALFVLECGVP
19071	49439	A	19180	1	303	
19072	49440	Α	19181	14	942	TKLTGSRG*LA*NPCM/HNNCE
	1			1		SCVDLLFVRGAGNCPECGTPLR
	ŀ			l		KSNFRVQLFEDPTVDKEVEIRK
						KVLKIYNKREEDFPSLREYNDF
				İ		LEEVEEIVFNLTNNVDLDNTKK
						KMEIYQKENKDVIQKNKLKLT
					1	REQEELEEALEVERQENEQRRL
	1	1	1		1	FIQKEEQLQQILKRKNKQAFLD
l	1	1	1		1	ELESSDLPVALLLAQHKDRSTQ
					1	LEMQLEKPKPVKPVTFSTGIKM
l		1	1		1	SVGITLCPAEEHTFNDERSFNLS
		1			1	SSWSKFNKPPSTLPFKVLDEER
l	1	1	1		1	LVELKVPNTLITKLVPFAISPCS
						EAIQDHPAILLAYKKTPFWRLQ
19073	49441	В	19182	49	456	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540.217	Nucleotide location of first codon for peptide	Nucleotide location of last codon for last amino acid of neptide sequence	Amino acid sequence ( X=Unknown,  *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				sequence		, ,
19074	49442	В	19183	53	333	
19075	49443	Ä	19184	2	208	VYPELQITNVVEANQPVTIQNW
	1	1				CKRGRKQCKTIPHL*FPYRCLG
						EPAGRGAGVDWGPGLEGRKRC CSC
19076	49444	В	19185	51	300	
19077	49445	В	19186	148	3568	
19078	49446	A	19187	1	3411	
19079	49447	Α	19188	2	2416	NSRGAACAGPRETAAVAARAE
		1				QGRGGSHSHSSALGAPRRVAM
	ł	1				LPGLALLLLAAWTARALEVPT
	l					DGNAGLLAEPQIAMFCGRLNM
						HMNVQNGKWDSDPSGTKTCID
		l				TKEGILQYCQEVYPELQITNVV
	į	1		İ		EANQPVTIQNWCKRGRKQCKT
				l		HPHFVIP\YRCLVGEFVSDALLV
						PDKCKFLHQERMDVCETHLHW
		1				HTVAKETCSEKSTNLHDYGML
	1					LPCGIDKFRGVEFVCCPLAEES
		1				DNVDSADAEE\DDSDVWW\AG
						ADTDYADGSEDKVVEVAEEEE
		ı				VAEVEEEEAD*LTRTDEDG\DE
						VEEEA\EEPYQEATERTT\SIATT
						TTTTTESVEEVVREVCSEQAET
		İ				GAVPSNDLPLVL*CD*REVCPIL
						LRRMWRQPEQL*HRRVLHGRV
						WQRJ\PTTAASTPDA\VDKYLET
					\	PGDENEHAHFQKAKERLEAKH
	i					RERMSQV\MREWEEAE\RQAK
	1					NLPKADKKAVIQHFQ\EKVESL
						*QEAANE\RQQLVETHMARVE
	1					AMLNDRRRLALENYITALQAV
	Į.	1				PPRPRHVFNMLKKYVRAEQKD
	1					RQHTLKHFEHVRMVDPKKAAQ
						IRSQVMTHLRVIYERMNQSLSL
	1			I		LYNVPAVAEEIQDEVDELLQKE
						QNYSDDVLANMISEPRISYGND
		1				ALMPSLTETKTTVELLPVNGEF
	1			I		SLDDLQPWHSFGADSVPANTE
	I					NEVE\PVDARPAADRGLTTRPG

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
19080	49448	A	19189	1	2355	I MKSIFTSEISSVLIFVNPEPGRVV
1,,000	17740	^	17107	ľ	2555	SFLGSGRREHAEERARGPRETA
		1		l		AVAARAEOGRGGSHSHSSALG
		1		į.		APRRVAMLPGLALLLLAAWTV
						WAL\EVPTDGNAGLLAEPQIAM
1		l				FCGRLNMHMNVQNVKWDSDP
		ı				S\GTKTCIDTKEGILQYCQEVYP
						ELQITNVVEANQPVTIQNWCKR
	1					GRK\QCKTHPHFVIPYRCLVGE
						VSDALL\VPDKCKFLHOERMGC
						FAETHLHWHT\AAKETLQ*RRS
ŀ		1				
		1				TNLHDYGMLLPCGIDKLRGVEF VCCPLAEESDNVDSADAEEDDS
						DVWWGGADTDYADGSEDKVV
		l				
		1				EVAEEEEVAEVEEEEADDDED DEDGDEVEEEAKEPYEEATERT
		1				TSIATTTTTTTESVEEVVRVPTT
				l		
		l				AASTPDAVDKYLETPGDENEH
		l				AHFQKAKERLEAKHRERMSQV
						MREWEEAERQAKN\LPKADKK
		1				AVF\QHFP\EKVESLEQEAANER
		1		İ		QQLVETHMARVEAMLNDPRRL
		l				ALE\NYI\TALQAV\PPRPRHVF\
				ĺ		NMLKKYVRARTEGLVSTSL*HF
						EHVR\MVDPKKAAQIRSQVM\T
		1		ł		HLRVIYERMNQSLS\LLYNVPA
		1				VAEEIQDEVDELLQKDANYS**
		l				RLWPTMISEPRI\SYG\NDAL\MP
						SLTETKTTRGSSVPVNEE\FSLD\
		1				DLEPVHFFWWLTSVPANTENE
		1				VE\PVDARPAADRGLTTR\PGSG
		_				LTNIKTEEISE\VKMDAEFRHDS
19081	49449	A	19190	103	463	PLLYAMSTGKRWLSFGSMIPPV
		l				AICASNKRIPWPFSMSSLFMAW
						NKEMMFPVSGSLYPVTARSAD
						RSFSLNSMPTRPLL*ASSTGNLK
						LLTGSTIKPVAAWASSNSRAVP
		_				GRTKPIFMAS
19082	49450 49451	A	19191	3	182 437	MANUA CICOCCCI CA DIALTOA
19083	49451	Ι^	19192	3	437	MVHAEISDEGFFLSAPIALTQA
		1				WLNIPKT\RRTFCK\KCGKHQPH
		1				K\VTQYKKGKDS\LYAQGKRRY
		ı			1	DRKQSGYGGQN*KPIFRKKAKT
		l		1		TKKIVLKALSALSPTCRSKSKC
		1		I		WLFKR\CKHF*TGEEIRKRKGQ
10004	10.152	L_	10102	241	401	VDPVLKCHLLFMEGH
19084	49452	С	19193	341	421	L

SEQ ID			SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
19085	49453	A	19194	15	1066	VLACTVEASVIGGQKREMNMO
		1				SIVREGFMEEAGPRIGFNLSFFI
	1	ı				QSTVTGSSSVGSTQLQPLSLPP/
		l				TAGQEPRGTGPLGSHNSCPAPE
	1	l				PVSYGRLNDPPATTHPGSFTRF
	1	l				HSKPLTSSCWDSEMEGCVSNL
		l			1	MVCNLASFLNVSTNPCAFFPW
		l				YFYYLLLL*AGWSPLHIAASAC
		1			1	RDEIVKALLGKGGVLNVYTNT
		l				DRFLHCFLLSSPSFQIAVMLLEG
		1			1	GANPDAKDHYEATAMHRAAA
		1				KGNLLARNPNHYIELVVINWSI
		1				VVPDFRHLACDEERVEEAKLL
	1					VSQGASIYIENKEEKTPLQV\AK
		l			1	GGLGF*YSREWVGRFKQLGFIL
		l				YFVLLCLLSPVSYKLMYLCTRI
19086	49454	Α	19195	1597	1923	
19087	49455	Α	19196	551	747	
19088	49456	Α	19197	1059	1296	
19089	49457	В	19198	1	1281	
19090	49458	Α	19199	3	565	LPGRLLLLNFRQRRQIDRPSMN
		l				DTRNLSRT\RKFHAPTRPTSEEN
		1				KWVIDVLSPAGRPTVP*DQKFF
		l				EK\LA\KMYQAPHPDV\ILVFGF
		l				RT\HFGGGKTTGFG\MIYDSPW
	i	1				MQRKNEP\KHRLAR\HGLYEKK
				l		KDLKKATEKERQEPELKKVQG
	1	1		I	1	GLAKGPLLGAGQKEEMKCLAV
						ELEIGSQPKELKVLQ
19091	49459	Α	19200	2	476	

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
19092	49460	A	19201	i	2448	MRGSILKECGSKERASQVDLEY
17072	17700	l^	17201	1	1-110	SRGNTASFAMCFHDRARIMKG
						SORSRKLTGGEGREEGERVENK
			1			DFLDLHGQIQVRLVVKTASLLS
					i	RVTYIAEVEGRETDAGWRNEL
						OVGRLDSGPDILVVSISTDHTLV
						DTHLEAVGGHSHEFPYFKNHL
						ACHVESELQRDRNGHRDAGWR
						NMRHGITDKEMQDSQGSSDNH
		1			1	VLGSLRSWSARAAPALPGLPEE
						AFVEMSTEGGFGGTSRSDAQQS
						LKSFWLRPRFFITELTLRAWIHT
						EDNNCRTYVAMAITKFDQLDF
		ł				LIDIVLRDELKPPKCQEEVLQSV
						TPAEPVQYYFTLAQQPTA\VQV
						QGQQQGQTTASSMTTMQPGQII
l		1			ļ	IAQLQQGQTTPVTTQVGEGQQ
		ŀ				VQIVQAQPQGQAQ*AQSGTGW
						TVQGQIQTLATSAQPITQTEVQ
		1				QRQQ*FSQFTDGQQLYQIQQVS
		1				IPAGQ\DLAQ\PMFIQSANQPSD
						GQAPRSHEVIAAAPAARRERER
						ELAGRGPFCPPPAGNVRALKSR
		1				RCLPGERRERARKKKPEGGAA
		1				ASERGETDSHPGASGQGPRDSG
						RVPLGMWSRRGLGVSRAPLHL
		İ				LLGVSTSFPLPLTPLIPTTAVVN
		1				PLKPLKNRIKAPHRRMPLVPGG
						SONLGTVRARISTROSHAEPST
						DNERVLSMTQDIHSIFLNLKNIT
		İ				WICTLOSCGFLLSNLCKDIVHK
						AGSGEARTRWSPRAQAGTHED
19093	49461	С	19202	124	369	
19094	49462	В	19203	739	870	
19095	49463	С	19204	787	969	
19096	49464	A	19205	101	331	
19097	49465	A	19206	137	415	
19098	49466	A	19207	86	221	
19099 19100	49467	A	19208	120	1347 899	FGARGNLKKAYSTRSKMAELN
19100	49408	<u>۱</u> ^	19209	120	099	THVNVKEKIYAVRSVVPNKSN
						NEIVLVLQQFDFNVDKAVQAF
						VDGSAIQVLKEWNMTGKKKN
		1				NKRKRSKSKQHQGNK\DAKDK
						VERPD\ACPLQPQPPQIQNGPM
			ŀ	1		NGCEKDSSSTDSANEKPALIPRE
						KKISILEEPSKALRGVTGPNIEK
	l	1		1		SAKDLQRCTVSLTRYRVMIKEE
	1	1		l		VDSSVKKITAAFAELHNCIIDKE
	1	1		I		ASLMAEMDKGIEEAMEILTAR
	1	1	l	I		Q\RKAEALKRLTDL\AS\QMAE

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /-possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
10101	140460	+-	10010	1011	2150	ADTKPERGVSSAVFASGSEGRE
19101	49469	Α	19210	211	2130	
				1		LGCVLLSSSETRLLSGTLLWIPF
						AYSTRSKMAELNTHVNVKEKI
						YAARSVVPNKSNNEIVLVLQQI
				1		DFNVDKAVQAFVDGSAIQVLK
				ı		EWNMTGNKKNYKRIRSKSKQI
		1	İ			QGNKDAKDKVERPEAGPLQPQ
		1				PPQIQNGPMNGCEKDSSTDS#
			1			n\ekpaliprekkisileepskal
			1			RG\VTEGNRLLQQKLSLGG\NP
			1	1		KPIHGTTERSDGLQWSAEQPCN
l						PSKPKAKTSPVKSNTPAAHLEI
						KPDEL\AKKRGPNIEKSS/VKDL
			l .			ORL/CTVFF*LEYRVMN*RERK
				i		WDSSGERRSKLPFAE\LHNCHE
						OKEV\SLMGRKWD*SLKEGRP
	1	1	i			WEILDWLVRKKSKKKLKRLTE
	1		i			LGQSRMAEMQLGPKLR\AEIKH
				1		FVSEAVNYDE\ELGKSCPGFSC
						DIEO\LK\AQIIALPGKITHPK\NN
						YFLKELPCSSLLPLLNAARSKE
		1				LGKTEVTFSRKSSTHNKPSEGK
						AANPKMVSSLPSTADPSHQT\M
		1	ļ			PANKONGSSNORRRFNPO\YHI
		1				
	ł					\NRLN\GPAKSQGSGNEAEPLGI
						G\NSRHGTQEGQPH/NRFGFRPI
				1		NKGRCQKIQEASLGIEGPPRAP
				1		AHFLKRPRAKGSHAADTFGRA
						RAFSGVS/GSVRGSQCNLFPT\R
		_				EVSTDAAVLSVPGCDRWVA
19102	49470	A	19211	93	180	
19103	49471	A	19212	3	39 888	
19104	49472	В	19213	1		COL COOL IDION (FTOCH CVCIV
19105	49473	Α	19214	863	1509	GCAGPCLVNQMFTSSILCKSHC
		1				HSLVSINQGHNAPWKAAG\PLF
						LKAGYC\QSFSPCDSLKYG\SWI
		1				EKDLTVPQPDTRKASVLRWISC
						RGKPLAVDMEEG\HCL\CLPPG
						N*NVLGCKTPIVHLFNSELGRK
l	1	1				AALWREARHVG\SNAALLFFTF
l	1	1				LRCLGGEKHKSGLHAHPGIVP\
l	1	1	100			LELNYDIDSFAHVFVFVVAVEL
		L		L		PLIITLLPYCIPLCCNNEK
19106	49474	С	19215	289	510	
19107	49475	В	19216	534	1686	
19108	49476	В	19217	1	1062	
19109	49477	В	19218	1	1878	
19110	49478	В	19219	1	747	
19111	49479	В	19220	230	786	
19112	49480	В	19221	67	6011	
19113	49481	В	19222	1	3455	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19114	49482	В	19223	1	4763	
19115	49483	В	19224	65	4534	
19116	49484	В	19225	512	4782	
19117	49485	В	19226	345	2194	
19118	49486	В	19227	267	7391	
19119	49487	Α	19228	578	739	
19120	49488	A	19229	419	1410	KOROARERHILPRIPQLSAVVTIE T-RR-RNFAELKIS/RIKKFA HKMLQKARRKLIYEKVKHCHK EYRQMYRTEIQMATMARKAG HKMLQKARRKLIYEKVKHCHK EYRQMYRTEIQMATMARKAG HKFYHPPKKLAFVIRISAISOVSP KWKNKQLCPLNHYFGLGMGD LRAFGLADGTOPSGGEITGMDD LRAFGLADGTOPSGGEITGMDD LRAFGLADGTOPSGGEITGMDD LRAFGLADGTOPSGGEITGMDD LRAFGLADGTOPSGGEITGMDD LRAFGLADGTOPSGEITGMDD LRAFGLADGTOPSGEITGMDD LRAFGLADGTOPSGEITGMDD LRAFGLADGTOPSGEITGMDD LRAFGLADGTOPSGEITGMDD LRAFGLADGTOPSGEITGMDD LRAFGLADGTOPSGEITGMDD RAFGLADGTOPSGEITGMD RAFGLADGTOPSGE
19121	49489	Α	19230	3	307	AGTMEGVEEKKKEVPAVPETL KKKRRNFAELKIKRLRKKFAQ KMLRKARRKLIYEKAKHYHKE YRQMYRTEIRMARMARKAGN FYVPAEPK\LAFVIRIRGI
19122	49490	A	19231	3	160	GRVLL*DKTSRGTIRQQQLLFT NICCSAASA/G*YPGKQGLEWT SSRLQQTCS
19123	49491	А	19232	303	570	GLCIRHVLVPSAAGLLEFAGGP LQTLFAWVSAAEAAEQQIWVN SKCC/CPDRSSGSFVSEEYLAV* GVGLTLSSASLMLGAVDWSCS HSA
19124	49492	A	19233	1	176	MQYVQQKPKLKFQVHICAYRK TVLQPPLLIPRQT/WVWSGPPA NSNRPAAGGADC*KEN

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19125	49493	А	19234	I	1977	MFAVLQAPLVIPRQT/WVWSGP PANSNRPAAEGPDC*KEN*RQT GSGVDLQQTPTDLQLRVLIVRR KTNEQKGHPHQNPICTSPSSKT
						KVDTTTNMGEKQSRKTENSKN QSASPPPNLKKKREKNQIDAIK
						NDKGDITTDPTEIQTTIREYYKH LYSNKLENLEEMGKFLDTYNLP
						GLNQEEVESLNRPITGSEIEVIIN SLPTKKSPGPDGFTAEFYORTK
						DKNHMIISIDEEKAFDKIQQPFM
						LKTLNKLGIDGTYLKIIRAIYDK PTANIILNGQKLEAFPLKAGTR
						QGCPLSPLLFNIVLEVLAREIRQ EKEIKGIQVGKEEVKLYLFADD
			]			MIVYLENPIISAQNLLKLISNFSK
						VSGYKINVQKSQAFLYTSNRQT ESQIMSELPVTIASKRIKYLGIQL
						TRGVKNLFKENYKPLLNKIKED TNKWKNIPCSWIGRINIMKMAI
						VPKVIYRFNAIPIKLPMTFFTEL
						EKTTLKCIWNQKRAHIVKSILS QKNKAGGIMLPDFKLYYKATV
						TKTAWYWYQNRHIDQWNRTE PSEIMPHIYSYLIFDKPDKTRNG
						ERIPYLIRWCWCWQNWLAICR KLKLDPFLTSYTKINSRWIKDL
						NVRPKTIKTLEENLGITIQDIGM
				:		GKDFMSKTPKAMATKAKIDK WDLIKLKSFCTAKETTIRVNRO
		Ļ				PTEWENISAIYSSDKGLISRIY
19126	49494	A	19235	206	456 385	NLCCSAASAGDTOANRVWSGT
19127	49493	A	19236	2	363	PTNSSRPEVSSGAMDGEGWGL
						PVDPLTPGHQDALPWQRCYHP CSSSSVPPRQACASPASCSSSAA
						W/TSASTGPWHSGCGSSCGSCC CWGSPSASVGVGAGAIRSRTV
19128	49496	В	19237	1	642	CWGSFSASVGVOAGAIRGRETV
19129	49497	Ā	19238	128	584	
19130	49498	A	19239	4054	4578	QSGPSAAGLLEFAGGPLQTLFA WVSAAEAAEQRILVNSRCCCLI VP\RKFCLRGVASHVRCQSAPY DVFCHGITLAKCWCSALGLPSL
						QSCEPNALFFINYPVCGI/TAPCC KVEGTMG\VGPKSPQL\SYNVL GSDNNGVLLGSMAIFTILILLIH
	L	L				EHGMFFHLFVSSFISLSSGL

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19131	49499	A	19240	I	948	MVLEKAREEVDPPSMLIPPVTQ CGQLPRSQCPQPTLSRMLTLEV GISLGIIVLMISLWPDTVKEYQS REALSFKKYNKNPGLLKFAGDP LOTLFA WVSPAEAAEOQISALC
						FLWKLRPRGAPTRCQPLLSYTR CLSAPAGSFVYTMRGKPPIQAS VMADASPPTKIEHPRTTSDCCV ASKNFKPVDLSLLCSMGVGSAE
						LDHWATWLQSPFQGSERFCLA GVPGTTGV*KETPAASSVSAQM AAQFCA*N/HRTLVV*APKGIL
	40.500		10241	171	1345	WVCGLRRPWEKRSICAGVHHS SWHSPSWLPLARGGSSSTPCTS WVRRCPTLHL YCPKEGTLDFNFAFNMTAVNV
19132	49500	A	19241	171	1343	ALIRDTKWLTLEVCREFQRGTC SRADADCKFAHPPRVCHVENG RVVACFDSLKSVTAVPFLFMAL GLSREPETVPASMVQTFSLGVG GGAGSV*PDENCKYLHPPFHLK TQLEINGRNNLIQQKTAAAMFA
						QQMQLMLQNAQMSSLGSFPMT PSIPANPPM'SFESLRYHILGMG LVPAELVPNTPVLIPGKPTSLQL PGSCLGPKLMAFQINWEVLPRN FQRGINC'SRGENDICRY'AHPTD ASMIEVASDNTVTICMGYIKGRR TVGVWGIKAKSSKQRILDTKGS
						HQGNSFVRGTDYLIPICTNMSK AKGTAFLKWMQKLVYNGSSG QCSPAFFCCAWKEHSEKAGRA SGAKCNRHRHTNPVFLMREGA IS
19133	49501	A	19242	61	544	KFNPIFVTSRPRARIRKRAFINAP SHIPKGRLLSFPPLSPKSLRPEG TNRADSHAPIPKRMIESSRLVR GHL*GSAKLAKVVPRFTRKY VIYIERIVQREKAINGTTVHIVGI HPSKQVVITKAKTGTKTRKKIP PNKKAQSRQVGKEKGIKYKER
19134	49502	Α	19243	652	1042	THEKMQE TPLSSCFLSREKATQLLFPAVVA VPMVLSAMGFTAAGIASSSIAA KMMSAAAIANGGGVASGSLVA TLQS/LG*VSWRGLPTVLPTELP RQACPTLSTLCFFPGATGLSGLT KFILGSIGSAIAAVIARFY
19135	49503	Α	19244	48	397	A IDOUGANA VIANT I

SEQ ID NO:	of peptide	Met hod	SEQ ID NO: in USSN	location of first	codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
19136	49504	Α	19245	42	296	GCVGVRPSLHPATSTASGSASP
						TLARAMASVSELACIYSALILH
						DDEVTVTEDKINA/APAEEKKV
						EAKKEESEESDDDMGFGLFD
19137	49505	Α	19246	172	519	LGPSFLHDDEVTVTEDKIQMPLI
						KAAGVNVEPFWPG/LCFAKAL
		l		İ		GKRSTLGSLILAMLGGPVGPGS
						QPAGCLQPAG\GSCPPSTCCWF
						QLEGEEKWEAKERKIPREF*LID
						MGFGLFD
19138	49506	Α	19247	3	175	
19139	49507	Α	19248	2	390	GWDWNCVWEPHHWLCQSL/N
						SVTQAGVQLCNLSSLQPLPLGF
						KQFSCLSLPSSWDYRNPSLKQQ
						LFSYAILGFALSEAMGLFCLMV
		1				AFLI\SLPCEGAVSTSHSSPASG
		_				WPRVFLFLYLPRQPGERGWLR
19140	49508	В	19249	139	13320	m in this country is an a sale
19141	49509	Α	19250	28	450	TNDFNLQNPGSCFPSACPAGVG
		l		1		SERLPVLGWFVGNRSFPPPPQST LSVLGKRLGRNGAIAAGVFGA
		1				LFIGYCIYFDRKRLK*POLKDAE
						AVQKFFLEEI*L\GEEILAKGVD
1						HLTNPSAFFG/OPNHFPLOMDSF
		1				GPFLRFQA
19142	49510	Α	19251	164	420	OITER QA
19143	49511	A	19252	1	329	STHTTYWEGCRTTSAGLLRKH
						EPGEEAF/FYHST\SKKPGIAGLI
		l			1	KVNVOFVRMMKRSIPWAELNP
		l				YHQAHKATGGPLKNMVLFTRQ
		ĺ		i		RLSIQPLTQEEFDFVLSLEEKEP
19144	49512	В	19253	39	368	
19145	49513	Λ	19254	1014	1290	
19146	49514	Α	19255	122	680	LARITRIVRTKVPCSVTMSRPRK
		l		l		RLAGTSGSDKGLSGKRTKTENS
		l		l		GEALAKVEDSNPQKTSATKNC
		1		l		LKNLSSHWLMKSEPESRLEKG
		1		l		VDVKFSIEDLTAQAKQTTCWD
		ĺ		l		GVRNYQAS/RNFLRAMKLGEE\
		l				AFFYP*QLAKKPGIAGLMKIVK
				l		EAYPDHTQF*EK\NPHYDPSSKE
I	1	1		I		DNPKWSMKSLILF

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=pnssible nucleotide insertion)
19147	49515	A	19256	2	1005	RISTSTLCPKPKKLIAPPGRAGIA ASMGLNEQKEFQKVAFDFAA REMAPNMAEWDQKDRKADGK GGAVTQEVQAQILIVKHGQKL VSRFQLSSFSVYDSVRTTQSKQ EHLQTDKGLSGKRTKTENSGE ALAKVEDSNPQKTSATKNCLK NLSSHWLMKSEPESRLEKGVD VKFSIEDLKVAQPQOTTCWEG VRNYQARNFLRAMKLGEIAF FYHSNCKIEFGIAGLMKIVKEA VYPDHTQFEKKQPPPI-PPSYQR GTTPKWPHGWWVQVWFGMM KRFHSPLAEULKSHHQAHKAIS GGPLIKNMVLFTRQRLSRQPLT VQEEFDPVUSLEEKEPS
19148	49516	A	19257	3	727	VRLOFLTPTLRAARTMAAPPOL ARALLVVVNALLRKRRYHAD VLKGFRNGAVYGAKIRGPSRR WVMTFLFREWAASREKLWAIL OATVHSWWILARFVPHLTRV FRCPAVPYITRARTYPAHAFPG AGLSFGGILVYGEKÇ+TENFOG NMYLLSTRPCLP*SRLAVRRK GLHP*NPRWDPFPVCLTAVVW GUVLWLFYHRSTLQPSLQSSM TYLYEDSNVWHDISDFLVYNK SRPSN
19149	49517	A	19258	1	849	MSGALDVILOMKEEDVIKEHA AGTHLGGTNLDFQMEQYIYKR KSDGIYINLKRTWEKFLLAAR AVVAIENPADVSVISSGNTGOR AVLKFAAATGATPIAGHTEPGT FTNQIQAAFREPRLLVYTDPRA DHOPLTESSYVNLPTIALCNTDS PLRYVDJICNNNGAHSDPEELE KEEQAAAEKAVTKEEFGGEWT PAPPEFTATOPEVADLSEGVQV PSVPIQQFPTDDWSTQPATENW SAAPTAQATEWKMQQSTILLE AESSSHQTTPNLPAPWSRTSQPPE

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
19150	49518	A	19259		1309	GNI.AAGKTIQAQDRDAVGILSS RTGESMENI.QKNILPKQRRRT REITFIMSGALDVLQMKEEDVL KFLAAIGTHI.GGTOFI.LSRGHG YFYKGKS/DGLSFIINPKRAREE! LLLPARQIVPHKTPSIDVSVISSG NTGQVCGTVRA/VCLKFAAAT GATHIAGRIFTPGTHFPRSKA AFIREPRILLVVT*PFGADPFALS. RSASYVNILPYHILRCGNTDSIOL. RYVDIAIPCNNKGAHSVGLMW WMLARGSFCAMBGTINSEHFW LEVMPDLYFYRDFEIEKEEQA AA*ERQVTKEEFQGEWTAPPA EVTATOPPEVADWSEGVQGAPL VPYSAIPPTEDWSSQPAMEDWS AAPTAQATEWCSRTSLRQNPSG LKKEGLYSARSISKTHVSKT ELJKEGGLYARSISKTHVSKT ELJKEGGLYARSISKTHVSKT
19151	49519	Α	19260		2495	AFTTRSTFSTNYIRSLGSVQAPS YGARPRQAARPASYAGAGGSG SRISVSRSTSPRGGMGSGGLAT GTSPGVMAGMGGGJCNEEETM QSLADRLASYLGQF*RSLEDR RTRKLGRAKFREHFGRKKOPQ VARDWSHYFKINEDLEGTEFFF KILVGQCPASVSARFDNAPSLL LD*F*FEKY*GQSWPMCPVLLE RUDIPLGSAKVIDDTNYHTDLQL LETEIRGSSRRELLFQ*RRNHEE: EVKGLQAQIASSGLTVEVDVDA KSQDLAKIMADIRAQYDUELA RKEPEKEA*TKYWSSADLREST TYCHPHKSA*GWKLAEDDASQ KLRRTNYQSLEDRFWTSMRKSE RPALENSP*GEVEAPLRPLQDW SSLGABICHLTRPPSWKIGEDFN AGRGQRPGPQGV*GPLLNHQG SSLGABICHLTRPPSWKIGEDFN LGDSSLDERNSMQTIQKTTTP G*YGLGKVS*STQLTFVLKAL KGSQLAKVS*STQLTFVLKAL KGSQLGKVVS*DQLTFKVLKAL KGSQLGKVVS*DQLTFKVLKAL KGQGAVVPFWGSRRPIKSFRVQ KKKKEKESF

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
19152	49520	A	19261	387	1125	CCRPCATPYALRSPLR*PACPPP
i		1			1	RWRPSSMPTSRPPVSPAASPTC
		1				GTCMLSP\CPPAEHLLHLPHAQP
						ODPALLOPCHPAPPLRPRALHA
		1				AHHVGWPAPHOPLLPPPVLCPC
		1				GGAGRGGG*RCPWRGPSSSSPG
		1				PTLIAGODPGAAOP*TWPO/PTL
		1			i	TSVSATASPKAP\LPLAAAVPGA
		l				PAEGCCPLLROALPAGOLPPGG
	ŀ	1				RRATSAVPPAVPGD/PPAQPTM
		1			İ	PGSMSCWALAPARPCPPGRCW
		1				AWRS
19153	49521	A	19262	3	1097	RGNSRLRYSHEDELQLPRLPEL
						FGNCROLLEEVEVAT\DPAGFR\
		1		1		IVQEK\VFKG\LDLLE\RAAEML\
		l				SOSTLEGRECREWKDLSPTHLIT
		1				FWGP\AFQGALTM\KQVNPSKR
					i	LRSFCSGAREHFI\NYLT\QCH\C
						YHVGQSFEL\PKT\MNNSAENH
	l			1		TANSSMAYPSLVAM\ASQRQA
						KIORYKOKKELEHRLSAMKSA
						VESGQADDERVRGYYLLHLQR
	1	1	İ			W\VDISLEEIESIDOEIKILRERDS
					i	SREASTSN\SSRQERPPVKPFHS
						HFGTWLHSQSTFGAGYSKGWP
		1		1		TYGR*VSWYE\QHRKLWSTYP
			ŀ			DQGNMPRAAPEGISEKAAQQQ
		l				EDOEEKEEEDDEPNNFHRARE
				1		W\DDWK\DTHP\RG\YGNRQNM
19154	49522	Α	19263	2	262	
19155	49523	Α	19264	3	1062	GRTAENPARAVSSPNFYAHRKT
		1	l			EVLFPCLTQPLARGPKKHLK\R
				1		VAAPKH\WMLDKLTRVFAPR\P
			ŀ			STG\PHKLR\ECLSRIIF\LRNRLK
		l				\YAL\TGDEVKKI\CMQR\FIK\ID
		1				GQGSELDINLPLLGFMGCPSAF
		ł				DKTGEENF\RLDLIDTQGVRFC
		1				WYIRI*PPWRKAKLQVWCQK*
		1				GKILCGPTKRESPSSGLTH*CPA
		1				PHPAYPPIPPHPR*NGYPIPD*I*E
		l				DLAKINLISIQSSEHW*TLCMGD
	1	l				LEGA*P*GRNWVLITPTERGHP
		l	i			GIFLTVGSR*KDANGQQAFGHF
		l				GLFQHFLVIGKGNKTHGISL\PR
		1				GKGIRLHHLLEERDKRLA\AKQ
			1	1		SOWGEMGSLGVDIVQIFWYRN
19156	49524	Α	19265	62	298	,

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			l	sequence		
19157	49525	A	19266	li .	555	MAWQMMQLLLLALVTAAGSA
17137	17525	ľ.	1,7200	1	1555	OPRSARARTDLLNVCMNAKHH
				İ		KTQPSPEDELYGQ/SP/WMCKG
		1			i	SCRKTKSWNI/HRKSKCEVGLA/
				1		WEACSVSAGTGRGPGCGRWV
			l	l		GAPOGP/CPRKCSSG*PTW/VOR
		1				SONMEEMAVVNOSWRKERILN
		l				VPLCKEDCERWWEDCRTSYTC
						KSNWHKGWNWTSAPSAVCDP
						LI.
19158	49526	Α	19267	216	974	MDMAWQMMQLLLLALVTAA
		-				GSAOPR\SARA\RTDLLNVCMN
			1			AKHHKTQPSPEDE\LYGQCSP\
						WKK\NACCTAS\TSQELHKDTS
						RLYNFNW\DHCG*KWNPTCK\R
						PLYPQDSCL\YECLTPTLGPW\IR
						QFNQSWRKERFLNV\PLCKEDC
						ERWWEDCRTSYTCKSNWHKG
				1		WNWTS\GINKGRPGAF*STFES
				l		YFPTPAALCEGLWSHSFKVSNY
				İ	i	SRGSGRCIQMWFDSAQGNPNE
						EVAKFYAAAMNAGAPSRGIIDS
19159	49527	Α	19268	345	2138	QRLTATSSWTTMAKNRRDRNS
						WGGFSEKTYEWSSEEEEPVKK
		l				AGPVQVLIVKDDHSFELDETAL
						NRILLSEAVRDKEVVAVSVAG
						AFRKGKSFLMDFMLRYMYNQE
				·		SVDWVGDYNEPLTGFSWRGGS
			1	•		ERETTGIQIWSEIFLINKPDGKK
						VAVLLMDTQGTFDSQSTLRDS
						ATVFALRHNDPASIQVYNLSQN
		1				VQ\EDDLQ\HLQLFT\EYGQDW
		1				AMGGKHFLEAIFRSLDYFFVRD
		1				WSFPYEFSYGADGGAKFLEKR
		1				LKVSGNQHEELQNVRKHIHSCF
		l				TNISCFLLPHPGLK\VATNPNFD
		1				GK\LKEIDDEFHQKL*KYLIPWA YFRSRGA*DI*RRSNGGLKI\T\C
						RGLVEYFKAYIKIYQGEELPHP
						KSMLQATAEANNLAAVATAK
		l				DTYNKKMEEICGGDKPFLAPN
		l				DLQTKHLAT*GRNLWKLFRGV
		1		1		KKMGGEEFSRRYLQQLESEIDE
		1		1		LY\TNISSHNDSK\NTFPCSSYPO
		1				PTLFCSHPLITYVIAGVTGFIGL
		1		l		DIIASLCNMIMGLTLITLCTWAY
	Í	1				IRYSGEYRELGAVIGPRWLOLC
		ı				GTREVQMRPWNKLYQCQQAT
		l				PTDILYPSKPFPLHPKVGNLTEQ
		1				IOKRKKMVMPKF
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